

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: April 2, 2004, 14:30:56 ; Search time 6 Seconds  
(without alignments)  
3.134 Million cell updates/sec

Title: us-10-006-191-19  
Perfect score: 1049  
Sequence: 1 ttgaactgattcacatctca.....gtgtatatatttttttataaa 1049

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 0.5

Searched: 501 seqs, 8964 residues

Total number of hits satisfying chosen parameters: 1002

Minimum DB seq length: 8  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 545 summaries

Database : rng.seq\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	34.4	3.3	40	1	AAQ34094
2	33.6	3.2	41	1	AAH77495
3	32	3.1	32	1	ABK66312
4	30.2	2.9	37	1	AAQ33710
5	25.2	2.4	30	1	AAZ98502
6	25	2.4	25	1	AAAI5467
7	23.4	2.2	25	1	AAI15468
8	23.4	2.2	27	1	AAI61970
9	23	2.2	24	1	AAH30425
10	23	2.2	24	1	AAH39074
11	22.2	2.1	27	1	AAQ34044
12	22.2	2.1	27	1	AAQ33678
13	22.2	2.1	27	1	AAQ33804
14	22.2	2.1	27	1	AAQ34181
15	22.2	2.1	27	1	AAQ34012
16	22.2	2.1	27	1	AAQ34143
17	22.2	2.1	27	1	AAH5733
18	22.2	2.1	27	1	AAH46005
19	22	2.1	22	1	AAH30426
20	21.8	2.1	25	1	AAQ33918
21	21.8	2.1	25	1	AAQ33642
22	21.8	2.1	25	1	AAQ33962
23	21.8	2.1	25	1	AAH5734
24	21.8	2.1	26	1	AAQ34083
25	21.8	2.1	26	1	AAQ33684
26	21.8	2.1	26	1	AAQ33704
27	21.8	2.1	26	1	AAQ33831
28	21.8	2.1	26	1	AAQ33837
29	21.8	2.1	27	1	AAQ33740
30	21.8	2.1	27	1	AAQ33951
31	21.8	2.1	27	1	AAH24300
32	21.8	2.1	27	1	AAH46017
33	21.8	2.1	27	1	AAH46001

C	34	21.8	2.1	27	1	AAH60473	Oligonucleotide cl
	35	21.4	2.0	23	1	AAQ33663	Microsatellite seq
	36	21.4	2.0	23	1	AAQ33773	Microsatellite seq
C	37	21.4	2.0	23	1	AAQ33885	Microsatellite seq
	38	21.4	2.0	23	1	AAH66105	Repeat sequence fo
	39	21.4	2.0	23	1	AAH39005	SNP specific upper
	40	21.4	2.0	24	1	AAQ33986	Microsatellite seq
	41	21.4	2.0	24	1	AAQ34158	Sequence of a micr
	42	21.4	2.0	24	1	AAQ33909	Microsatellite seq
	43	21.4	2.0	24	1	AAQ34065	Microsatellite seq
	44	21.4	2.0	24	1	AAQ34024	Microsatellite seq
C	45	21.4	2.0	24	1	AAQ33707	Microsatellite seq
	46	21.4	2.0	24	1	AAH66096	Repeat sequence fo
	47	21.4	2.0	24	1	AAH46015	Synthetic oligonuc
	48	21.4	2.0	24	1	AAH46016	Synthetic oligonuc
	49	21.4	2.0	24	1	AAH98862	Immunostimulatory
	50	21.4	2.0	24	1	ABH78584	Angiogenesis inhib
	51	21.4	2.0	24	1	ACH03377	Immunostimulatory
	52	21.4	2.0	24	1	ADH37364	Immunostimulatory
	53	21.4	2.0	25	1	AAH33861	Microsatellite seq
C	54	21.4	2.0	25	1	AAH40163	SNP specific SNPE
	55	21.4	2.0	25	1	AAH38303	SNP specific SNPE
	56	21.4	2.0	26	1	AAQ47179	MHC DR A intron bi
	57	21.2	2.0	26	1	AAQ44016	Target sequence #8
	58	21	2.0	21	1	AAQ33891	Microsatellite seq
	59	21	2.0	21	1	AAQ33879	Microsatellite seq
C	60	21	2.0	21	1	AAH65738	Repeat sequence fr
	61	21	2.0	21	1	AAH46013	Synthetic oligonuc
	62	21	2.0	21	1	AAH99702	Immunostimulatory
	63	21	2.0	21	1	ABH78423	Angiogenesis inhib
C	64	21	2.0	21	1	ABH77131	Human connective t
	65	21	2.0	21	1	ACH03241	Immunostimulatory
	66	21	2.0	21	1	ADH37204	Immunostimulatory
	67	21	2.0	22	1	AAQ33810	Microsatellite seq
	68	21	2.0	22	1	AAQ33675	Microsatellite seq
	69	21	2.0	22	1	AAQ34038	Microsatellite seq
	70	21	2.0	22	1	AAQ34080	Microsatellite seq
	71	21	2.0	22	1	AAQ33991	Microsatellite seq
C	72	21	2.0	22	1	AAH83952	Oligonucleotide cl
	73	21	2.0	22	1	AAH65727	Repeat sequence fr
C	74	21	2.0	22	1	AAH64448	SSR motif #8. Uni
	75	21	2.0	23	1	AAH60472	Oligonucleotide cl
C	76	21	2.0	25	1	AAH40155	SNP specific SNPE
	77	21	2.0	25	1	AAH40159	SNP specific SNPE
C	78	20.6	2.0	23	1	ADH69512	5' anchored (ISSR)
	79	20	1.9	20	1	AAQ34170	Sequence of a micr
	80	20	1.9	20	1	AAQ33816	Microsatellite seq
	81	20	1.9	20	1	AAQ33672	Microsatellite seq
C	82	20	1.9	20	1	AAH30427	Compound simple se
	83	20	1.9	20	1	AAH93829	Antitumoral phosph
	84	20	1.9	20	1	AAH06824	Oligonucleotide wh
	85	20	1.9	20	1	AAH39091	20-mer oligonucleo
	86	20	1.9	20	1	AAH13762	Simple sequence re
C	87	20	1.9	20	1	AAH13705	Simple sequence re
	88	20	1.9	20	1	AAH75569	Mrell related prob
C	89	20	1.9	20	1	AAH62932	Human PEPCK-cytoso
	90	20	1.9	20	1	AAH28355	DNA oligomer #5.
C	91	20	1.9	20	1	AAH48201	Antibody binding o
	92	20	1.9	20	1	AAH64445	SSR motif #5. Uni
C	93	20	1.9	20	1	AAH64449	SSR motif #9. Uni
	94	20	1.9	20	1	ABH87132	Human connective t
	95	20	1.9	20	1	AAH45125	Oligonucleotide sy
C	96	20	1.9	20	1	ABA96307	Oligonucleotide SE
	97	20	1.9	20	1	ABA96306	Oligonucleotide (C
C	98	20	1.9	20	1	ABH24438	Oligonucleotide (T
	99	20	1.9	20	1	ABH24439	Human connective t
C	100	20	1.9	20	1	ABH25647	Human connective t
	101	20	1.9	20	1	ABH25669	Human connective t
C	102	20	1.9	20	1	ABH25654	Human connective t
	103	20	1.9	20	1	ABH25649	Human connective t
C	104	20	1.9	20	1	ABH25648	Human connective t
	105	20	1.9	20	1	ABH25653	Human connective t
C	106	20	1.9	20	1	ABH25656	Human connective t

C 107	20	1.9	20	1	ADB25671	Human connective t
C 108	20	1.9	20	1	ADB25666	Human connective t
C 109	20	1.9	20	1	ADB25702	Human connective t
C 110	20	1.9	20	1	ADB25652	Human connective t
C 111	20	1.9	20	1	ADB25703	Human connective t
C 112	20	1.9	20	1	ADB25655	Human connective t
C 113	20	1.9	20	1	ADB25650	Human connective t
C 114	20	1.9	20	1	ADB25651	Human connective t
C 115	20	1.9	20	1	ADB25700	Human connective t
C 116	20	1.9	20	1	ADB25704	Human connective t
C 117	20	1.9	20	1	ADB25667	Human connective t
C 118	20	1.9	20	1	ADB25672	Human connective t
C 119	20	1.9	20	1	ADB25699	Human connective t
C 120	20	1.9	20	1	ADB25701	Human connective t
C 121	20	1.9	20	1	ADB25646	Human connective t
C 122	20	1.9	20	1	ADB25668	Human connective t
C 123	20	1.9	20	1	ADB25670	Human connective t
C 124	20	1.9	20	1	ADB26665	Polynucleotide (ds
C 125	20	1.9	21	1	AAQ34015	Microsatellite seq
C 126	20	1.9	21	1	AAH90296	Oligonucleotide RT
C 127	20	1.9	21	1	AAH46014	Synthetic oligonuc
C 128	20	1.9	21	1	ABN88973	Phosphorothioate 2
C 129	20	1.9	21	1	ABN88972	Phosphorothioate 2
C 130	19.8	1.9	24	1	AB257678	Human zinc finger
C 131	19.4	1.8	21	1	AAQ33789	Microsatellite seq
C 132	19.4	1.8	21	1	AAV58080	ICAM-1 antisense c
C 133	19.4	1.8	21	1	ABV38616	Human ICAM-1, E-se
C 134	19.4	1.8	21	1	ABV38629	Human NADPH quinon
C 135	19.4	1.8	21	1	ABV37831	Human NADPH quinon
C 136	19.4	1.8	22	1	AAQ33716	Microsatellite seq
C 137	19.4	1.8	22	1	AAV64456	SSR motif #16. Un
C 138	19.4	1.8	23	1	ADP69447	5' anchored (ISSR)
C 139	19.4	1.8	24	1	AAV39357	SNP specific upper
C 140	19.4	1.8	24	1	ABZ70239	Murine tricarboxyl
C 141	19	1.8	24	1	AAQ33728	Microsatellite seq
C 142	19	1.8	19	1	AAV30412	Compound simple se
C 143	19	1.8	19	1	AAV66033	Repeat sequence fo
C 144	19	1.8	19	1	AAV28941	SSA primer 4 for a
C 145	19	1.8	19	1	AAV28942	SSA primer 4 for a
C 146	19	1.8	19	1	AAV66739	Heterologous inser
C 147	19	1.8	19	1	AAV66738	Heterologous inser
C 148	19	1.8	19	1	ADP69517	ISSR-related PCR p
C 149	19	1.8	21	1	AAV85976	CA repeat fluoroge
C 150	19	1.8	21	1	ABL44374	Human chromosome 1
C 151	18.4	1.8	20	1	ABV38503	H. discus derived
C 152	18.4	1.8	20	1	ABV37833	Human NADPH quinon
C 153	18.4	1.8	20	1	ADB25760	Mouse connective t
C 154	18	1.7	18	1	AAQ34135	Sequence of a micr
C 155	18	1.7	18	1	AAQ33722	Microsatellite seq
C 156	18	1.7	18	1	AAQ33950	Microsatellite seq
C 157	18	1.7	18	1	AAQ33937	Simple sequence re
C 158	18	1.7	18	1	AAQ46599	Simple sequence re
C 159	18	1.7	18	1	AAQ46588	Simple sequence re
C 160	18	1.7	18	1	AAV21968	Nuclease resistant
C 161	18	1.7	18	1	AAV77460	US5912147 primer 4
C 162	18	1.7	18	1	AAV77461	US5912147 primer 5
C 163	18	1.7	18	1	AAV76437	Sequencing reagent
C 164	18	1.7	18	1	AAV33765	Simple sequence re
C 165	18	1.7	18	1	AAV33732	Simple sequence re
C 166	18	1.7	18	1	AAV33723	Simple sequence re
C 167	18	1.7	18	1	AAV33729	Simple sequence re
C 168	18	1.7	18	1	AAH46012	Synthetic oligonuc
C 169	18	1.7	18	1	AAH46011	Synthetic oligonuc
C 170	18	1.7	20	1	AAV64454	SSR motif #14. Un
C 171	18	1.7	20	1	AAQ49455	Primer for detecti
C 172	18	1.7	20	1	ADD69468	3' anchored (ISSR)
C 173	17.8	1.7	21	1	AAQ75727	Reverse transcript
C 174	17.8	1.7	21	1	ABV37830	Human NADPH quinon
C 175	17.8	1.7	21	1	ABV37832	Human NADPH quinon
C 176	17.8	1.7	22	1	AAQ33888	Microsatellite seq
C 177	17.8	1.7	22	1	AAV64469	SSR motif #18. Un
C 178	17.8	1.7	22	1	ABV37834	Human NADPH quinon
C 179	17.4	1.7	20	1	AAV62964	Mouse PEPCK-cytoso
C 180	17.4	1.7	20	1	AAV21755	Mouse Survivin ant
C 181	17.4	1.7	20	1	ABV37835	Human NADPH quinon
C 182	17	1.6	17	1	AAQ34164	Sequence of a micr
C 183	17	1.6	17	1	AAQ33783	Microsatellite seq
C 184	17	1.6	17	1	AAV56865	WO513834 oligonuc
C 185	17	1.6	17	1	AAV66099	Repeat sequence fo
C 186	17	1.6	17	1	AAV91062	Methylphosphonat
C 187	17	1.6	17	1	AAV17594	5' variation gener
C 188	17	1.6	17	1	ADB45728	Tumour suppression
C 189	17	1.6	18	1	AAV77487	US5912147 primer 3
C 190	17	1.6	18	1	AAV77486	US5912147 primer 3
C 191	17	1.6	18	1	AAV77484	US5912147 primer 2
C 192	17	1.6	18	1	AAV77459	US5912147 primer 3
C 193	17	1.6	18	1	AAV77488	US5912147 primer 3
C 194	17	1.6	18	1	AAV77457	US5912147 primer 1
C 195	16.8	1.6	20	1	AAQ75591	Reverse transcript
C 196	16.8	1.6	20	1	AAV73096	Human MCL1 gene re
C 197	16.8	1.6	20	1	AAV73096	Human MCL1 gene re
C 198	16.8	1.6	20	1	AAV50667	Human uridine diph
C 199	16.8	1.6	20	1	AAV50667	Human uridine diph
C 200	16.8	1.6	20	1	AAV31716	Human oligonucleot
C 201	16.8	1.6	20	1	ABV80012	EST polymorphic DN
C 202	16.8	1.6	20	1	ADB25742	Mouse connective t
C 203	16.8	1.6	21	1	AAQ75729	Reverse transcript
C 204	16.8	1.6	21	1	AAQ75730	Reverse transcript
C 205	16.8	1.6	21	1	AAQ75728	Reverse transcript
C 206	16.8	1.6	21	1	AAQ60082	Reverse PCR primer
C 207	16.8	1.6	21	1	ABV47931	Human MIP-3 beta R
C 208	16.8	1.6	21	1	ABV30425	Compound simple se
C 209	16.6	1.6	24	1	ADD69518	ISSR-related PCR p
C 210	16.6	1.6	17	1	AAQ33786	Microsatellite seq
C 211	16.4	1.6	18	1	AAV19941	Microsatellite seq
C 212	16.4	1.6	18	1	AAV19941	Primer SEQ ID NO:1
C 213	16.4	1.6	18	1	AAV77485	US5912147 primer 2
C 214	16.4	1.6	18	1	AAV77494	US5912147 primer 3
C 215	16.4	1.6	18	1	AAV77493	US5912147 primer 3
C 216	16.4	1.6	18	1	AAV77464	US5912147 primer 8
C 217	16.4	1.6	18	1	AAV77491	US5912147 primer 3
C 218	16.4	1.6	18	1	AAV77489	US5912147 primer 3
C 219	16.4	1.6	18	1	AAV77463	US5912147 primer 7
C 220	16.4	1.6	18	1	AAV33733	Simple sequence re
C 221	16.4	1.6	18	1	AAV33764	Simple sequence re
C 222	16.4	1.6	18	1	AAV34450	SSR motif #10. Un
C 223	16.4	1.6	18	1	ABV37779	EST polymorphic DN
C 224	16.4	1.6	18	1	ABV37779	EST polymorphic DN
C 225	16.4	1.6	19	1	AAH91159	Human inflammatory
C 226	16.4	1.6	19	1	ABV30423	Human UGT1a1 promo
C 227	16.4	1.6	19	1	ABV30423	Human UGT1a1 promo
C 228	16.4	1.6	19	1	AAV50681	Human uridine diph
C 229	16.4	1.6	19	1	AAV50681	Human uridine diph
C 230	16.4	1.6	19	1	AAV50681	Murine capn12 exon
C 231	16	1.5	16	1	AAQ33743	Microsatellite seq
C 232	16	1.5	16	1	AAQ33743	Microsatellite seq
C 233	16	1.5	16	1	AAQ33903	Microsatellite seq
C 234	16	1.5	16	1	AAQ68236	Purine-pyrimidine
C 235	16	1.5	16	1	AAQ68233	Purine-pyrimidine
C 236	16	1.5	16	1	AAQ68233	Purine-pyrimidine
C 237	16	1.5	16	1	AAQ68233	Purine-pyrimidine
C 238	16	1.5	16	1	AAV66090	Repeat sequence fo
C 239	16	1.5	16	1	AAV66090	H. discus derived
C 240	16	1.5	17	1	AAV17599	5' variation gener
C 241	16	1.5	17	1	AAV17597	5' variation gener
C 242	16	1.5	17	1	AAV17595	5' variation gener
C 243	16	1.5	17	1	AAV17596	5' variation gener
C 244	16	1.5	17	1	AAV17598	5' variation gener
C 245	16	1.5	18	1	AAV77462	US5912147 primer 6
C 246	16	1.5	18	1	AAV77458	US5912147 primer 2
C 247	16	1.5	18	1	AAV77492	US5912147 primer 3
C 248	16	1.5	18	1	AAV77490	US5912147 primer 3
C 249	16	1.5	20	1	ABV89513	Human oligonucleot
C 250	15.8	1.5	19	1	AAQ75552	Reverse transcript
C 251	15.8	1.5	19	1	AAQ75552	Sequence of a micr
C 252	15.6	1.5	18	1	AAV27514	5' anchored simple



PT sources, using set of distinct gene specific primers.

XX

XX

PS Example 3; SEQ ID NO 400; 11pp; English.

CC The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine MboI DNA fragments of between 250 and 500 bp with an (AC)<sub>15</sub> and a (TC)<sub>15</sub> oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and MboI sites, the frequency of (TC)<sub>15</sub> > 9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information for ca. 230 such bovine microsatellites is summarised in the specification and indexed herein (see below). The sequences upstream and downstream of the microsatellite sequence were used to generate the

Fri Apr 2 14:41:45 2004

mcgarry191-19.rng

Page 3

253	15.4	1.5	17	1	AAV91399	Human C-raf target	c 326	14	1.3	15	1	AA150678	Human uridine diph
254	15.4	1.5	18	1	AAV21967	Nuclease resistant	c 327	14	1.3	17	1	AAT81559	Human c-myb hammer
c 255	15.4	1.5	18	1	AAV21967	Nuclease resistant	c 328	14	1.3	17	1	AAT81559	Human c-myb hammer
256	15.4	1.5	18	1	AAH37514	SNP specific lower	c 329	14	1.3	17	1	AAT74947	Nucleotide sequence
257	15.4	1.5	18	1	ABL38718	Immunostimulatory	c 330	14	1.3	17	1	ABD45500	Tumour suppressor
c 258	15.4	1.5	18	1	ABL38718	Immunostimulatory	c 331	13.8	1.3	17	1	AAT53762	Rat ICAM hammerhea
c 259	15.2	1.4	18	1	AAT27912	5'-anchored simple	c 332	13.8	1.3	17	1	AAT81448	Human c-myb hammer
c 260	15.2	1.4	41	1	AAH77495	Human zinc finger	c 333	13.8	1.3	17	1	AAT27920	5'-anchored simple
261	15	1.4	15	1	AAQ33764	Microsatellite seq	c 334	13.8	1.3	17	1	AAH69800	Human flt1 VEGF re
262	15	1.4	15	1	AAH31678	Tag sequence of a	c 335	13.8	1.3	17	1	AAH73299	Mouse flk-1 VEGF r
263	15	1.4	15	1	AAH46010	Synthetic oligonuc	c 336	13.8	1.3	17	1	AAH73299	Mouse flk-1 VEGF r
264	15	1.4	15	1	ABK32632	Human pancreatic c	c 337	13.8	1.3	17	1	AAH73299	Mouse flk-1 VEGF r
265	15	1.4	16	1	ABK90419	Human UGT1a1 promo	c 338	13.8	1.3	17	1	AAH18370	Human C-raf target
c 266	15	1.4	16	1	ABK90419	Human UGT1a1 promo	c 339	13.8	1.3	17	1	AAH18370	Human C-raf target
c 267	15	1.4	16	1	AAH50677	Human uridine diph	c 340	13.8	1.3	17	1	AAH50677	Human uridine diph
c 268	15	1.4	16	1	AAH50677	Human uridine diph	c 341	13.8	1.3	17	1	AAH50677	Human uridine diph
c 269	15	1.4	17	1	ABK90422	Human UGT1a1 promo	c 342	13.8	1.3	17	1	AAH50677	Human uridine diph
c 270	15	1.4	17	1	ABK90422	Human UGT1a1 promo	c 343	13.8	1.3	17	1	AAH50677	Human uridine diph
c 271	15	1.4	17	1	AAH50679	Human uridine diph	c 344	13.8	1.3	17	1	AAH50679	Human uridine diph
c 272	15	1.4	17	1	AAH50679	Human uridine diph	c 345	13.8	1.3	17	1	AAH50679	Human uridine diph
c 273	15	1.4	17	1	ABZ60766	Human K-Ras DNazym	c 346	13.8	1.3	17	1	AAH50197	2'-Methoxyethoxy-m
c 274	15	1.4	18	1	AAT27913	5'-anchored simple	c 347	13.8	1.3	17	1	AAH50197	2'-Methoxyethoxy-m
c 275	15	1.4	18	1	AAT27913	5'-anchored simple	c 348	13.8	1.3	17	1	AAH50197	2'-Methoxyethoxy-m
c 276	15	1.4	18	1	ABZ1102	Haematopoietic cel	c 349	13.8	1.3	17	1	ABV82841	Human HTPL scannin
c 277	15	1.4	18	1	ABZ1102	Haematopoietic cel	c 350	13.8	1.3	17	1	ABV82841	Human HTPL scannin
c 278	15	1.4	18	1	ADC70018	Primer oligo used	c 351	13.8	1.3	17	1	ABV82841	Human HTPL scannin
c 279	15	1.4	18	1	ADH84378	Human lymphoid cel	c 352	13.8	1.3	17	1	ABV82841	Human HTPL scannin
c 280	15	1.4	32	1	ABK66312	Human gene specifi	c 353	13.8	1.3	17	1	ABV82841	Human HTPL scannin
c 281	14.8	1.4	18	1	AAT94667	Anchored poly(7) o	c 354	13.8	1.3	17	1	ABV82841	Human HTPL scannin
c 282	14.8	1.4	18	1	AAT94667	Anchored poly(7) o	c 355	13.8	1.3	17	1	ABV82841	Human HTPL scannin
c 283	14.8	1.4	18	1	AAT94667	Anchored poly(7) o	c 356	13.8	1.3	17	1	ABV82841	Human HTPL scannin
c 284	14.6	1.4	15	1	ADD69515	Human integrin bet	c 357	13.8	1.3	17	1	ABV82841	Human HTPL scannin
c 285	14.6	1.4	15	1	ADD69515	Human integrin bet	c 358	13.8	1.3	17	1	ABV82841	Human HTPL scannin
c 286	14.4	1.4	16	1	AAQ51146	ISSR-related PCR p	c 359	13.8	1.3	17	1	ABV82841	Human HTPL scannin
c 287	14.4	1.4	16	1	AAQ51146	ISSR-related PCR p	c 360	13.8	1.3	17	1	ABV82841	Human HTPL scannin
c 288	14.4	1.4	16	1	AAQ51146	ISSR-related PCR p	c 361	13.8	1.3	17	1	ABV82841	Human HTPL scannin
c 289	14.4	1.4	16	1	AAQ51146	ISSR-related PCR p	c 362	13.8	1.3	17	1	ABV82841	Human HTPL scannin
c 290	14.4	1.4	16	1	AAQ51146	ISSR-related PCR p	c 363	13.8	1.3	17	1	ABV82841	Human HTPL scannin
c 291	14.4	1.4	16	1	AAQ51146	ISSR-related PCR p	c 364	13.6	1.3	15	1	ABK15668	Human UBE3A gene A
c 292	14.4	1.4	16	1	AAQ51146	ISSR-related PCR p	c 365	13.6	1.3	15	1	ABK15668	Human UBE3A gene A
c 293	14.4	1.4	16	1	AAQ51146	ISSR-related PCR p	c 366	13.4	1.3	15	1	ABK15668	Human UBE3A gene A
c 294	14.4	1.4	16	1	AAQ51146	ISSR-related PCR p	c 367	13.4	1.3	15	1	ABK15668	Human UBE3A gene A
c 295	14.4	1.4	16	1	AAQ51146	ISSR-related PCR p	c 368	13.4	1.3	15	1	ABK15668	Human UBE3A gene A
c 296	14.4	1.4	16	1	AAQ51146	ISSR-related PCR p	c 369	13.4	1.3	15	1	ABK15668	Human UBE3A gene A
c 297	14.4	1.4	16	1	AAQ51146	ISSR-related PCR p	c 370	13.4	1.3	15	1	ABK15668	Human UBE3A gene A
c 298	14.4	1.4	16	1	AAQ51146	ISSR-related PCR p	c 371	13.4	1.3	15	1	ABK15668	Human UBE3A gene A
c 299	14.4	1.4	16	1	AAQ51146	ISSR-related PCR p	c 372	13	1.2	13	1	AAA10358	DNA ligand binding
c 300	14.4	1.4	16	1	AAQ51146	ISSR-related PCR p	c 373	13	1.2	13	1	AAA10358	DNA ligand binding
c 301	14.4	1.4	16	1	AAQ51146	ISSR-related PCR p	c 374	13	1.2	13	1	AAA10358	DNA ligand binding
c 302	14.4	1.4	16	1	AAQ51146	ISSR-related PCR p	c 375	13	1.2	13	1	AAA10358	DNA ligand binding
c 303	14.4	1.4	16	1	AAQ51146	ISSR-related PCR p	c 376	13	1.2	13	1	AAA10358	DNA ligand binding
c 304	14.4	1.4	16	1	AAQ51146	ISSR-related PCR p	c 377	13	1.2	13	1	AAA10358	DNA ligand binding
c 305	14.4	1.4	16	1	AAQ51146	ISSR-related PCR p	c 378	13	1.2	13	1	AAA10358	DNA ligand binding
c 306	14.4	1.4	16	1	AAQ51146	ISSR-related PCR p	c 379	13	1.2	13	1	AAA10358	DNA ligand binding
c 307	14.4	1.4	16	1	AAQ51146	ISSR-related PCR p	c 380	13	1.2	13	1	AAA10358	DNA ligand binding
c 308	14.4	1.4	16	1	AAQ51146	ISSR-related PCR p	c 381	13	1.2	13	1	AAA10358	DNA ligand binding
c 309	14.4	1.4	16	1	AAQ51146	ISSR-related PCR p	c 382	13	1.2	13	1	AAA10358	DNA ligand binding
c 310	14.4	1.4	16	1	AAQ51146	ISSR-related PCR p	c 383	13	1.2	13	1	AAA10358	DNA ligand binding
c 311	14.4	1.4	16	1	AAQ51146	ISSR-related PCR p	c 384	13	1.2	13	1	AAA10358	DNA ligand binding
c 312	14.4	1.4	16	1	AAQ51146	ISSR-related PCR p	c 385	13	1.2	13	1	AAA10358	DNA ligand binding
c 313	14.2	1.4	20	1	AAH31526	Sequence of an oli	c 386	13	1.2	13	1	AAA10358	DNA ligand binding
c 314	14	1.3	14	1	AAH31526	Sequence of an oli	c 387	13	1.2	13	1	AAA10358	DNA ligand binding
c 315	14	1.3	14	1	AAH31526	Sequence of an oli	c 388	13	1.2	13	1	AAA10358	DNA ligand binding
c 316	14	1.3	14	1	AAH31526	Sequence of an oli	c 389	13	1.2	13	1	AAA10358	DNA ligand binding
c 317	14	1.3	14	1	AAH31526	Sequence of an oli	c 390	13	1.2	13	1	AAA10358	DNA ligand binding
c 318	14	1.3	14	1	AAH31526	Sequence of an oli	c 391	13	1.2	13	1	AAA10358	DNA ligand binding

1793 TGTGTGTGTGTGTGTGTATATATATATATG 1828

XX  
05-MAR-2003  
RD

CC sequences which can be used as DNA markers. The new method markedly  
 CC improves the efficiency of isolation of satellite sequences in comparison  
 CC to prior art methods which are reliant on base sequences. Sequences  
 CC AA298483-514 represent sequences from Haliotis discus, used in the method  
 CC of the invention  
 XX  
 SQ Sequence 30 BP; 15 A; 13 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 2.4%; Score 25.2; DB 1; Length 30;  
 Best Local Similarity 90.0%; Pred. No. 20;  
 Matches 27; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTGTATATATA 1822  
 DB 30 TGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1

RESULT 6  
 AAA15467/c  
 ID AAA15467 standard; DNA; 25 BP.  
 XX  
 AC AAA15467;  
 XX  
 DT 21-SEP-2000 (first entry)  
 XX  
 DE Antisense primer for a rat connective tissue growth factor DNA.  
 XX  
 KW Rat; connective tissue growth factor; CTGF; cell proliferative disorder;  
 KW connective tissue cell; scleroderma; arthritis; cirrhosis;  
 KW hepatic fibrosis; renal fibrosis; atherosclerosis; cardiac fibrosis;  
 KW adhesion; surgical scarring; antisense primer; DNA-RNA hybrid; ss.  
 XX  
 OS Rattus sp.

XX  
 FH Key Location/Qualifiers  
 FT misc\_RNA 13..25  
 FT /\*tag= a  
 XX  
 FN WO200027868-A2.  
 XX  
 PD 18-MAY-2000.  
 XX  
 PF 05-NOV-1999; 99WO-US026189.  
 XX  
 PR 06-NOV-1998; 98US-00187478.  
 PR 14-APR-1999; 99US-00292036.  
 XX  
 PA (FIBR-) FIBROGEN INC.

XX  
 PI Schmidt BF, Allen ML, Sverdrup F, Carmichael DF;  
 XX  
 DR WPI; 2000-376484/32.  
 XX  
 PT New rat connective tissue growth factor, its related gene and antisense  
 PT sequences useful for modulating CTGF and treatment of cell proliferative  
 PT disorders.  
 XX  
 PS Claim 24; Page 44; 55pp; English.

XX The present sequence represents an antisense primer which is used to  
 CC inhibit expression of the rat connective tissue growth factor (CTGF)  
 CC gene. The polypeptide may play a significant role in the normal  
 CC development, growth and repair of mammalian tissue. Antisense sequences  
 CC can be used to inhibit the expression of CTGF in a cell. In particular,  
 CC the antisense sequences are useful for ameliorating cell proliferative  
 CC disorders associated with CTGF, e.g. overgrowth of cells, e.g. connective  
 CC tissue cells. The regulation of CTGF activity comprises down-regulation.  
 CC The disorders, which can be treated, are chosen from scleroderma,  
 CC arthritis, cirrhosis, hepatic fibrosis, renal fibrosis, atherosclerosis,  
 CC cardiac fibrosis, adhesions and surgical scarring. The antisense  
 CC sequences can also be used to detect expression of CTGF in a sample

XX Sequence 25 BP; 6 A; 8 C; 4 G; 2 T; 5 U; 0 Other;

Query Match 2.4%; Score 25; DB 1; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 18;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1718 ATTAGACTGCACAGCTTGTGCAAG 1742  
 DB 25 ATTAGACTGCACAGCTTGTGCAAG 1

RESULT 7  
 AAA15468/c  
 ID AAA15468 standard; DNA; 25 BP.  
 XX  
 AC AAA15468;  
 XX  
 DT 21-SEP-2000 (first entry)  
 XX  
 DE Antisense primer for a rat connective tissue growth factor DNA.

XX Rat; connective tissue growth factor; CTGF; cell proliferative disorder;  
 KW connective tissue cell; scleroderma; arthritis; cirrhosis;  
 KW hepatic fibrosis; renal fibrosis; atherosclerosis; cardiac fibrosis;  
 KW adhesion; surgical scarring; antisense primer; DNA-RNA hybrid; ss.  
 XX  
 OS Rattus sp.

XX  
 FH Key Location/Qualifiers  
 FT misc\_RNA 10..22  
 FT /\*tag= a  
 XX  
 FN WO200027868-A2.  
 XX  
 PD 18-MAY-2000.  
 XX  
 PF 05-NOV-1999; 99WO-US026189.  
 XX  
 PR 06-NOV-1998; 98US-00187478.  
 PR 14-APR-1999; 99US-00292036.  
 XX  
 PA (FIBR-) FIBROGEN INC.

XX  
 PI Schmidt BF, Allen ML, Sverdrup F, Carmichael DF;  
 XX  
 DR WPI; 2000-376484/32.  
 XX  
 PT New rat connective tissue growth factor, its related gene and antisense  
 PT sequences useful for modulating CTGF and treatment of cell proliferative  
 PT disorders.  
 XX  
 PS Claim 24; Page 44; 55pp; English.

XX The present sequence represents an antisense primer which is used to  
 CC inhibit expression of the rat connective tissue growth factor (CTGF)  
 CC gene. The polypeptide may play a significant role in the normal  
 CC development, growth and repair of mammalian tissue. Antisense sequences  
 CC can be used to inhibit the expression of CTGF in a cell. In particular,  
 CC the antisense sequences are useful for ameliorating cell proliferative  
 CC disorders associated with CTGF, e.g. overgrowth of cells, e.g. connective  
 CC tissue cells. The regulation of CTGF activity comprises down-regulation.  
 CC The disorders, which can be treated, are chosen from scleroderma,  
 CC arthritis, cirrhosis, hepatic fibrosis, renal fibrosis, atherosclerosis,  
 CC cardiac fibrosis, adhesions and surgical scarring. The antisense  
 CC sequences can also be used to detect expression of CTGF in a sample

SQ Sequence 25 BP; 5 A; 7 C; 5 G; 4 T; 4 U; 0 Other;

Query Match 2.2%; Score 23.4; DB 1; Length 25;  
 Best Local Similarity 96.0%; Pred. No. 28;  
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1742 GTGAATTTCCTGTAAACAAGCCAGA 1766  
 |||||||

Db 25 GTGAATTTCGGTAAACAGCCAGA 1

RESULT 8

AA161970/c

ID AA161970 standard; DNA; 27 BP.

XX

AC AA161970;

XX

DT 16-OCT-2001 (first entry)

XX

DE Soybean 240017 region G3 DNA forward primer, SEQ ID NO: 601.

XX

KW Soybean; antihelminthic; gene therapy; soybean cyst nematode; SCN;

XX

KW SCN resistance; rhg1; Rhg4; SCN resistant allele; plant breeding;

XX

KW 240017 region G3; 318013 region A3; 515002 region G2; PCR primer;

XX

OS Glycine max.

XX

PN WO200151627-A2.

XX

PD 19-JUL-2001.

XX

XX

PF 05-JAN-2001; 2001WO-US000552.

XX

PR 07-JAN-2000; 2000US-0174880P.

XX

PA (MONS ) MONSANTO CO.

XX

PI Hauge BM, Wang ML, Parsons JD, Parnell LD;

XX

PI WPI; 2001-425872/45.

XX

DR New purified nucleic acid for producing a soybean plant having soybean

XX

PT cyst nematode resistance and for use in plant breeding programs.

XX

PS Claim 25; Page 1178; 1353pp; English.

XX

CC The invention relates to nucleic acid molecules from regions of the

XX

CC soybean genome which are associated with soybean cyst nematode (SCN)

XX

CC resistance. The nucleic acids are used to transform plants, and can

XX

CC produce soybean plants having an rhg1 or an Rhg4 SCN resistant allele.

XX

CC The nucleic acids can be used for investigating rhg1 or Rhg4 haplotypes

XX

CC of soybean plants and for introgressing SCN resistance or partial SCN

XX

CC resistance into soybean plants. They can also be used in plant breeding

XX

CC programmes. The invention also relates to proteins encoded by such

XX

CC nucleic acid molecules, as well as antibodies capable of recognising

XX

CC these proteins. The present sequence is a primer used to amplify a region

XX

CC of the soybean genome

XX

SQ Sequence 27 BP; 12 A; 11 C; 0 G; 4 T; 0 U; 0 Other;

XX

Query Match 2.2%; Score 23.4; DB 1; Length 27;

Best Local Similarity 96.0%; Pred. No. 30;

Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

XX

Oy 1795 TGTGTGTGTGTGTGTGTGTATAT 1819

Db 27 TGTGTGTGTGTGTGTGTATAAT 3

RESULT 9

AA130425/c

ID AA130425 standard; DNA; 24 BP.

XX

AC AA130425;

XX

DT 28-JAN-1997 (first entry)

XX

DE Compound simple sequence repeat primer (CA)4.5(TA)7.5.

XX

KW Detection; polymorphism; perfect compound simple sequence repeat;

XX

KW adaptor directed primer; genome; genetic; fingerprinting;

XX

KW

KW amplified fragment length polymorphism assay; microsatellite region;

XX

KW genetic trait marking; germplasm comparisons; compound; ss.

XX

OS Synthetic.

XX

PN WO9617082-A2.

XX

XX

PD -06-JUN-1996.

XX

XX

PF 21-NOV-1995; 95WO-US015150.

XX

XX

PR 28-NOV-1994; 94US-00346456.

XX

XX

PA (DUPO ) DU PONT DE NEMOURS & CO E I.

XX

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PI Morgante M, Vogel JM;

XX

XX

DR WPI; 1996-277795/28.

XX

XX

PT Modified amplified fragment length polymorphism assay - for detection of

XX

PT polymorphism esp. in microsatellite regions.

XX

XX

PS Disclosure; Fig 1c; 173pp; English.

XX

CC Detecting polymorphisms between 2 nucleic acid samples, esp. in

XX

CC microsatellite regions, comprises digesting the nucleic acid to generate

XX

CC fragments, ligating adaptor segments to their ends, amplifying them using

XX

CC primer directed amplification and comparing the prods. to detect

XX

CC differences. The primers used in the amplification comprise a primer

XX

CC consisting of a perfect cpd. simple sequence repeat (SSR), and an adaptor

XX

CC directed primer, comprising a sequence complementary to an adaptor

XX

CC segment. The present sequence is an example of a compound SSR primer. The

XX

CC method represents a modified amplified fragment length polymorphism

XX

CC assay, which is partic. useful for genome fingerprinting, i.e. for

XX

CC genetic trait marking and germplasm comparisons

XX

SQ Sequence 24 BP; 12 A; 4 C; 0 G; 8 T; 0 U; 0 Other;

XX

Query Match 2.2%; Score 23; DB 1; Length 24;

Best Local Similarity 100.0%; Pred. No. 30;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX

Oy 1805 TGTGTGTGTATATATATATATAT 1827

Db 24 TGTGTGTGTATATATATATATAT 2

RESULT 10

AAH39074/c

ID AAH39074 standard; DNA; 24 BP.

XX

AC AAH39074;

XX

DT 14-AUG-2001 (first entry)

XX

XX

DE SNP specific lower PCR primer SEQ ID 1870.

XX

XX

KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;

XX

KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;

XX

KW Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolemia;

XX

KW polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;

XX

KW acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;

XX

KW inflammation; forensic investigation; paternity analysis; PCR primer; ss.

XX

OS Homo sapiens.

XX

PN WO200129262-A2.

XX

XX

PD 26-APR-2001.

XX

XX

PF 13-OCT-2000; 2000WO-US028436.

XX

XX

PR 15-OCT-1999; 99US-0160096P.

XX (ORCH-) ORCHID BIOSCIENCES INC.  
 XX Picoult-Newburg L, Pohl M;  
 XX WPI; 1992-284684/34.  
 XX New genotyping oligonucleotide, useful for detecting the presence,  
 XX absence or identity of single polynucleotide polymorphism in a nucleic  
 XX acid sample.  
 XX Claim 1; Page 59; 83pp; English.  
 XX Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide  
 XX primer extension (SNPE) primers, and the sequences of regions flanking  
 XX sites of single nucleotide polymorphisms SNPs. The present invention  
 XX includes kits for determining the presence or absence of a SNP, using the  
 XX oligonucleotides of the invention. The PCR primers are used to amplify a  
 XX SNP flanking sequence, the SNPE primer is used as a genotyping primer.  
 XX The oligonucleotides are useful for genotyping a nucleic acid sample by  
 XX performing a single-nucleotide primer extension reaction. The  
 XX oligonucleotides are useful for determining the presence, absence or  
 XX identity of a SNP and for genotyping nucleic acid samples, for e.g. to  
 XX assess by association analysis the genotype of an individual or group of  
 XX individuals, having a pathological phenotypic trait suspected of being  
 XX caused by one or more SNPs. Phenotypic traits include diseases e.g.  
 XX agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular  
 XX dystrophy, familial hypercholesterolaemia, polycystic kidney disease,  
 XX osteogenesis imperfecta and acute intermittent porphyria. Phenotypic  
 XX traits also include symptoms of or susceptibility to multifactorial  
 XX disease of which a component is or may be genetic such as autoimmune  
 XX diseases, including, rheumatoid arthritis, multiple sclerosis,  
 XX inflammation, cancer, nervous system diseases and infection by pathogenic  
 XX microorganism. The method is also useful in forensic investigations and  
 XX paternity analysis. The present sequence represents a PCR primer specific  
 XX for a human SNP containing DNA sequence  
 XX  
 XX SQ Sequence 24 BP; 12 A; 11 C; 0 G; 1 T; 0 U; 0 Other;  
 Query Match 2.2%; Score 23; DB 1; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 30;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1791 ATTGTGTGTGTGTGTGTGTGTGTGTGTGT 1813  
 Db 23 ATTGTGTGTGTGTGTGTGTGTGTGTGTGT 1  
 RESULT 11  
 AAQ34044  
 ID AAQ34044 standard; DNA; 27 BP.  
 XX  
 XX AAQ34044;  
 XX  
 XX 25-MAR-2003 (revised)  
 XX 02-FEB-1993 (first entry)  
 XX  
 XX Microsatellite sequence from clone TGLA435.  
 XX PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;  
 XX genetic mapping; traits; amplification; ss.  
 XX Bos taurus.  
 XX WO9213102-A1.  
 XX 06-AUG-1992.  
 XX 15-JAN-1992; 92WO-US000340.  
 XX 15-JAN-1991; 91US-00642342.  
 XX (GENM-) GENMARK.  
 XX  
 XX Georges M, Massey JM;  
 XX WPI; 1992-284684/34.  
 XX Polymorphic bovine DNA markers - used in genetic identification, gene  
 XX mapping, and selective breeding.  
 XX Table 7; Page 201; 517pp; English.

XX Georges M, Massey JM;  
 XX WPI; 1992-284684/34.  
 XX Polymorphic bovine DNA markers - used in genetic identification, gene  
 XX mapping, and selective breeding.  
 XX Table 7; Page 348; 517pp; English.  
 XX The sequence is that of a bovine microsatellite sequence obtd. by  
 XX screening a library of bovine MboI DNA fragments of between 250 and 500  
 XX bp with an (AC)<sub>15</sub> and a (TC)<sub>15</sub> oligonucleotide probe. One out of 50  
 XX clones cross-hybridised. Assuming independent distribution of  
 XX microsatellites and MboI sites, the frequency of (TC)<sub>n</sub> > 9 microsatellites  
 XX in the bovine genome is estimated at >100,000. The sequence information  
 XX for ca. 230 such bovine microsatellites is summarised in the  
 XX specification and indexed herein (see below). The sequences upstream and  
 XX downstream of the microsatellite sequence were used to generate the  
 XX required PCR primers for in vitro amplification of the corresp.  
 XX microsatellite (using the program OPTIPRIM). The microsatellites may be  
 XX used to identify individuals, for parentage testing, and in the genetic  
 XX mapping of economic trait loci, or genes involved in the determination of  
 XX economically important traits esp. in cattle, to allow selective  
 XX breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN  
 XX field.)  
 XX SQ Sequence 27 BP; 0 A; 0 C; 13 G; 14 T; 0 U; 0 Other;  
 Query Match 2.1%; Score 22.2; DB 1; Length 27;  
 Best Local Similarity 88.9%; Pred. No. 42;  
 Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1793 TGTGTGTGTGTGTGTGTGTGTGTGTATAT 1819  
 Db 1 TGTGTGTGTGTGTGTGTGTGTGTGTGTGT 27  
 RESULT 12  
 AAQ33678  
 ID AAQ33678 standard; DNA; 27 BP.  
 XX  
 XX AAQ33678;  
 XX  
 XX 25-MAR-2003 (revised)  
 XX 02-FEB-1993 (first entry)  
 XX  
 XX Microsatellite sequence from clone TGLA12.  
 XX PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;  
 XX genetic mapping; traits; amplification; ss.  
 XX Bos taurus.  
 XX WO9213102-A1.  
 XX 06-AUG-1992.  
 XX 15-JAN-1992; 92WO-US000340.  
 XX 15-JAN-1991; 91US-00642342.  
 XX (GENM-) GENMARK.  
 XX  
 XX Georges M, Massey JM;  
 XX WPI; 1992-284684/34.  
 XX Polymorphic bovine DNA markers - used in genetic identification, gene  
 XX mapping, and selective breeding.  
 XX Table 7; Page 201; 517pp; English.

CC The sequence is that of a bovine microsatellite sequence obt'd. by  
 CC screening a library of bovine MboI DNA fragments of between 250 and 500  
 CC bp with an (AC)<sub>15</sub> and a (TC)<sub>15</sub> oligonucleotide probe. One out of 50  
 CC clones cross-hybridised. Assuming independent distribution of  
 CC microsatellites and MboI sites, the frequency of (T6)<sub>n</sub> >9 microsatellites  
 CC in the bovine genome is estimated at >100,000. The sequence information  
 CC for ca. 230 such bovine microsatellites is summarised in the  
 CC specification and indexed herein (see below). The sequences upstream and  
 CC downstream of the microsatellite sequence were used to generate the  
 CC required PCR primers for in vitro amplification of the corresp.  
 CC microsatellite (using the program OPTIPRIM). The microsatellites may be  
 CC used to identify individuals, for parentage testing, and in the genetic  
 CC mapping of economic trait loci, or genes involved in the determination of  
 CC economically important traits esp. in cattle, to allow selective  
 CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN  
 CC field.)

XX SQ Sequence 27 BP; 0 A; 0 C; 13 G; 14 T; 0 U; 0 Other;

Query Match 2.1%; Score 22.2; DB 1; Length 27;  
 Best Local Similarity 88.9%; Pred. No. 42;  
 Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTGTATAT 1819

DB 1 TGTGTGTGTGTGTGTGTGTGTGTGTGT 27

#### RESULT 13

AAQ33804

ID AAQ33804 standard; DNA; 27 BP.

XX AC AAQ33804;

XX DT 25-MAR-2003 (revised)

XX DT 02-FEB-1993 (first entry)

XX DE Microsatellite sequence from clone TGLA210.

XX KW PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;  
 XX genetic mapping; traits; amplification; ss.

XX OS Bos taurus.

XX PN WO9213102-Al.

XX PD 06-AUG-1992.

XX PF 15-JAN-1992; 92WO-US000340.

XX PR 15-JAN-1991; 91US-00642342.

XX PA (GENM-) GENMARK.

XX PI Georges M, Massey JM;

XX XX WFI; 1992-284684/34.

XX PT Polymorphic bovine DNA markers - used in genetic identification, gene  
 XX mapping, and selective breeding.

XX PS Table 7; Page 251; 517pp; English.

XX CC The sequence is that of a bovine microsatellite sequence obt'd. by  
 CC screening a library of bovine MboI DNA fragments of between 250 and 500  
 CC bp with an (AC)<sub>15</sub> and a (TC)<sub>15</sub> oligonucleotide probe. One out of 50  
 CC clones cross-hybridised. Assuming independent distribution of  
 CC microsatellites and MboI sites, the frequency of (T6)<sub>n</sub> >9 microsatellites  
 CC in the bovine genome is estimated at >100,000. The sequence information  
 CC for ca. 230 such bovine microsatellites is summarised in the  
 CC specification and indexed herein (see below). The sequences upstream and  
 CC downstream of the microsatellite sequence were used to generate the  
 CC required PCR primers for in vitro amplification of the corresp.

CC microsatellite (using the program OPTIPRIM). The microsatellites may be  
 CC used to identify individuals, for parentage testing, and in the genetic  
 CC mapping of economic trait loci, or genes involved in the determination of  
 CC economically important traits esp. in cattle, to allow selective  
 CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN  
 CC field.)

XX SQ Sequence 27 BP; 0 A; 0 C; 13 G; 14 T; 0 U; 0 Other;

Query Match 2.1%; Score 22.2; DB 1; Length 27;  
 Best Local Similarity 88.9%; Pred. No. 42;  
 Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTATAT 1819

DB 1 TGTGTGTGTGTGTGTGTGTGTGTGTGT 27

#### RESULT 14

AAQ34181

ID AAQ34181 standard; DNA; 27 BP.

XX AC AAQ34181;

XX DT 25-MAR-2003 (revised)

XX DT 02-FEB-1993 (first entry)

XX DE Microsatellite sequence from clone TGLA98.

XX KW PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;  
 XX genetic mapping; traits; amplification; ss.

XX OS Bos taurus.

XX PN WO9213102-Al.

XX PD 06-AUG-1992.

XX PF 15-JAN-1992; 92WO-US000340.

XX PR 15-JAN-1991; 91US-00642342.

XX PA (GENM-) GENMARK.

XX PI Georges M, Massey JM;

XX XX WFI; 1992-284684/34.

XX PT Polymorphic bovine DNA markers - used in genetic identification, gene  
 XX mapping, and selective breeding.

XX PS Table 7; Page 403; 517pp; English.

XX CC The sequence is a bovine microsatellite sequence obt'd. by screening a  
 CC library of bovine MboI DNA fragments of between 250 and 500 bp with an  
 CC (AC)<sub>15</sub> and a (TC)<sub>15</sub> oligonucleotide probe. One out of 50 clones cross  
 CC hybridised. Assuming independent distribution of microsatellites and MboI  
 CC sites, the frequency of (T6)<sub>n</sub> >9 microsatellites in the bovine genome is  
 CC estimated at >100,000. The sequence information for ca. 230 such bovine  
 CC microsatellites is summarised in the specification and indexed herein  
 CC (see below). The sequences upstream and downstream of the microsatellite  
 CC sequence were used to generate the required PCR primers for in vitro  
 CC amplification of the corresp. microsatellite (using the program  
 CC OPTIPRIM). The microsatellites may be used to identify individuals, for  
 CC parentage testing, and in the genetic mapping of economic trait loci, or  
 CC genes involved in the determination of economically important traits esp. in  
 CC cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on  
 CC 25-MAR-2003 to correct PN field.)

XX SQ Sequence 27 BP; 0 A; 0 C; 13 G; 14 T; 0 U; 0 Other;

Query Match 2.1%; Score 22.2; DB 1; Length 27;  
 Best Local Similarity 88.9%; Pred. No. 42;

```

Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1793 TGTGTGTGTGTGTGTGTGTATAT 1819
DB 1 TGTGTGTGTGTGTGTGTGTGTGTGT 27

RESULT 15
AAQ34012
ID AAQ34012 standard; DNA; 27 BP.
XX
AC AAQ34012;
XX
DT 25-MAR-2003 (revised)
DT 02-FEB-1993 (first entry)
XX
DE Microsatellite sequence from clone TGLA417.
XX
KW PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
KW genetic mapping; traits; amplification; ss.
XX
OS Bos taurus.
XX
PN WO9213102-A1..
XX
PD 06-AUG-1992.
XX
PF 15-JAN-1992; 92WO-US000340.
XX
PR 15-JAN-1991; 91US-00642342.
XX
PA (GENM-) GENMARK.
XX
PI Georges M, Massey JM;
XX
DR WPI; 1992-284684/34.
XX
PT Polymorphic bovine DNA markers - used in genetic identification, gene
PT mapping, and selective breeding.
XX
PS Table 7; Page 335; 517pp; English.
XX
CC The sequence is that of a bovine microsatellite sequence obtd. by
CC screening a library of bovine MboI DNA fragments of between 250 and 500
CC bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
CC clones cross-hybridised. Assuming independent distribution of
CC microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites
CC in the bovine genome is estimated at >100,000. The sequence information
CC for ca. 230 such bovine microsatellites is summarised in the
CC specification and indexed herein (see below). The sequences upstream and
CC downstream of the microsatellite sequence were used to generate the
CC required PCR primers for in vitro amplification of the corresp.
CC microsatellite (using the program OPTIPRIM). The microsatellites may be
CC used to identify individuals, for parentage testing, and in the genetic
CC mapping of economic trait loci, or genes involved the determination of
CC economically important traits esp. in cattle, to allow selective
CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
SQ Sequence 27 BP; 0 A; 0 C; 13 G; 14 T; 0 U; 0 Other;

Query Match 2.1%; Score 22.2; DB 1; Length 27;
Best Local Similarity 88.9%; Pred. No. 42;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTATAT 1819
DB 1 TGTGTGTGTGTGTGTGTGTGTGTGT 27

RESULT 16
AAQ34143
ID AAQ34143 standard; DNA; 27 BP.
XX
AC AAQ34143;
XX
DT 25-MAR-2003 (revised)
DT 02-FEB-1993 (first entry)
XX
DE Sequence of a microsatellite from clone TGLA76.
XX
KW PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
KW genetic mapping; traits; amplification; ss.
XX
OS Bos taurus.
XX
PN WO9213102-A1.
XX
PD 06-AUG-1992.
XX
PF 15-JAN-1992; 92WO-US000340.
XX
PR 15-JAN-1991; 91US-00642342.
XX
PA (GENM-) GENMARK.
XX
PI Georges M, Massey JM;
XX
DR WPI; 1992-284684/34.
XX
PT Polymorphic bovine DNA markers - used in genetic identification, gene
PT mapping, and selective breeding.
XX
PS Table 7; Page 388; 517pp; English.
XX
CC The sequence is that of a bovine microsatellite sequence obtd. by
CC screening a library of bovine MboI DNA fragments of between 250 and 500
CC bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
CC clones cross-hybridised. Assuming independent distribution of
CC microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites
CC in the bovine genome is estimated at >100,000. The sequence information
CC for ca. 230 such bovine microsatellites is summarised in the
CC specification and indexed herein (see below). The sequences upstream and
CC downstream of the microsatellite sequence were used to generate the
CC required PCR primers for in vitro amplification of the corresp.
CC microsatellite (using the program OPTIPRIM). The microsatellites may be
CC used to identify individuals, for parentage testing, and in the genetic
CC mapping of economic trait loci, or genes involved the determination of
CC economically important traits esp. in cattle, to allow selective
CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
SQ Sequence 27 BP; 0 A; 0 C; 13 G; 14 T; 0 U; 0 Other;

Query Match 2.1%; Score 22.2; DB 1; Length 27;
Best Local Similarity 88.9%; Pred. No. 42;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTATAT 1819
DB 1 TGTGTGTGTGTGTGTGTGTGTGTGT 27

RESULT 17
AAQ34143/c
ID AAQ34143 standard; DNA; 27 BP.
XX
AC AAQ34143;
XX
DT 25-MAR-2003 (revised)
DT 17-JUN-1997 (first entry)
XX
DE Repeat sequence from polymorphic marker clone Mfd31.
XX
KW Polymorphism; repeat sequence; genetic marker; primer; amplification;
KW PCR; polymerase chain reaction; paternity; maternity; human; pedigree;

```

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XX AAQ34143;
AC
XX 25-MAR-2003 (revised)
DT 02-FEB-1993 (first entry)
XX
DE Sequence of a microsatellite from clone TGLA76.
XX
KW PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
KW genetic mapping; traits; amplification; ss.
XX
OS Bos taurus.
XX
PN WO9213102-A1.
XX
PD 06-AUG-1992.
XX
PF 15-JAN-1992; 92WO-US000340.
XX
PR 15-JAN-1991; 91US-00642342.
XX
PA (GENM-) GENMARK.
XX
PI Georges M, Massey JM;
XX
DR WPI; 1992-284684/34.
XX
PT Polymorphic bovine DNA markers - used in genetic identification, gene
PT mapping, and selective breeding.
XX
PS Table 7; Page 388; 517pp; English.
XX
CC The sequence is that of a bovine microsatellite sequence obtd. by
CC screening a library of bovine MboI DNA fragments of between 250 and 500
CC bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
CC clones cross-hybridised. Assuming independent distribution of
CC microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites
CC in the bovine genome is estimated at >100,000. The sequence information
CC for ca. 230 such bovine microsatellites is summarised in the
CC specification and indexed herein (see below). The sequences upstream and
CC downstream of the microsatellite sequence were used to generate the
CC required PCR primers for in vitro amplification of the corresp.
CC microsatellite (using the program OPTIPRIM). The microsatellites may be
CC used to identify individuals, for parentage testing, and in the genetic
CC mapping of economic trait loci, or genes involved the determination of
CC economically important traits esp. in cattle, to allow selective
CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
SQ Sequence 27 BP; 0 A; 0 C; 13 G; 14 T; 0 U; 0 Other;

Query Match 2.1%; Score 22.2; DB 1; Length 27;
Best Local Similarity 88.9%; Pred. No. 42;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTATAT 1819
DB 1 TGTGTGTGTGTGTGTGTGTGTGTGT 27

RESULT 17
AAQ34143/c
ID AAQ34143 standard; DNA; 27 BP.
XX
AC AAQ34143;
XX
DT 25-MAR-2003 (revised)
DT 17-JUN-1997 (first entry)
XX
DE Repeat sequence from polymorphic marker clone Mfd31.
XX
KW Polymorphism; repeat sequence; genetic marker; primer; amplification;
KW PCR; polymerase chain reaction; paternity; maternity; human; pedigree;

```

KW linkage analysis; genetic disease; animal; plant; breeding; locus;  
KW hybridisation; chromosome; ds.

XX Homo sapiens.

XX US5582979-A.

XX 10-DEC-1996.

XX 04-APR-1994; 94US-00222177.

XX 21-APR-1989; 89US-00341562.

XX 05-SEP-1991; 91US-00754351.

XX (MARS-) MARSHFIELD CLINIC.

XX Weber JL;

XX WPI; 1997-042299/04.

XX Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n -  
XX using novel nucleic acid mols. as primers.

XX Claim 1; Col 9-10; 186pp; English.

XX The invention relates to the isolation of polymorphic repeat sequences  
XX having the sequence (dC-dA)n (dG-dT)n which can be used as genetic  
XX markers. Primers based on these sequences can be used to detect these  
XX repeats, especially for use in e.g. paternity or maternity testing, human  
XX genetic analysis such as linkage analysis of genetic disease, commercial  
XX animal or plant breeding or pedigree analysis. Clones containing the  
XX repeat sequences were isolated by hybridisation of chromosome-specific  
XX phage libraries with a synthetic poly(dC-dA). (dG-dT) probe. Over 100  
XX repeat blocks were isolated. The inserts from the clones were amplified  
XX by primers AAH65798-T66047. Those clones where the repeat sequence has  
XX been determined are shown in AAH65704-797. This repeat sequence is from  
XX the marker clone Mdf31 which contains the repeat sequence having the  
XX formula: (AC)13A. (Updated on 25-MAR-2003 to correct PF field.)

XX Sequence 27 BP; 14 A; 13 C; 0 G; 0 T; 0 U; 0 Other;

XX Query Match 2.1%; Score 22.2; DB 1; Length 27;

XX Best Local Similarity 88.9%; Pred. No. 42;

XX Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTGTGTGTATAT 1819

DB 27 TGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1

RESULT 18

AAH46005

ID AAH46005 standard; DNA; 27 BP.

XX AC AAH46005;

XX 12-SEP-2001 (first entry)

XX Synthetic oligonucleotide 5.

XX Synthetic oligonucleotide; dinucleotide repeat; cytostatic; apoptosis;  
KW cell cycle arrest; cell proliferation; caspase; cytokine; interleukin;  
KW tumour necrosis factor; TNF; cancer; carcinoma; sarcoma; leukemia;  
KW lymphoma; ss.

XX Synthetic.

XX WO200144465-A2.

XX 21-JUN-2001.

XX 12-DEC-2000; 2000WO-CA001467.

XX

PR 13-DEC-1999; 99US-0170325P.

PR 29-AUG-2000; 2000US-0228925P.

XX (BION-) BIONICHE LIFE SCI INC.

XX Phillips NC, Fillion MC;

XX WPI; 2001-398150/42.

XX Composition comprising synthetic oligonucleotides which comprise multiple  
XX repeats of dinucleotides such as GT, TG useful for treating cancer by  
XX inducing cell cycle arrest, inhibiting proliferation, activating  
XX caspases.

XX Example 4; Page 16; 77pp; English.

XX The present sequence is that of a synthetic oligonucleotide useful to the  
XX invention. The invention relates to a composition, comprising a 2 to 20  
XX base 3'-OH, 5'-OH synthetic oligonucleotide which comprises multiple  
XX repeats of dinucleotides such as GT, TG, etc., according to specific  
XX formula and having cytostatic activity. The oligonucleotide compositions  
XX are useful for inducing cell cycle arrest, inhibition of proliferation,  
XX activation of caspases and induction of apoptosis or production of  
XX cytokines such as interleukin (IL)-1-beta, IL-6, IL-10, IL-12 and tumour  
XX necrosis factor (TNF)-alpha by immune system cells, in an animal having  
XX cancer such as primary carcinoma, secondary carcinoma, primary sarcoma  
XX and secondary sarcoma such as, leukemia, lymphoma, breast, prostate,  
XX colorectal, ovarian or bone cancer. The compositions induce apoptosis  
XX independent of Fas, p53/p21, p21/waf-1/Cip1, p15(ink4B), p16(ink4), drug  
XX resistance, caspase 3, transforming growth factor (TGF)-beta 1 receptor  
XX and hormone dependence

XX Sequence 27 BP; 0 A; 0 C; 13 G; 14 T; 0 U; 0 Other;

XX Query Match 2.1%; Score 22.2; DB 1; Length 27;

XX Best Local Similarity 88.9%; Pred. No. 42;

XX Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTGTGTGTATAT 1819

DB 1 TGTGTGTGTGTGTGTGTGTGTGTGTGTGT 27

RESULT 19

AAAT30426/C

ID AAAT30426 standard; DNA; 22 BP.

XX AC AAAT30426;

XX 28-JAN-1997 (first entry)

XX Compound simple sequence repeat primer (CA)6.5(TA)4.5.

XX Detection; polymorphism; perfect compound simple sequence repeat;  
KW adaptor directed primer; genome; genetic; fingerprinting;  
KW amplified fragment length polymorphism assay; microsatellite region;  
KW genetic trait marking; germplasm comparisons; compound; ss.

XX Synthetic.

XX WO9617082-A2.

XX 06-JUN-1996.

XX 21-NOV-1995; 95WO-US015150.

XX 28-NOV-1994; 94US-00346456.

XX (DUPO) DU PONT DE NEMOURS & CO E I.

XX Morgante M, Vogel JM;

XX WPI; 1996-277795/28.

XX



XX Modified amplified fragment length polymorphism assay - for detection of  
PT polymorphism esp. in microsatellite regions.  
XX  
PS Disclosure; Fig 1c; 173pp; English.  
XX  
CC Detecting polymorphisms between 2 nucleic acid samples, esp. in  
CC microsatellite regions, comprises digesting the nucleic acid to generate  
CC fragments, ligating adaptor segments to their ends, amplifying them using  
CC primer directed amplification and comparing the prods. to detect  
CC differences. The primers used in the amplification comprise a primer  
CC consisting of a perfect cpd. simple sequence repeat (SSR), and an adaptor  
CC directed primer, comprising a sequence complementary to an adaptor  
CC segment. The present sequence is an example of a compound SSR primer. The  
CC method represents a modified amplified fragment length polymorphism  
CC assay, which is partic. useful for genome fingerprinting, i.e. for  
CC genetic trait marking and germplasm comparisons  
XX  
SQ Sequence 22 BP; 11 A; 6 C; 0 G; 5 T; 0 U; 0 Other;  
Query Match 2.1%; Score 22; DB 1; Length 22;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1801 TGTGTGTGTGTGTATATATA 1822  
DB 22 TGTGTGTGTGTGTATATATA 1  
RESULT 20  
AAQ33918  
ID AAQ33918 standard; DNA; 25 BP.  
AC AAQ33918;  
XX  
XX 25-MAR-2003 (revised)  
DT 02-FEB-1993 (first entry)  
XX  
DE Microsatellite sequence from clone TGLA327.  
XX  
KW PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;  
KW genetic mapping; traits; amplification; ss.  
XX  
OS Bos taurus.  
XX  
XX WO9213102-A1.  
XX  
XX 06-AUG-1992.  
XX  
XX 15-JAN-1992; 92WO-US000340.  
XX  
XX 15-JAN-1991; 91US-00642342.  
XX  
XX (GENM-) GENMARK.  
XX  
XX Georges M, Massey JW;  
XX  
XX WPI. 1992-284684/34.  
XX  
XX Polymorphic bovine DNA markers - used in genetic identification, gene  
XX mapping, and selective breeding.  
XX  
XX Table 7; Page 297; 517pp; English.  
XX  
XX The sequence is that of a bovine microsatellite sequence obtd. by  
XX screening a library of bovine MboI DNA fragments of between 250 and 500  
XX bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50  
XX clones cross-hybridised. Assuming independent distribution of  
XX microsatellites and MboI sites, the frequency of (T6)n > 9 microsatellites  
XX in the bovine genome is estimated at >100, 000. The sequence information  
XX for ca. 230 such bovine microsatellites is summarised in the  
XX specification and indexed herein (see below). The sequences upstream and  
XX downstream of the microsatellite sequence were used to generate the

CC required PCR primers for in vitro amplification of the corresp.  
CC microsatellite (using the program OPTIPRIM). The microsatellites may be  
CC used to identify individuals, for parentage testing, and in the genetic  
CC mapping of economic trait loci, or genes involved in the determination of  
CC economically important traits esp. in cattle, to allow selective  
CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN  
CC field.)  
XX  
SQ Sequence 25 BP; 0 A; 0 C; 12 G; 13 T; 0 U; 0 Other;  
Query Match 2.1%; Score 21.8; DB 1; Length 25;  
Best Local Similarity 92.0%; Pred. No. 44;  
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1793 TGTGTGTGTGTGTGTGTATAT 1817  
DB 1 TGTGTGTGTGTGTGTGTGTGTGT 25  
RESULT 21  
AAQ33642  
ID AAQ33642 standard; DNA; 25 BP.  
XX  
AC AAQ33642;  
XX  
XX 25-MAR-2003 (revised)  
DT 02-FEB-1993 (first entry)  
XX  
DE Microsatellite sequence from clone MTGT13B.  
XX  
KW PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;  
KW genetic mapping; traits; amplification; ss.  
XX  
OS Bos taurus.  
XX  
XX WO9213102-A1.  
XX  
XX 06-AUG-1992.  
XX  
XX 15-JAN-1992; 92WO-US000340.  
XX  
XX 15-JAN-1991; 91US-00642342.  
XX  
XX (GENM-) GENMARK.  
XX  
XX Georges M, Massey JM;  
XX  
XX WPI. 1992-284684/34.  
XX  
XX Polymorphic bovine DNA markers - used in genetic identification, gene  
XX mapping, and selective breeding.  
XX  
XX Table 7; Page 186; 517pp; English.  
XX  
XX The sequence is that of a bovine microsatellite sequence obtd. by  
XX screening a library of bovine MboI DNA fragments of between 250 and 500  
XX bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50  
XX clones cross-hybridised. Assuming independent distribution of  
XX microsatellites and MboI sites, the frequency of (T6)n > 9 microsatellites  
XX in the bovine genome is estimated at >100, 000. The sequence information  
XX for ca. 230 such bovine microsatellites is summarised in the  
XX specification and indexed herein (see below). The sequences upstream and  
XX downstream of the microsatellite sequence were used to generate the  
XX  
XX required PCR primers for in vitro amplification of the corresp.  
XX microsatellite (using the program OPTIPRIM). The microsatellites may be  
XX used to identify individuals, for parentage testing, and in the genetic  
XX mapping of economic trait loci, or genes involved in the determination of  
XX economically important traits esp. in cattle, to allow selective  
XX breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN  
XX field.)  
XX  
SQ Sequence 25 BP; 0 A; 0 C; 12 G; 13 T; 0 U; 0 Other;

Query Match 2.1%; Score 21.8; DB 1; Length 25;  
Best Local Similarity 92.0%; Pred. No. 44;  
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTAT 1817  
DB 1 TGTGTGTGTGTGTGTGTGTGT 25

RESULT 22  
AAQ33962  
ID AAQ33962 standard; DNA; 25 BP.  
XX AAQ33962;  
XX  
XX 25-MAR-2003 (revised)  
DT 02-FEB-1993 (first entry)  
XX  
DE Microsatellite sequence from clone TGLA354.  
XX  
XX PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;  
KW genetic mapping; traits; amplification; ss.  
XX  
XX Bos taurus.  
XX  
XX WO9213102-A1.  
XX  
XX 06-AUG-1992.  
XX  
XX 15-JAN-1992; 92WO-US000340.  
XX  
XX 15-JAN-1991; 91US-00642342.  
XX  
XX (GENM-) GENMARK.  
XX  
XX Georges M, Massey JM;  
XX  
XX WPI; 1992-284684/34.  
XX  
XX Polymorphic bovine DNA markers - used in genetic identification, gene  
PT mapping, and selective breeding.  
XX  
XX Table 7; Page 315; 517pp; English.  
XX  
XX The sequence is that of a bovine microsatellite sequence obtd. by  
CC screening a library of bovine MboI DNA fragments of between 250 and 500  
CC bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50  
CC clones cross-hybridised. Assuming independent distribution of  
CC microsatellites and MboI sites, the frequency of (16)n > 9 microsatellites  
CC in the bovine genome is estimated at >100,000. The sequence information  
CC for ca. 230 such bovine microsatellites is summarised in the  
CC specification and indexed herein (see below). The sequences upstream and  
CC downstream of the microsatellite sequence were used to generate the  
CC required PCR primers for in vitro amplification of the corresp.  
CC microsatellite (using the program OPTIPRIM). The microsatellites may be  
CC used to identify individuals, for parentage testing, and in the genetic  
CC mapping of economic trait loci, or genes involved in the determination of  
CC economically important traits esp. in cattle, to allow selective  
CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN  
CC field.)  
XX  
XX Sequence 25 BP; 0 A; 0 C; 12 G; 13 T; 0 U; 0 Other;

Query Match 2.1%; Score 21.8; DB 1; Length 25;  
Best Local Similarity 92.0%; Pred. No. 44;  
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTAT 1817  
DB 1 TGTGTGTGTGTGTGTGTGTGT 25

RESULT 23

AAAT65734/c  
ID AAAT65734 standard; DNA; 25 BP.  
XX AAAT65734;  
XX  
XX 25-MAR-2003 (revised)  
DT 17-JUN-1997 (first entry)  
XX  
XX Repeat sequence from polymorphic marker clone Mfd32.

XX Polymorphism; repeat sequence; genetic marker; primer; amplification;  
KW PCR; polymerase chain reaction; paternity; maternity; human; pedigree;  
KW linkage analysis; genetic disease; animal; plant; breeding; locus;  
KW hybridisation; chromosome; ds.  
XX  
XX Homo sapiens.  
OS  
XX US5582979-A.  
XX  
XX 10-DEC-1996.  
PD  
XX 04-APR-1994; 94US-00222177.  
PF  
XX 21-APR-1989; 89US-00341562.  
PR  
XX 05-SEP-1991; 91US-00754351.  
PR  
XX (MARS-) MARSHFIELD CLINIC.  
XX  
XX Weber JL;  
XX  
XX WPI; 1997-042299/04.  
XX  
XX Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n -  
PT using novel nucleic acid mols. as primers.  
XX  
XX Disclosure; Col 9-10; 186pp; English.  
XX  
XX The invention relates to the isolation of polymorphic repeat sequences  
CC having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic  
CC markers. Primers based on these sequences can be used to detect these  
CC repeats, especially for use in e.g. paternity or maternity testing, human  
CC genetic analysis such as linkage analysis of genetic disease, commercial  
CC animal or plant breeding or pedigree analysis. Clones containing the  
CC repeat sequences were isolated by hybridisation of chromosome-specific  
CC phage libraries with a synthetic poly(dC-dA).(dG-dT) probe. Over 100  
CC repeat blocks were isolated. The inserts from the clones were amplified  
CC by primers AAT65798-T66047. Those clones where the repeat sequence has  
CC been determined are shown in AAT65704-797. This repeat sequence is from  
CC the marker clone Maf32 which contains the repeat sequence having the  
CC formula: (AC)12A. (Updated on 25-MAR-2003 to correct PF field.)  
XX  
XX Sequence 25 BP; 13 A; 12 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 2.1%; Score 21.8; DB 1; Length 25;  
Best Local Similarity 92.0%; Pred. No. 44;  
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTAT 1817  
DB 25 TGTGTGTGTGTGTGTGTGTGT 1

RESULT 24  
AAQ34083  
ID AAQ34083 standard; DNA; 26 BP.  
XX AAQ34083;  
XX  
XX 25-MAR-2003 (revised)  
DT 02-FEB-1993 (first entry)  
XX  
XX Microsatellite sequence from clone TGLA49.  
DE  
XX

KW PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;  
 KW genetic mapping; traits; amplification; ss.  
 XX Bos taurus.

OS

XX WO9213102-A1.

XX 06-AUG-1992.

XX 15-JAN-1992; 92WO-US000340.

XX 15-JAN-1991; 91US-00642342.

XX (GENM-) GENMARK.

XX Georges M, Massey JM;

XX WPI; 1992-284684/34.

XX Polymorphic bovine DNA markers - used in genetic identification, gene  
 PT mapping, and selective breeding.  
 XX Table 7; Page 364; 517pp; English.

XX The sequence is that of a bovine microsatellite sequence obtd. by  
 CC screening a library of bovine MboI DNA fragments of between 250 and 500  
 CC bp with an (AC)<sub>15</sub> and a (TC)<sub>15</sub> oligonucleotide probe. One out of 50  
 CC clones cross-hybridised. Assuming independent distribution of  
 CC microsatellites and MboI sites, the frequency of (T6)<sub>n</sub> > 9 microsatellites  
 CC in the bovine genome is estimated at >100, 000. The sequence information  
 CC for ca. 230 such bovine microsatellites is summarised in the  
 CC specification and indexed herein (see below). The sequences upstream and  
 CC downstream of the microsatellite sequence were used to generate the  
 CC required PCR primers for in vitro amplification of the corresp.  
 CC microsatellite (using the program OPTIPRIM). The microsatellites may be  
 CC used to identify individuals, for parentage testing, and in the genetic  
 CC mapping of economic trait loci, or genes involved in the determination of  
 CC economically important traits esp. in cattle, to allow selective  
 CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN  
 CC field.)

XX SQ Sequence 26 BP; 0 A; 0 C; 13 G; 13 T; 0 U; 0 Other;  
 Query Match 2.1%; Score 21.8; DB 1; Length 26;  
 Best Local Similarity 92.0%; Pred. No. 45;  
 Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 OY 1793 TGTGTGTGTGTGTGTGTGTAT 1817  
 DB 1 TGTGTGTGTGTGTGTGTGTGTGTGT 25

RESULT 25

AAQ33684

ID AAQ33684 standard; DNA; 26 BP.

XX AAQ33684;

XX 25-MAR-2003 (revised)

DT 02-FEB-1993 (first entry)

XX Microsatellite sequence from clone TGLA123.

XX PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;  
 KW genetic mapping; traits; amplification; ss.  
 XX Bos taurus.

XX WO9213102-A1.

XX 06-AUG-1992.

XX 15-JAN-1992; 92WO-US000340.

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15-JAN-1991; 91US-00642342.

(GENM-) GENMARK.

Georges M, Massey JM;

WPI; 1992-284684/34.

Polymorphic bovine DNA markers - used in genetic identification, gene  
 mapping, and selective breeding.

Table 7; Page 203; 517pp; English.

The sequence is that of a bovine microsatellite sequence obtd. by  
 screening a library of bovine MboI DNA fragments of between 250 and 500  
 bp with an (AC)<sub>15</sub> and a (TC)<sub>15</sub> oligonucleotide probe. One out of 50  
 clones cross-hybridised. Assuming independent distribution of  
 microsatellites and MboI sites, the frequency of (T6)<sub>n</sub> > 9 microsatellites  
 in the bovine genome is estimated at >100, 000. The sequence information  
 for ca. 230 such bovine microsatellites is summarised in the  
 specification and indexed herein (see below). The sequences upstream and  
 downstream of the microsatellite sequence were used to generate the  
 required PCR primers for in vitro amplification of the corresp.  
 microsatellite (using the program OPTIPRIM). The microsatellites may be  
 used to identify individuals, for parentage testing, and in the genetic  
 mapping of economic trait loci, or genes involved in the determination of  
 economically important traits esp. in cattle, to allow selective  
 breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN  
 field.)

SQ Sequence 26 BP; 0 A; 0 C; 13 G; 13 T; 0 U; 0 Other;

Query Match 2.1%; Score 21.8; DB 1; Length 26;

Best Local Similarity 92.0%; Pred. No. 45;

Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1793 TGTGTGTGTGTGTGTGTGTAT 1817

DB 2 TGTGTGTGTGTGTGTGTGTGTGT 26

RESULT 26

AAQ33704

ID AAQ33704 standard; DNA; 26 BP.

XX AAQ33704;

XX 25-MAR-2003 (revised)

DT 02-FEB-1993 (first entry)

XX Microsatellite sequence from clone TGLA130.

XX PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;  
 KW genetic mapping; traits; amplification; ss.  
 XX Bos taurus.

XX WO9213102-A1.

XX 06-AUG-1992.

XX 15-JAN-1992; 92WO-US000340.

XX 15-JAN-1991; 91US-00642342.

XX (GENM-) GENMARK.

XX Georges M, Massey JM;

XX WPI; 1992-284684/34.

Polymorphic bovine DNA markers - used in genetic identification, gene

PT mapping, and selective breeding.  
XX Table 7; Page 211; 517pp; English.  
XX The sequence is that of a bovine microsatellite sequence obtd. by  
CC screening a library of bovine MboI DNA fragments of between 250 and 500  
CC bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50  
CC clones cross-hybridised. Assuming independent distribution of  
CC microsatellites and MboI sites, the frequency of (T6)n > 9 microsatellites  
CC in the bovine genome is estimated at >100, 000. The sequence information  
CC for ca. 230 such bovine microsatellites is summarised in the  
CC specification and indexed herein (see below). The sequences upstream and  
CC downstream of the microsatellite sequence were used to generate the  
CC required PCR primers for in vitro amplification of the corresp.  
CC microsatellite (using the program OPTIPRIM). The microsatellites may be  
CC used to identify individuals, for parentage testing, and in the genetic  
CC mapping of economic trait loci, or genes involved in the determination of  
CC economically important traits esp. in cattle, to allow selective  
CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN  
CC field.)  
XX  
SQ Sequence 26 BP; 0 A; 0 C; 13 G; 13 T; 0 U; 0 Other;  
Query Match 2.1%; Score 21.8; DB 1; Length 26;  
Best Local Similarity 92.0%; Pred. No. 45;  
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1793 TGTGTGTGTGTGTGTGTGTGTAT 1817  
DB 2 TGTGTGTGTGTGTGTGTGTGTGTGT 26  
RESULT 27  
AAQ33831  
ID AAQ33831 standard; DNA; 26 BP.  
AC AAQ33831;  
XX  
XX  
DT 25-MAR-2003 (revised)  
DT 02-FEB-1993 (first entry)  
XX  
DE Microsatellite sequence from clone TGLA231.  
XX  
XX PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;  
KW genetic mapping; traits; amplification; ss.  
KW  
XX Bos taurus.  
OS  
XX WO9213102-A1.  
PN  
XX  
XX 06-AUG-1992.  
PD  
XX 15-JAN-1992; 92WO-US000340.  
PF  
XX 15-JAN-1991; 91US-00642342.  
PR  
XX (GENM-) GENMARK.  
XX  
XX Georges M, Massey JM;  
PI  
XX WPI; 1992-284684/34.  
XX  
XX Polymorphic bovine DNA markers - used in genetic identification, gene  
PT mapping, and selective breeding.  
PT  
XX Table 7; Page 262; 517pp; English.  
XX  
XX The sequence is that of a bovine microsatellite sequence obtd. by  
CC screening a library of bovine MboI DNA fragments of between 250 and 500  
CC bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50  
CC clones cross-hybridised. Assuming independent distribution of  
CC microsatellites and MboI sites, the frequency of (T6)n > 9 microsatellites  
CC in the bovine genome is estimated at >100, 000. The sequence information

CC for ca. 230 such bovine microsatellites is summarised in the  
CC specification and indexed herein (see below). The sequences upstream and  
CC downstream of the microsatellite sequence were used to generate the  
CC required PCR primers for in vitro amplification of the corresp.  
CC microsatellite (using the program OPTIPRIM). The microsatellites may be  
CC used to identify individuals, for parentage testing, and in the genetic  
CC mapping of economic trait loci, or genes involved in the determination of  
CC economically important traits esp. in cattle, to allow selective  
CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN  
CC field.)  
XX  
SQ Sequence 26 BP; 0 A; 0 C; 13 G; 13 T; 0 U; 0 Other;  
Query Match 2.1%; Score 21.8; DB 1; Length 26;  
Best Local Similarity 92.0%; Pred. No. 45;  
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1793 TGTGTGTGTGTGTGTGTGTAT 1817  
DB 1 TGTGTGTGTGTGTGTGTGTGTGTGT 25  
RESULT 28  
AAQ33837  
ID AAQ33837 standard; DNA; 26 BP.  
AC AAQ33837;  
XX  
XX 25-MAR-2003 (revised)  
DT 02-FEB-1993 (first entry)  
XX  
DE Microsatellite sequence from clone TGLA25.  
XX  
XX PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;  
KW genetic mapping; traits; amplification; ss.  
KW  
XX Bos taurus.  
OS  
XX WO9213102-A1.  
PN  
XX  
XX 06-AUG-1992.  
PD  
XX 15-JAN-1992; 92WO-US000340.  
PF  
XX 15-JAN-1991; 91US-00642342.  
PR  
XX (GENM-) GENMARK.  
XX  
XX Georges M, Massey JM;  
PI  
XX WPI; 1992-284684/34.  
XX  
XX Polymorphic bovine DNA markers - used in genetic identification, gene  
PT mapping, and selective breeding.  
PT  
XX Table 7; Page 264; 517pp; English.  
XX  
XX The sequence is that of a bovine microsatellite sequence obtd. by  
CC screening a library of bovine MboI DNA fragments of between 250 and 500  
CC bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50  
CC clones cross-hybridised. Assuming independent distribution of  
CC microsatellites and MboI sites, the frequency of (T6)n > 9 microsatellites  
CC in the bovine genome is estimated at >100, 000. The sequence information  
CC for ca. 230 such bovine microsatellites is summarised in the  
CC specification and indexed herein (see below). The sequences upstream and  
CC downstream of the microsatellite sequence were used to generate the  
CC required PCR primers for in vitro amplification of the corresp.  
CC microsatellite (using the program OPTIPRIM). The microsatellites may be  
CC used to identify individuals, for parentage testing, and in the genetic  
CC mapping of economic trait loci, or genes involved in the determination of  
CC economically important traits esp. in cattle, to allow selective  
CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN  
CC field.)

XX SQ Sequence 26 BP; 0 A; 0 C; 13 G; 13 T; 0 U; 0 Other;  
Query Match 2.1%; Score 21.8; DB 1; Length 26;  
Best Local Similarity 92.0%; Pred. No. 45;  
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1793 TGTGTGTGTGTGTGTGTGTAT 1817  
DB 1 TGTGTGTGTGTGTGTGTGTGT 25  
RESULT 29  
ID AAO33740 standard; DNA; 27 BP.  
XX AC AAO33740;  
XX 25-MAR-2003 (revised)  
DT 02-FEB-1993 (first entry)  
XX XX  
Microsatellite sequence from clone TGLA154.  
PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;  
genetic mapping; traits; amplification; ss.  
XX OS Bos taurus.  
XX PN WO9213102-A1.  
XX PD 06-AUG-1992.  
XX PF 15-JAN-1992; 92WO-US000340.  
XX PR 15-JAN-1991; 91US-00642342.  
XX PA (GENN-) GENMARK.  
XX PI Georges M, Massey JW;  
XX DR WPI; 1992-284684/34.  
XX XX Polymorphic bovine DNA markers - used in genetic identification, gene  
PT mapping, and selective breeding.  
PS Table 7; Page 226; 517pp; English.  
XX The sequence is that of a bovine microsatellite sequence obtd. by  
XX screening a library of bovine MboI DNA fragments of between 250 and 500  
XX bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50  
XX clones cross-hybridised. Assuming independent distribution of  
XX microsatellites and MboI sites, the frequency of 1/61n > 9 microsatellites  
XX in the bovine genome is estimated at >100, 000. The sequence information  
XX for ca. 230 such bovine microsatellites is summarised in the  
XX specification and indexed herein (see below). The sequences upstream and  
XX downstream of the microsatellite sequence were used to generate the  
XX required PCR primers for in vitro amplification of the corresp.  
XX microsatellite (using the program OPTIPRIM). The microsatellites may be  
XX used to identify individuals, for parentage testing, and in the genetic  
XX mapping of economic trait loci, or genes involved in the determination of  
XX economically important traits esp. in cattle, to allow selective  
XX breeding. See also AAO33501-34437. (Updated on 25-MAR-2003 to correct PN  
XX field.)  
XX SQ Sequence 27 BP; 2 A; 0 C; 12 G; 13 T; 0 U; 0 Other;  
Query Match 2.1%; Score 21.8; DB 1; Length 27;  
Best Local Similarity 92.0%; Pred. No. 47;  
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1797 TGTGTGTGTGTGTGTGTATATAT 1821  
DB 1 TGTGTGTGTGTGTGTGTATGTGT 25

XX SQ Sequence 26 BP; 0 A; 0 C; 13 G; 13 T; 0 U; 0 Other;  
Query Match 2.1%; Score 21.8; DB 1; Length 26;  
Best Local Similarity 92.0%; Pred. No. 45;  
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1793 TGTGTGTGTGTGTGTGTGTAT 1817  
DB 1 TGTGTGTGTGTGTGTGTGTGT 25  
RESULT 29  
ID AAO33740 standard; DNA; 27 BP.  
XX AC AAO33740;  
XX 25-MAR-2003 (revised)  
DT 02-FEB-1993 (first entry)  
XX XX  
Microsatellite sequence from clone TGLA154.  
PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;  
genetic mapping; traits; amplification; ss.  
XX OS Bos taurus.  
XX PN WO9213102-A1.  
XX PD 06-AUG-1992.  
XX PF 15-JAN-1992; 92WO-US000340.  
XX PR 15-JAN-1991; 91US-00642342.  
XX PA (GENN-) GENMARK.  
XX PI Georges M, Massey JW;  
XX DR WPI; 1992-284684/34.  
XX XX Polymorphic bovine DNA markers - used in genetic identification, gene  
PT mapping, and selective breeding.  
PS Table 7; Page 226; 517pp; English.  
XX The sequence is that of a bovine microsatellite sequence obtd. by  
XX screening a library of bovine MboI DNA fragments of between 250 and 500  
XX bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50  
XX clones cross-hybridised. Assuming independent distribution of  
XX microsatellites and MboI sites, the frequency of 1/61n > 9 microsatellites  
XX in the bovine genome is estimated at >100, 000. The sequence information  
XX for ca. 230 such bovine microsatellites is summarised in the  
XX specification and indexed herein (see below). The sequences upstream and  
XX downstream of the microsatellite sequence were used to generate the  
XX required PCR primers for in vitro amplification of the corresp.  
XX microsatellite (using the program OPTIPRIM). The microsatellites may be  
XX used to identify individuals, for parentage testing, and in the genetic  
XX mapping of economic trait loci, or genes involved in the determination of  
XX economically important traits esp. in cattle, to allow selective  
XX breeding. See also AAO33501-34437. (Updated on 25-MAR-2003 to correct PN  
XX field.)  
XX SQ Sequence 27 BP; 2 A; 0 C; 12 G; 13 T; 0 U; 0 Other;  
Query Match 2.1%; Score 21.8; DB 1; Length 27;  
Best Local Similarity 92.0%; Pred. No. 47;  
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1797 TGTGTGTGTGTGTGTGTATATAT 1821  
DB 1 TGTGTGTGTGTGTGTGTATGTGT 25

RESULT 30  
AAQ83951/C  
ID AAQ83951 standard; DNA; 27 BP.  
XX AC AAQ83951;  
XX 25-MAR-2003 (revised)  
DT 04-OCT-1995 (first entry)  
XX XX  
Oligonucleotide clamp 1, containing loop-and-branch forming region.  
XX KW HIV; pol; nef; oligonucleotide clamp; branched; macromolecule; ss.  
XX OS Synthetic.  
XX FH Key Location/Qualifiers  
FT modified\_base 1 /\*tag= a  
FT /\*note= "Modified with SP(O-)(=O)-"  
FT modified\_base 27 /\*tag= b  
FT /\*note= "Modified with -OP(O-)(=O)S"  
XX PN WO9501365-A1.  
XX PD 12-JAN-1995..  
XX PF 05-JUL-1994; 94WO-US007557.  
XX PR 02-JUL-1993; 93US-00087386.  
XX PA (LYNX-) LYNX THERAPEUTICS INC.  
XX PI Grynazov SM;  
XX DR WPI; 1995-060944/08.  
XX XX Synthesis of branched polymers and novel branched polymeric structures -  
PT used as molecular probes esp. for detecting poly-nucleotide (S).  
XX PS Example 7; Page 33; 52pp; English.  
XX This sequence represents an oligonucleotide clamp which was used to bind  
XX a target sequence comprising a segment of the HIV pol and nef genes in  
XX single stranded or double stranded forms. This molecule forms a loop-and-  
XX branch configuration. An oligonucleotide clamp is a compound capable of  
XX forming a covalently closed macromolecule or a stable circular complex  
XX after specifically binding to the target polynucleotide. Oligonucleotide  
XX clamps generally comprise one or more oligonucleotide moieties capable of  
XX specific binding to the target molecule and one or more pairs of binding  
XX moieties covalently linked to the oligonucleotide moieties. Upon  
XX annealing of the oligonucleotides moieties to the target polynucleotide,  
XX the binding moieties of a pair are brought into juxtaposition so that they  
XX form a stable covalent or non-covalent linkage or complex. The  
XX interaction of the binding moieties effectively clamps the specifically  
XX annealed oligonucleotide moieties to the target polynucleotide. (Updated  
XX on 25-MAR-2003 to correct PN field.)  
XX SQ Sequence 27 BP; 13 A; 14 C; 0 G; 0 T; 0 U; 0 Other;  
Query Match 2.1%; Score 21.8; DB 1; Length 27;  
Best Local Similarity 92.0%; Pred. No. 47;  
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1793 TGTGTGTGTGTGTGTGTGTATAT 1817  
DB 26 TGTGTGTGTGTGTGTGTGTGTGT 2  
RESULT 31  
AAH24300



KW tumour necrosis factor; TNF; cancer; carcinoma; sarcoma; leukemia;  
 KW lymphoma; ss.

OS Synthetic.

PN WO200144465-A2.

XX 21-JUN-2001.

XX 12-DEC-2000; 2000WO-CA001467.

XX 13-DEC-1999; 99US-0170325P.

PR 29-AUG-2000; 2000US-0228925P.

XX (BION-) BIONICHE LIFE SCI INC.

XX Phillips NC, Fillion MC;

XX WPI; 2001-398150/42.

XX Composition comprising synthetic oligonucleotides which comprise multiple  
 PT repeats of dinucleotides such as GT, TG useful for treating cancer by  
 PT inducing cell cycle arrest, inhibiting proliferation, activating  
 PT caspases.

XX Example 4; Page 16; 77pp; English.

XX The present sequence is that of a synthetic oligonucleotide useful to the  
 CC invention. The invention relates to a composition, comprising a 2 to 20  
 CC base 3'-OH, 5'-OH synthetic oligonucleotide which comprises multiple  
 CC repeats of dinucleotides such as GT, TG, etc., according to specific  
 CC formula and having cytostatic activity. The oligonucleotide compositions  
 CC are useful for inducing cell cycle arrest, inhibition of proliferation,  
 CC activation of caspases and induction of apoptosis or production of  
 CC cytokines such as interleukin (IL)-1-beta, IL-6, IL-10, IL-12 and tumour  
 CC necrosis factor (TNF)-alpha by immune system cells, in an animal having  
 CC cancer such as primary carcinoma, secondary carcinoma, primary sarcoma  
 CC and secondary sarcoma such as, leukemia, lymphoma, breast, prostate,  
 CC colorectal, ovarian or bone cancer. The compositions induce apoptosis  
 CC independent of Fas, p53/p21, p21/waf-1/Cip, p15(ink4B), p16(ink4), drug  
 CC resistance, caspase 3, transforming growth factor (TGF)-beta 1 receptor  
 CC and hormone dependence

XX Sequence 27 BP; 0 A; 0 C; 14 G; 13 T; 0 U; 0 Other;

Query Match 2.1%; Score 21.8; DB 1; Length 27;  
 Best Local Similarity 92.0%; Pred. No. 47;  
 Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTGTATAT 1817

Db 2 TGTGTGTGTGTGTGTGTGTGTGTGT 26

RESULT 34

AAF60473/c

ID AAF60473 standard; DNA; 27 BP.

XX AC

XX AAF60473;

XX 27-APR-2001 (first entry)

XX Oligonucleotide clamp #19.

XX Oligonucleotide clamp; ds.

XX Unidentified.

XX US6180777-B1.

XX 30-JAN-2001.

XX 03-JAN-1997; 97US-00787321.

XX 12-JAN-1996; 96US-0009918P.

XX (FARB ) BAYER CORP.

XX Horn T;

XX WPI; 2001-201911/20.

XX Synthesizing branched nucleic acids useful as diagnostic and molecular  
 PT probes, involves combining first units having haloalkylamino groups and  
 PT second units having thiol or phosphorothioate groups.

XX Disclosure; Col 29-30; 20pp; English.

XX The present invention relates to a method for synthesising a branched or  
 CC multiply connected macromolecular structure, comprising oligonucleotide  
 CC clamps (OC). The macromolecular structure is capable of specifically  
 CC binding to a target molecule, and can therefore be used as probes. At  
 CC least one OC comprises a target binding sequence that binds specifically  
 CC and stably with the target molecule, and at least two OCs comprise signal  
 CC generation moieties capable of generating a detectable signal in the  
 CC presence of the target molecule. In addition the OCs are connected to one  
 CC another by thioalkylamino, or thiophosphorylalkylamino bridges. The  
 CC present sequence is an OC used in the present invention

XX Sequence 27 BP; 13 A; 14 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 2.1%; Score 21.8; DB 1; Length 27;  
 Best Local Similarity 92.0%; Pred. No. 47;  
 Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTATAT 1817

Db 26 TGTGTGTGTGTGTGTGTGTGTGTGT 2

RESULT 35

AAQ33663

ID AAQ33663 standard; DNA; 23 BP.

XX AC AAQ33663;

XX 25-MAR-2003 (revised)

DT 02-FEB-1993 (first entry)

XX Microsatellite sequence from clone TGLA110.

XX PCR; selection; primers; Optiprimer; breeding; cattle; parentage;

XX genetic mapping; traits; amplification; ss.

XX Bos taurus.

XX WO9213102-A1.

XX 06-AUG-1992.

XX 15-JAN-1992; 92WO-US000340.

XX 15-JAN-1991; 91US-00642342.

XX (GENM-) GENMARK.

XX Georges M, Massey JM;

XX WPI; 1992-284684/34.

XX Polymorphic bovine DNA markers - used in genetic identification, gene  
 PT mapping, and selective breeding.

XX Table 7; Page 195; 517pp; English.

XX The sequence is that of a bovine microsatellite sequence obtd. by

CC screening a library of bovine MboI DNA fragments of between 250 and 500  
 CC bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50  
 CC clones cross-hybridised. Assuming independent distribution of  
 CC microsatellites and MboI sites, the frequency of (76)n > 9 microsatellites  
 CC in the bovine genome is estimated at >100, 000. The sequence information  
 CC for ca. 230 such bovine microsatellites is summarised in the  
 CC specification and indexed herein (see below). The sequences upstream and  
 CC downstream of the microsatellite sequence were used to generate the  
 CC required PCR primers for in vitro amplification of the corresp.  
 CC microsatellite (using the program OPTIPRIM). The microsatellites may be  
 CC used to identify individuals, for parentage testing, and in the genetic  
 CC mapping of economic trait loci, or genes involved in the determination of  
 CC economically important traits esp. in cattle, to allow selective  
 CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN  
 CC field.)

XX  
 SQ Sequence 23 BP; 0 A; 0 C; 11 G; 12 T; 0 U; 0 Other;  
 Query Match 2.0%; Score 21.4; DB 1; Length 23;  
 Best Local Similarity 95.7%; Pred. No. 46;  
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTAT 1815  
 |||||  
 DB 1 TGTGTGTGTGTGTGTGTGT 23

## RESULT 36

AAQ33773  
 ID AAQ33773 standard; DNA; 23 BP.

XX  
 AC AAQ33773;

XX 25-MAR-2003 (revised)

DT 02-FEB-1993 (first entry)

DE Microsatellite sequence from clone TGLA176.

XX PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;

KW genetic mapping; traits; amplification; ss.

XX Bos taurus.

XX WO9213102-A1.

XX 06-AUG-1992.

XX 15-JAN-1992; 92WO-US000340.

XX 15-JAN-1991; 91US-00642342.

XX (GENM-) GENMARK.

XX Georges M, Massey JM;

XX WPI; 1992-284684/34.

XX Polymorphic bovine DNA markers - used in genetic identification, gene  
 mapping, and selective breeding.

XX Table 7; Page 239; 517pp; English.

XX The sequence is that of a bovine microsatellite sequence obtd. by  
 CC screening a library of bovine MboI DNA fragments of between 250 and 500  
 CC bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50  
 CC clones cross-hybridised. Assuming independent distribution of  
 CC microsatellites and MboI sites, the frequency of (76)n > 9 microsatellites  
 CC in the bovine genome is estimated at >100, 000. The sequence information  
 CC for ca. 230 such bovine microsatellites is summarised in the  
 CC specification and indexed herein (see below). The sequences upstream and  
 CC downstream of the microsatellite sequence were used to generate the  
 CC required PCR primers for in vitro amplification of the corresp.  
 CC microsatellite (using the program OPTIPRIM). The microsatellites may be

CC used to identify individuals, for parentage testing, and in the genetic  
 CC mapping of economic trait loci, or genes involved in the determination of  
 CC economically important traits esp. in cattle, to allow selective  
 CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN  
 CC field.)

XX Sequence 23 BP; 0 A; 0 C; 11 G; 12 T; 0 U; 0 Other;

Query Match 2.0%; Score 21.4; DB 1; Length 23;

Best Local Similarity 95.7%; Pred. No. 46;

Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTAT 1815

|||||  
 DB 1 TGTGTGTGTGTGTGTGTGT 23

## RESULT 37

AAQ33885

ID AAQ33885 standard; DNA; 23 BP.

XX AAQ33885;

XX 25-MAR-2003 (revised)

DT 02-FEB-1993 (first entry)

XX Microsatellite sequence from clone TGLA304.

XX PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;

KW genetic mapping; traits; amplification; ss.

XX Bos taurus.

XX WO9213102-A1.

XX 06-AUG-1992.

XX 15-JAN-1992; 92WO-US000340.

XX 15-JAN-1991; 91US-00642342.

XX (GENM-) GENMARK.

XX Georges M, Massey JM;

XX WPI; 1992-284684/34.

XX Polymorphic bovine DNA markers - used in genetic identification, gene  
 mapping, and selective breeding.

XX Table 7; Page 283; 517pp; English.

XX The sequence is that of a bovine microsatellite sequence obtd. by  
 CC screening a library of bovine MboI DNA fragments of between 250 and 500  
 CC bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50  
 CC clones cross-hybridised. Assuming independent distribution of  
 CC microsatellites and MboI sites, the frequency of (76)n > 9 microsatellites  
 CC in the bovine genome is estimated at >100, 000. The sequence information  
 CC for ca. 230 such bovine microsatellites is summarised in the  
 CC specification and indexed herein (see below). The sequences upstream and  
 CC downstream of the microsatellite sequence were used to generate the  
 CC required PCR primers for in vitro amplification of the corresp.  
 CC microsatellite (using the program OPTIPRIM). The microsatellites may be  
 CC used to identify individuals, for parentage testing, and in the genetic  
 CC mapping of economic trait loci, or genes involved in the determination of  
 CC economically important traits esp. in cattle, to allow selective  
 CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN  
 CC field.)

XX Sequence 23 BP; 0 A; 0 C; 11 G; 12 T; 0 U; 0 Other;

Query Match 2.0%; Score 21.4; DB 1; Length 23;

Best Local Similarity 95.7%; Pred. No. 46;



DT	14-AUG-2001	(first entry)
DE		
DE	SNP specific upper PCR primer SEQ ID 1801.	
XX		
XX	Single nucleotide polymorphism; SNP; single nucleotide primer extension;	
XX	SNPE; genotyping; agammaglobulinemia; diabetes insipidus; cancer;	
KW	Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;	
KW	polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;	
KW	acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;	
KW	inflammation; forensic investigation; paternity analysis; PCR primer; sa.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200129262-A2.	
XX		
PD	26-APR-2001.	
XX		
PF	13-OCT-2000; 2000WO-US028436.	
XX		
PR	15-OCT-1999; 99US-0160096P.	
XX		
PA	(ORCH-) ORCHID BIOSCIENCES INC.	
XX		
PI	Picoult-Newburg L, Pohl M;	
XX		
DR	WPI; 2001-290930/30.	
XX		
PT	New genotyping oligonucleotide, useful for detecting the presence,	
PT	absence or identity of single polynucleotide polymorphism in a nucleic	
PT	acid sample.	
XX		
PS	Claim 1; Page 59; 83pp; English.	
XX		
XX	Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide	
CC	primer extension (SNPE) primers, and the sequences of regions flanking	
CC	sites of single nucleotide polymorphisms SNPs. The present invention	
CC	includes kits for determining the presence or absence of a SNP, using the	
CC	oligonucleotides of the invention. the PCR primers are used to amplify a	
CC	SNP flanking sequence, the SNPE primer is used as a genotyping primer.	
CC	The oligonucleotides are useful for genotyping a nucleic acid sample by	
CC	performing a single-nucleotide primer extension reaction. The	
CC	oligonucleotides are useful for determining the presence, absence or	
CC	identity of a SNP and for genotyping nucleic acid samples, for e.g. to	
CC	assess by association analysis the genotype of an individual or group of	
CC	individuals, having a pathological phenotypic trait suspected of being	
CC	caused by one or more SNPs. Phenotypic traits include diseases e.g.	
CC	agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular	
CC	dystrophy, familial hypercholesterolaemia, polycystic kidney disease,	
CC	osteogenesis imperfecta and acute intermittent porphyria. Phenotypic	
CC	traits also include symptoms of or susceptibility to multifactorial	
CC	disease of which a component is or may be genetic such as autoimmune	
CC	diseases, including, rheumatoid arthritis, multiple sclerosis,	
CC	inflammation, cancer, nervous system diseases and infection by pathogenic	
CC	microorganism. The method is also useful in forensic investigations and	
CC	paternity analysis. The present sequence represents a PCR primer specific	
CC	for a human SNP containing DNA sequence	
XX		

	Query Match	2.0%;	Score 21.4;	DB 1;	Length 23;.
	Best Local Similarity	95.7%;	Pred. NO. 46;		
	Matches 22;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
QY	1790	TATTGTGCTGTGTGTGTG	1812		
Dd	1	TTTGTGTGTGTGTGTGTG	23		
	RESULT 40				
	AAQ33986				
	ID AAQ33986 standard; DNA; 24 BP.				
	XX				
	AC AAQ33986;				

```

XX 25-MAR-2003 (revised)
DT 02-FEB-1993 (first entry)
XX
XX Microsatellite sequence from clone TGLA382.
XX
XX PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
KW genetic mapping; traits; amplification; ss.
XX
XX Bos taurus.
OS
XX WO9213102-A1.
XX
XX 06-AUG-1992.
XX
XX 15-JAN-1992; 92WO-US000340.
XX
XX 15-JAN-1991; 91US-00642342.
XX
XX (GENM-) GENMARK.
XX
XX Georges M, Massey JM;
PI
XX WPI; 1992-284684/34.
XX
XX Polymorphic bovine DNA markers - used in genetic identification, gene
PT mapping, and selective breeding.
XX
XX Table 7; Page 324; 517pp; English.
XX
XX The sequence is that of a bovine microsatellite sequence obtd. by
CC screening a library of bovine MboI DNA fragments of between 250 and 500
CC bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
CC clones cross-hybridised. Assuming independent distribution of
CC microsatellites and MboI sites, the frequency of (T6)n > 9 microsatellites
CC in the bovine genome is estimated at >100,000. The sequence information
CC for ca. 230 such bovine microsatellites is summarised in the
CC specification and indexed herein (see below). The sequences upstream and
CC downstream of the microsatellite sequence were used to generate the
CC required PCR primers for in vitro amplification of the corresp.
CC microsatellite (using the program OPTIPRIM). The microsatellites may be
CC used to identify individuals, for parentage testing, and in the genetic
CC mapping of economic trait loci, or genes involved the determinism of
CC economically important traits esp. in cattle, to allow selective
CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
XX Sequence 24 BP; 0 A; 0 C; 12 G; 12 T; 0 U; 0 Other;
SQ
Query Match 2.0%; Score 21.4; DB 1; Length 24;
Best Local Similarity 95.7%; Pred. No. 47;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTAT 1815
DB 2 TGTGTGTGTGTGTGTGTGTGT 24

RESULT 41
AAQ341158
ID AAQ341158 standard; DNA; 24 BP.
XX
XX AAQ341158;
XX
XX 25-MAR-2003 (revised)
DT 02-FEB-1993 (first entry)
XX
XX Sequence of a microsatellite from clone TGLA80.
DE
XX PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
KW genetic mapping; traits; amplification; ss.
XX
XX Bos taurus.
OS

```

```

XX WO9213102-A1.
XX
XX 06-AUG-1992.
XX
XX 15-JAN-1992; 92WO-US000340.
XX
XX 15-JAN-1991; 91US-00642342.
XX
XX (GENM-) GENMARK.
XX
XX Georges M, Massey JM;
PI
XX WPI; 1992-284684/34.
XX
XX Polymorphic bovine DNA markers - used in genetic identification, gene
PT mapping, and selective breeding.
XX
XX Table 7; Page 394; 517pp; English.
XX
XX The sequence is that of a bovine microsatellite sequence obtd. by
CC screening a library of bovine MboI DNA fragments of between 250 and 500
CC bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
CC clones cross-hybridised. Assuming independent distribution of
CC microsatellites and MboI sites, the frequency of (T6)n > 9 microsatellites
CC in the bovine genome is estimated at >100,000. The sequence information
CC for ca. 230 such bovine microsatellites is summarised in the
CC specification and indexed herein (see below). The sequences upstream and
CC downstream of the microsatellite sequence were used to generate the
CC required PCR primers for in vitro amplification of the corresp.
CC microsatellite (using the program OPTIPRIM). The microsatellites may be
CC used to identify individuals, for parentage testing, and in the genetic
CC mapping of economic trait loci, or genes involved the determinism of
CC economically important traits esp. in cattle, to allow selective
CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
XX Sequence 24 BP; 0 A; 0 C; 12 G; 12 T; 0 U; 0 Other;
SQ
Query Match 2.0%; Score 21.4; DB 1; Length 24;
Best Local Similarity 95.7%; Pred. No. 47;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTAT 1815
DB 1 TGTGTGTGTGTGTGTGTGTGT 23

RESULT 42
AAQ33909
ID AAQ33909 standard; DNA; 24 BP.
XX
XX AAQ33909;
XX
XX 25-MAR-2003 (revised)
DT 02-FEB-1993 (first entry)
XX
XX Microsatellite sequence from clone TGLA322.
DE
XX PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
KW genetic mapping; traits; amplification; ss.
XX
XX Bos taurus.
OS
XX WO9213102-A1.
XX
XX 06-AUG-1992.
XX
XX 15-JAN-1992; 92WO-US000340.
XX
XX 15-JAN-1991; 91US-00642342.
XX
XX (GENM-) GENMARK.
XX

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XX Georges M, Massey JM;  
PI WPI; 1992-284684/34.  
XX Polymorphic bovine DNA markers - used in genetic identification, gene  
PT mapping, and selective breeding.  
XX Table 7; Page 293; 517pp; English.  
XX The sequence is that of a bovine microsatellite sequence obtd. by  
CC screening a library of bovine MboI DNA fragments of between 250 and 500  
CC bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50  
CC clones cross-hybridised. Assuming independent distribution of  
CC microsatellites and MboI sites, the frequency of (T6)n > 9 microsatellites  
CC in the bovine genome is estimated at >100, 000. The sequence information  
CC for ca. 230 such bovine microsatellites is summarised in the  
CC specification and indexed herein (see below). The sequences upstream and  
CC downstream of the microsatellite sequence were used to generate the  
CC required PCR primers for in vitro amplification of the corresp.  
CC microsatellite (using the program OPTIPRIM). The microsatellites may be  
CC used to identify individuals, for parentage testing, and in the genetic  
CC mapping of economic trait loci, or genes involved in the determination of  
CC economically important traits esp. in cattle, to allow selective  
CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN  
CC field.)  
XX SQ Sequence 24 BP; 0 A; 0 C; 12 G; 12 T; 0 U; 0 Other;  
Query Match 2.0%; Score 21.4; DB 1; Length 24;  
Best Local Similarity 95.7%; Pred. No. 47;  
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1793 TGTGTGTGTGTGTGTGTGTAT 1815  
DB 2 TGTGTGTGTGTGTGTGTGTGT 24  
RESULT 43  
AAQ34065  
ID AAQ34065 standard; DNA; 24 BP.  
XX AC AAQ34065;  
XX 25-MAR-2003 (revised)  
DT 02-FEB-1993 (first entry)  
XX Microsatellite sequence from clone TGLA444.  
XX PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;  
XX genetic mapping; traits; amplification; ss.  
XX Bos taurus.  
XX WO9213102-A1.  
XX 06-AUG-1992.  
XX 15-JAN-1992; 92WO-US000340.  
XX 15-JAN-1991; 91US-00642342.  
XX (GENM-) GENMARK.  
XX Georges M, Massey JM;  
XX WPI; 1992-284684/34.  
XX Polymorphic bovine DNA markers - used in genetic identification, gene  
PT mapping, and selective breeding.  
XX Table 7; Page 357; 517pp; English.

CC The sequence is that of a bovine microsatellite sequence obtd. by  
CC screening a library of bovine MboI DNA fragments of between 250 and 500  
CC bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50  
CC clones cross-hybridised. Assuming independent distribution of  
CC microsatellites and MboI sites, the frequency of (T6)n > 9 microsatellites  
CC in the bovine genome is estimated at >100, 000. The sequence information  
CC for ca. 230 such bovine microsatellites is summarised in the  
CC specification and indexed herein (see below). The sequences upstream and  
CC downstream of the microsatellite sequence were used to generate the  
CC required PCR primers for in vitro amplification of the corresp.  
CC microsatellite (using the program OPTIPRIM). The microsatellites may be  
CC used to identify individuals, for parentage testing, and in the genetic  
CC mapping of economic trait loci, or genes involved in the determination of  
CC economically important traits esp. in cattle, to allow selective  
CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN  
CC field.)  
XX SQ Sequence 24 BP; 0 A; 0 C; 12 G; 12 T; 0 U; 0 Other;  
Query Match 2.0%; Score 21.4; DB 1; Length 24;  
Best Local Similarity 95.7%; Pred. No. 47;  
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1793 TGTGTGTGTGTGTGTGTGTAT 1815  
DB 2 TGTGTGTGTGTGTGTGTGTGT 24  
RESULT 44  
AAQ34024  
ID AAQ34024 standard; DNA; 24 BP.  
XX AC AAQ34024;  
XX 25-MAR-2003 (revised)  
DT 02-FEB-1993 (first entry)  
XX Microsatellite sequence from clone TGLA423.  
XX PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;  
XX genetic mapping; traits; amplification; ss.  
XX Bos taurus.  
XX WO9213102-A1.  
XX 06-AUG-1992.  
XX 15-JAN-1992; 92WO-US000340.  
XX 15-JAN-1991; 91US-00642342.  
XX (GENM-) GENMARK.  
XX Georges M, Massey JM;  
XX WPI; 1992-284684/34.  
XX Polymorphic bovine DNA markers - used in genetic identification, gene  
PT mapping, and selective breeding.  
XX Table 7; Page 340; 517pp; English.  
XX The sequence is that of a bovine microsatellite sequence obtd. by  
CC screening a library of bovine MboI DNA fragments of between 250 and 500  
CC bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50  
CC clones cross-hybridised. Assuming independent distribution of  
CC microsatellites and MboI sites, the frequency of (T6)n > 9 microsatellites  
CC in the bovine genome is estimated at >100, 000. The sequence information  
CC for ca. 230 such bovine microsatellites is summarised in the  
CC specification and indexed herein (see below). The sequences upstream and  
CC downstream of the microsatellite sequence were used to generate the  
CC required PCR primers for in vitro amplification of the corresp.

CC microsatellite (using the program OPTIPRIM). The microsatellites may be  
CC used to identify individuals, for parentage testing, and in the genetic  
CC mapping of economic trait loci, or genes involved in the determination of  
CC economically important traits esp. in cattle, to allow selective  
CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN  
CC field.)  
XX  
SQ Sequence 24 BP; 0 A; 0 C; 12 G; 12 T; 0 U; 0 Other;

Query Match 2.0%; Score 21.4; DB 1; Length 24;  
Best Local Similarity 95.7%; Pred. No. 47;  
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1793 TGTGTGTGTGTGTGTGTGTAT 1815  
Db 1 TGTGTGTGTGTGTGTGTGTGTGTGT 23

RESULT 45  
AAQ33707  
ID AAQ33707 standard; DNA; 24 BP.  
XX  
AC AAQ33707;  
DT 25-MAR-2003 (revised)  
DT 02-FEB-1993 (first entry)  
XX  
DE Microsatellite sequence from clone TGLA131.  
XX  
KW PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;  
KW genetic mapping; traits; amplification; ss.  
XX  
OS Bos taurus.  
XX  
FN WO9213102-A1.  
XX  
PD 06-AUG-1992.  
XX  
PF 15-JAN-1992; 92WO-US000340.  
XX  
PR 15-JAN-1991; 91US-00642342.  
XX  
PA (GENM-) GENMARK.  
XX  
PI Georges M, Massey JM;  
XX  
XX WPI; 1992-284684/34.

XX Polymorphic bovine DNA markers - used in genetic identification, gene  
XX mapping, and selective breeding.  
XX  
XX Table 7; Page 213; 517pp; English.  
XX  
XX The sequence is that of a bovine microsatellite sequence obtd. by  
XX screening a library of bovine MboI DNA fragments of between 250 and 500  
XX bp with an (AC)<sub>15</sub> and a (TC)<sub>15</sub> oligonucleotide probe. One out of 50  
XX clones cross-hybridised. Assuming independent distribution of  
XX microsatellites and MboI sites, the frequency of (TC)<sub>n</sub> > 9 microsatellites  
XX in the bovine genome is estimated at >100,000. The sequence information  
XX for ca. 230 such bovine microsatellites is summarised in the  
XX specification and indexed herein (see below). The sequences upstream and  
XX downstream of the microsatellite sequence were used to generate the  
XX required PCR primers for in vitro amplification of the corresp.  
XX microsatellite (using the program OPTIPRIM). The microsatellites may be  
XX used to identify individuals, for parentage testing, and in the genetic  
XX mapping of economic trait loci, or genes involved in the determination of  
XX economically important traits esp. in cattle, to allow selective  
XX breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN  
XX field.)  
SQ Sequence 24 BP; 0 A; 0 C; 12 G; 12 T; 0 U; 0 Other;

Query Match 2.0%; Score 21.4; DB 1; Length 24;  
Best Local Similarity 95.7%; Pred. No. 47;  
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1793 TGTGTGTGTGTGTGTGTGTAT 1815  
Db 1 TGTGTGTGTGTGTGTGTGTGTGTGT 23

Best Local Similarity 95.7%; Pred. No. 47;  
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1793 TGTGTGTGTGTGTGTGTGTAT 1815  
Db 1 TGTGTGTGTGTGTGTGTGTGTGTGT 23

RESULT 46  
AAT66096/c  
ID AAT66096 standard; DNA; 24 BP.  
XX  
AC AAT66096;  
DT 25-MAR-2003 (revised)  
DT 18-JUN-1997 (first entry)  
XX  
DE Repeat sequence found in the human chromosomal clone JW42.

XX Polymorphism; repeat sequence; genetic marker; primer; amplification;  
KW PCR; polymerase chain reaction; paternity; maternity; human; pedigree;  
KW linkage analysis; genetic disease; animal; plant; breeding; locus;  
KW hybridisation; chromosome; ds.  
XX  
OS Homo sapiens.  
XX  
FN US5582979-A.  
XX  
PD 10-DEC-1996.  
XX  
PF 04-APR-1994; 94US-00222177.  
XX  
PR 21-APR-1989; 89US-00341562.  
PR 05-SEP-1991; 91US-00754351.  
XX  
PA (MARS-) MARSHFIELD CLINIC.  
XX  
PI Weber JL;  
XX  
XX WPI; 1997-042299/04.

XX Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n -  
XX using novel nucleic acid mols. as primers.  
XX  
XX Example 9; Col 61-62; 186pp; English.  
XX  
XX The invention relates to the isolation of polymorphic repeat sequences  
XX having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic  
XX markers. Primers based on these sequences can be used to detect these  
XX repeats, especially for use in e.g. paternity or maternity testing, human  
XX genetic analysis such as linkage analysis of genetic diseases, commercial  
XX animal or plant breeding or pedigree analysis. The sequences AAT66084-  
XX T66107 represent repeat sequences of low informativeness found in  
XX specific human genes. This repeat sequence is found in the human  
XX chromosomal clone JW42. The sequence is amplified by primers AAT66097-8.  
XX (Updated on 25-MAR-2003 to correct PF field.)  
SQ Sequence 24 BP; 12 A; 12 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 2.0%; Score 21.4; DB 1; Length 24;  
Best Local Similarity 95.7%; Pred. No. 47;  
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1793 TGTGTGTGTGTGTGTGTGTAT 1815  
Db 24 TGTGTGTGTGTGTGTGTGTGTGTGT 2

XX 12-SEP-2001 (first entry)  
 XX  
 DE Synthetic oligonucleotide 15.  
 XX  
 KW Synthetic oligonucleotide; dinucleotide repeat; cytostatic; apoptosis;  
 KW cell cycle arrest; cell proliferation; caspase; cytokine; interleukin;  
 KW tumour necrosis factor; TNF; cancer; carcinoma; sarcoma; leukemia;  
 XX lymphoma; ss.  
 XX  
 OS Synthetic.  
 XX  
 OS WO200144465-A2.  
 XX  
 PN 21-JUN-2001.  
 XX  
 PD 12-DEC-2000; 2000WO-CA001467.  
 XX  
 PF 13-DEC-1999; 99US-0170325P.  
 XX  
 PR 29-AUG-2000; 2000US-0228925P.  
 XX  
 XX (BION-) BIONICHE LIFE SCI INC.  
 PA  
 XX Phillips NC, Fillion MC;  
 PI  
 XX WPI; 2001-398150/42.  
 XX  
 XX Composition comprising synthetic oligonucleotides which comprise multiple  
 XX repeats of dinucleotides such as GT, TG useful for treating cancer by  
 XX inducing cell cycle arrest, inhibiting proliferation, activating  
 XX caspases.  
 XX  
 XX Example 4; Page 17; 77pp; English.  
 PS  
 XX The present sequence is that of a synthetic oligonucleotide useful to the  
 XX invention. The invention relates to a composition, comprising a 2 to 20  
 XX base 3'-OH, 5'-OH synthetic oligonucleotide which comprises multiple  
 XX repeats of dinucleotides such as GT, TG, etc., according to specific  
 XX formula and having cytostatic activity. The oligonucleotide compositions  
 XX are useful for inducing cell cycle arrest, inhibition of proliferation,  
 XX activation of caspases and induction of apoptosis or production of  
 XX cytokines such as interleukin (IL)-1-beta, IL-6, IL-10, IL-12 and tumour  
 XX necrosis factor (TNF)-alpha by immune system cells, in an animal having  
 XX cancer such as primary carcinoma, secondary carcinoma, primary sarcoma  
 XX and secondary sarcoma such as, leukemia, lymphoma, breast, prostate,  
 XX colorectal, ovarian or bone cancer. The compositions induce apoptosis  
 XX independent of Fas, p53/p21, p21/waf-1/CIP, p15(ink4b), p16(ink4), drug  
 XX resistance, caspase 3, transforming growth factor (TGF)-beta 1 receptor  
 XX and hormone dependence  
 XX  
 SQ Sequence 24 BP; 0 A; 0 C; 12 G; 12 T; 0 U; 0 Other;  
 XX  
 XX Query Match 2.0%; Score 21.4; DB 1; Length 24;  
 XX Best Local Similarity 95.7%; Pred. No. 47;  
 XX Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 XX  
 QY 1793 TGTGTGTGTGTGTGTGTGTAT 1815  
 Db 1 TGTGTGTGTGTGTGTGTGTGTGT 23  
 XX  
 XX RESULT 48  
 XX AAH46016  
 ID AAH46016 standard; DNA; 24 BP.  
 XX  
 XX AAH46016;  
 AC  
 XX 12-SEP-2001 (first entry)  
 DT  
 XX Synthetic oligonucleotide 16.  
 DE  
 XX Synthetic oligonucleotide; dinucleotide repeat; cytostatic; apoptosis;  
 KW cell cycle arrest; cell proliferation; caspase; cytokine; interleukin;

KW tumour necrosis factor; TNF; cancer; carcinoma; sarcoma; leukemia;  
 KW lymphoma; ss.  
 XX  
 OS Synthetic.  
 XX  
 OS WO200144465-A2.  
 XX  
 PN 21-JUN-2001.  
 XX  
 PD 12-DEC-2000; 2000WO-CA001467.  
 XX  
 PF 13-DEC-1999; 99US-0170325P.  
 XX  
 PR 29-AUG-2000; 2000US-0228925P.  
 XX  
 XX (BION-) BIONICHE LIFE SCI INC.  
 PA  
 XX Phillips NC, Fillion MC;  
 PI  
 XX WPI; 2001-398150/42.  
 XX  
 XX Composition comprising synthetic oligonucleotides which comprise multiple  
 XX repeats of dinucleotides such as GT, TG useful for treating cancer by  
 XX inducing cell cycle arrest, inhibiting proliferation, activating  
 XX caspases.  
 XX  
 XX Claim 6; Page 17; 77pp; English.  
 PS  
 XX The present sequence is that of a synthetic oligonucleotide useful to the  
 XX invention. The invention relates to a composition, comprising a 2 to 20  
 XX base 3'-OH, 5'-OH synthetic oligonucleotide which comprises multiple  
 XX repeats of dinucleotides such as GT, TG, etc., according to specific  
 XX formula and having cytostatic activity. The oligonucleotide compositions  
 XX are useful for inducing cell cycle arrest, inhibition of proliferation,  
 XX activation of caspases and induction of apoptosis or production of  
 XX cytokines such as interleukin (IL)-1-beta, IL-6, IL-10, IL-12 and tumour  
 XX necrosis factor (TNF)-alpha by immune system cells, in an animal having  
 XX cancer such as primary carcinoma, secondary carcinoma, primary sarcoma  
 XX and secondary sarcoma such as, leukemia, lymphoma, breast, prostate,  
 XX colorectal, ovarian or bone cancer. The compositions induce apoptosis  
 XX independent of Fas, p53/p21, p21/waf-1/CIP, p15(ink4b), p16(ink4), drug  
 XX resistance, caspase 3, transforming growth factor (TGF)-beta 1 receptor  
 XX and hormone dependence  
 XX  
 SQ Sequence 24 BP; 0 A; 0 C; 12 G; 12 T; 0 U; 0 Other;  
 XX  
 XX Query Match 2.0%; Score 21.4; DB 1; Length 24;  
 XX Best Local Similarity 95.7%; Pred. No. 47;  
 XX Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 XX  
 QY 1793 TGTGTGTGTGTGTGTGTGTAT 1815  
 Db 2 TGTGTGTGTGTGTGTGTGTGTGT 24  
 XX  
 XX RESULT 49  
 XX AAF99862  
 ID AAF99862 standard; DNA; 24 BP.  
 XX  
 XX AAF99862;  
 AC  
 XX 12-JUN-2001 (first entry)  
 DT  
 XX Immunostimulatory nucleic acid #978.  
 DE  
 XX Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;  
 KW immunostimulatory; tumour; viral infection; bacterial infection;  
 KW fungal infection; parasitic infection; cancer; asthma;  
 KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.  
 XX  
 OS Synthetic.  
 XX  
 OS WO200122972-A2.  
 PN  
 XX

PD 05-APR-2001.  
XX  
PF 25-SEP-2000; 2000WO-US026383.  
XX  
XX 25-SEP-1999; 99US-0156113P.  
PR 27-SEP-1999; 99US-0156135P.  
XX 23-AUG-2000; 2000US-0227436P.  
XX  
XX (IOWA ) UNIV IOWA RES FOUND.  
PA (COLE-) COLEY PHARM GMBH.  
XX  
XX Krieg AM, Schetter C, Vollmer J;  
PI WPI; 2001-273485/28.  
XX  
XX Vaccinating against tumors, infectious diseases, allergies and asthma  
PT using immunostimulatory Py-rich and TG nucleic acids.  
XX  
XX Claim 101; Page 59; 338pp; English.  
XX  
XX The present invention relates to a method for stimulating an immune  
CC response. The method comprises administering an immunostimulatory nucleic  
CC acid to a non-rodent subject in sufficient quantity to stimulate an  
CC immune response. The present sequence is one such immunostimulatory  
CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich  
CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects  
CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae  
CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,  
CC haemophilus, campylobacter, clostridium, Escherichia coli and/or  
CC staphylococcus), fungal antigens and/or parasitic antigens. The method is  
CC also useful for preventing cancer, asthma, infectious disease, allergy or  
CC immune deficiency. The present sequence can also be used to redirect a  
CC Th2 to a Th1 immune response and to activate immune cells. Note: the  
CC present sequence may have a phosphorothioate backbone  
XX  
XX Sequence 24 BP; 0 A; 0 C; 12 G; 12 T; 0 U; 0 Other;  
SQ  
Query Match 2.0%; Score 21.4; DB 1; Length 24;  
Best Local Similarity 95.7%; Pred. No. 47;  
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1793 TGTGTGTGTGTGTGTGTGTAT 1815  
DB 1 TGTGTGTGTGTGTGTGTGTGTGTGTGT 23  
RESULT 50  
ABS78584  
ID ABS78584 standard; DNA; 24 BP.  
XX  
AC ABS78584;  
XX  
XX 13-DEC-2002 (first entry)  
DT  
XX  
DE Angiogenesis inhibitory oligonucleotide #1068.  
XX  
XX Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;  
XX tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;  
XX diabetic retinopathy; retinopathy of prematurity; macular degeneration;  
XX corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;  
XX rubecosis; Osler-Webber Syndrome; myocardial angiogenesis;  
XX plaque neovascularisation; telangiectasia; haemophilic joint;  
XX angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;  
XX scleroderma; hypertrophic scar.  
XX  
OS Synthetic.  
XX  
XX WO200253141-A2.  
PN  
XX 11-JUL-2002.  
PD  
XX 14-DEC-2001; 2001WO-US048458.  
XX  
XX

PR 14-DEC-2000; 2000US-0255534P.  
XX  
XX (COLE-) COLEY PHARM GROUP INC.  
XX  
XX Bratzler RL;  
XX  
XX WPI; 2002-566690/60.  
XX  
XX Inhibiting angiogenesis in a subject, involves administering at least one  
PT antiangiogenic nucleic acid molecule to the subject.  
PT  
XX  
XX Claim 2; Page 38; 276pp; English.  
XX  
XX The invention relates to inhibiting angiogenesis in a subject, comprising  
CC administering at least one antiangiogenic nucleic acid molecule. Also  
CC included is a kit comprising a first container housing the antiangiogenic  
CC nucleic acids, and instructions for administering them to a subject  
CC having a condition characterised by unwanted angiogenesis. The method is  
CC useful for inhibiting angiogenesis associated with solid tumour growth,  
CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,  
CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,  
CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,  
CC rubecosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque  
CC neovascularisation, telangiectasia, haemophilic joints, angiofibroma,  
CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and  
CC hypertrophic scars. The present sequence is an antiangiogenic nucleic  
CC acid of the invention  
XX  
XX Sequence 24 BP; 0 A; 0 C; 12 G; 12 T; 0 U; 0 Other;  
SQ  
Query Match 2.0%; Score 21.4; DB 1; Length 24;  
Best Local Similarity 95.7%; Pred. No. 47;  
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1793 TGTGTGTGTGTGTGTGTGTAT 1815  
DB 1 TGTGTGTGTGTGTGTGTGTGTGTGTGT 23  
RESULT 51  
ACH03377  
ID ACH03377 standard; DNA; 24 BP.  
XX  
XX ACH03377;  
AC  
XX  
XX 25-SEP-2003 (first entry)  
DT  
XX  
DE Immunostimulatory nucleic acid #1012.  
XX  
XX Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;  
XX antiulcer; gene therapy; vaccine; non-allergic inflammatory disease;  
XX psoriasis; eczema; allergic contact dermatitis; latex dermatitis;  
XX inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.  
XX  
OS Synthetic.  
XX  
XX US20003050268-A1.  
PN  
XX 13-MAR-2003.  
PD  
XX 29-MAR-2002; 2002US-00112653.  
PF  
XX 29-MAR-2001; 2001US-0279642P.  
PR  
XX (KRIE/) KRIEG A M.  
PA (BERG/) BERG D J.  
XX  
XX Krieg AM, Berg DJ;  
PI  
XX WPI; 2003-521815/49.  
DR  
XX  
XX Treating non-allergic inflammatory diseases, such as psoriasis, eczema,  
PT allergic contact dermatitis, latex dermatitis or inflammatory bowel

PT disease by administering an immunostimulatory nucleic acid.  
XX  
PS Disclosure; Page 36; 229pp; English.  
XX

CC The invention describes a method of treating non-allergic inflammatory  
CC disease comprising administering to a subject having or at risk of  
CC developing a non-allergic inflammatory disease an immunostimulatory  
CC nucleic acid for prevention or treatment of the disease. The method is  
CC useful for treating non-allergic inflammatory diseases, such as  
CC psoriasis, eczema, allergic contact dermatitis, latex dermatitis or  
CC inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.  
CC This sequence represents an immunostimulatory nucleic acid  
XX  
SQ Sequence 24 BP; 0 A; 0 C; 12 G; 12 T; 0 U; 0 Other;

Query Match 2.0%; Score 21.4; DB 1; Length 24;  
Best Local Similarity 95.7%; Pred. No. 47;  
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTAT 1815  
DB 1 TGTGTGTGTGTGTGTGTGT 23

RESULT 52  
ADB37364  
ID ADB37364 standard; DNA; 24 BP.  
XX  
AC ADB37364;  
XX

DT 04-DEC-2003 (first entry)  
XX  
DE Immunostimulatory nucleic acid #978.  
XX  
KW ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;  
KW hypo-responsive subject; immunostimulatory.  
XX  
XX Synthetic.

OS US2003087848-A1.  
PN  
XX  
PD 08-MAY-2003.  
XX

PF 02-FEB-2001; 2001US-00776479.  
XX  
PR 03-FEB-2000; 2000US-0179991P.  
XX  
PA (BRAT/) BRATZLER R L.  
PA (PETE/) PETERSEN D M.  
PA (FOUR/) FOURON Y.

XX Bratzler RL, Petersen DM, Fouron Y;  
XX WPI; 2003-657977/62.  
XX  
XX Treating and/or preventing allergy or asthma using an immunostimulatory  
XX nucleic acid alone or in combination with an asthma/allergy medicament.  
XX  
PS Disclosure; Page 20; 221pp; English.  
XX

CC The invention relates to a method of treating or preventing allergy or  
CC asthma which comprises administering to a subject a poly-G nucleic acid  
CC in an aerosol formulation. The methods and compositions of the present  
CC invention are useful for diagnosing and/or treating asthma and allergy  
CC especially in a hypo-responsive subject. The present sequence represents  
CC an immunostimulatory nucleic acid of the invention.  
XX  
SQ Sequence 24 BP; 0 A; 0 C; 12 G; 12 T; 0 U; 0 Other;

Query Match 2.0%; Score 21.4; DB 1; Length 24;  
Best Local Similarity 95.7%; Pred. No. 47;  
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTAT 1815  
DB 1 TGTGTGTGTGTGTGTGTGT 23

RESULT 53  
AAQ33861  
ID AAQ33861 standard; DNA; 25 BP.  
XX  
AC AAQ33861;  
XX  
DT 25-MAR-2003 (revised)  
DT 02-FEB-1993 (first entry)  
XX

DE Microsatellite sequence from clone TGLA264.  
XX  
XX PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;  
KW genetic mapping; traits; amplification; ss.  
XX  
OS Bos taurus.  
XX  
PN WO92113102-A1.  
XX  
PD 06-AUG-1992.  
XX

PF 15-JAN-1992; 92WO-US000340.  
XX  
PR 15-JAN-1991; 91US-00642342.  
XX  
XX (GENM-) GENMARK.  
XX

PA Georges M. Massey JM;  
XX  
PI WPI; 1992-284684/34.  
XX  
DR Polymorphic bovine DNA markers - used in genetic identification, gene  
XX mapping, and selective breeding.  
PT  
XX Table 7; Page 274; 517pp; English.  
XX

CC The sequence is that of a bovine microsatellite sequence obtd. by  
CC screening a library of bovine MboI DNA fragments of between 250 and 500  
CC bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50  
CC clones cross-hybridised. Assuming independent distribution of  
CC microsatellites and MboI sites, the frequency of (T6)n > 9 microsatellites  
CC in the bovine genome is estimated at >100, 000. The sequence information  
CC for ca. 230 such bovine microsatellites is summarised in the  
CC specification and indexed herein (see below). The sequences upstream and  
CC downstream of the microsatellite sequence were used to generate the  
CC required PCR primers for in vitro amplification of the corresp.  
CC microsatellite (using the program OPTIPRIM). The microsatellites may be  
CC used to identify individuals, for parentage testing, and in the genetic  
CC mapping of economic trait loci, or genes involved in the determination of  
CC economically important traits esp. in cattle, to allow selective  
CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN  
CC field.)  
XX  
SQ Sequence 25 BP; 0 A; 0 C; 13 G; 12 T; 0 U; 0 Other;

Query Match 2.0%; Score 21.4; DB 1; Length 25;  
Best Local Similarity 95.7%; Pred. No. 49;  
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTAT 1815  
DB 2 TGTGTGTGTGTGTGTGTGT 24

RESULT 54  
AAH40163/c  
ID AAH40163 standard; DNA; 25 BP.  
XX  
XX AAH40163;









```
XX SQ Sequence 21 BP; 11 A; 10 C; 0 G; 0 T; 0 U; 0 Other;
Query Match 2.0%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGT 1813
DB 21 TGTGTGTGTGTGTGTGTGT 1

RESULT 61
AAH46013
ID AAH46013 standard; DNA; 21 BP.
XX
AC AAH46013;
XX
DT 12-SEP-2001 (first entry)
XX
DE Synthetic oligonucleotide 13.
XX
KW Synthetic oligonucleotide; dinucleotide repeat; cytostatic; apoptosis;
KW cell cycle arrest; cell proliferation; caspase; cytokine; interleukin;
KW tumour necrosis factor; TNF; cancer; carcinoma; sarcoma; leukemia;
KW lymphoma; ss.
XX
OS Synthetic.
XX
PN WO200144465-A2.
XX
PD 21-JUN-2001.
XX
PF 12-DEC-2000; 2000WO-CAC01467.
XX
PR 13-DEC-1999; 99US-0170325P.
XX
PR 29-AUG-2000; 2000US-0228925P.
XX
PA (BION-) BIONICHE LIFE SCI INC.
XX
PI Phillips NC, Fillion MC;
XX
DR WPI; 2001-398150/42.
XX
CC Composition comprising synthetic oligonucleotides which comprise multiple
PT repeats of dinucleotides such as GT; TG useful for treating cancer by
PT inducing cell cycle arrest, inhibiting proliferation, activating
PT caspases.
XX
PS Example 4; Page 17; 77pp; English.
XX
CC The present sequence is that of a synthetic oligonucleotide useful to the
CC invention. The invention relates to a composition, comprising a 2 to 20
CC base 3'-OH, 5'-OH synthetic oligonucleotide which comprises multiple
CC repeats of dinucleotides such as GT, TG, etc., according to specific
CC formula and having cytostatic activity. The oligonucleotide compositions
CC are useful for inducing cell cycle arrest, inhibition of proliferation,
CC activation of caspases and induction of apoptosis or production of
CC cytokines such as interleukin (IL)-1-beta, IL-6, IL-10, IL-12 and tumour
CC necrosis factor (TNF)-alpha by immune system cells, in an animal having
CC cancer such as primary carcinoma, secondary carcinoma, primary sarcoma
CC and secondary sarcoma such as, leukemia, lymphoma, breast, prostate,
CC colorectal, ovarian or bone cancer. The compositions induce apoptosis
CC independent of Fas, p53/p21, p21/waf-1/CIP, p15(ink4B), p16(ink4), drug
CC resistance, caspase 3, transforming growth factor (TGF)-beta 1 receptor
CC and hormone dependence
XX
SQ Sequence 21 BP; 0 A; 0 C; 10 G; 11 T; 0 U; 0 Other;
Query Match 2.0%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1793 TGTGTGTGTGTGTGTGTGT 1813
DB 1 TGTGTGTGTGTGTGTGTGT 21

RESULT 62
AAF99702
ID AAF99702 standard; DNA; 21 BP.
XX
AC AAF99702;
XX
DT 12-JUN-2001 (first entry)
XX
DE Immunostimulatory nucleic acid #818.
XX
KW Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
KW immunostimulatory; tumour; viral infection; bacterial infection;
KW fungal infection; parasitic infection; cancer; asthma;
KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX
OS Synthetic.
XX
PN WO200122972-A2.
XX
PD 05-APR-2001.
XX
PF 25-SEP-2000; 2000WO-US026383.
XX
PR 25-SEP-1999; 99US-0156113P.
XX
PR 27-SEP-1999; 99US-0156135P.
XX
PR 23-AUG-2000; 2000US-0227436P.
XX
PA (IOWA) UNIV IOWA RES FOUND.
XX
PA (COLE-) COLEY PHARM GMBH.
XX
PI Krieg AM, Schetter C, Vollmer J;
XX
DR WPI; 2001-273485/28.
XX
PT Vaccinating against tumors, infectious diseases, allergies and asthma
PT using immunostimulatory Py-rich and TG nucleic acids.
XX
PS Claim 101; Page 56; 339pp; English.
XX
CC The present invention relates to a method for stimulating an immune
CC response. The method comprises administering an immunostimulatory nucleic
CC acid to a non-rodent subject in sufficient quantity to stimulate an
CC immune response. The present sequence is one such immunostimulatory
CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
CC haemophilus, campylobacter, clostridium, Escherichia coli and/or
CC staphylococcus), fungal antigens and/or parasitic antigens. The method is
CC also useful for preventing cancer, asthma, infectious disease, allergy or
CC immune deficiency. The present sequence can also be used to redirect a
CC Th2 to a Th1 immune response and to activate immune cells. Note: the
CC present sequence may have a phosphorothioate backbone
XX
SQ Sequence 21 BP; 0 A; 0 C; 10 G; 11 T; 0 U; 0 Other;
Query Match 2.0%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGT 1813
DB 1 TGTGTGTGTGTGTGTGTGT 21

RESULT 63
ABS78423
ID ABS78423 standard; DNA; 21 BP.
```

XX ABS78423;  
XX 13-DEC-2002 (first entry)  
XX  
XX Angiogenesis inhibitory oligonucleotide #907.  
XX  
XX Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;  
XX tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;  
XX diabetic retinopathy; retinopathy of prematurity; macular degeneration;  
XX corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;  
XX rubeosis; Osler-Weber Syndrome; myocardial angiogenesis;  
XX plaque neovascularisation; telangiectasia; haemophilic joint;  
XX angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;  
XX scleroderma; hypertrophic scar.  
XX  
XX Synthetic.  
XX  
XX WO200253141-A2.  
XX  
XX 11-JUL-2002.  
XX  
XX 14-DEC-2001; 2001WO-US048458.  
XX  
XX 14-DEC-2000; 2000US-0255534P.  
XX  
XX (COLE-) COLEY PHARM GROUP INC.  
XX  
XX Bratzler RL;  
XX  
XX WPI; 2002-566690/60.  
XX  
XX Inhibiting angiogenesis in a subject, involves administering at least one  
XX antiangiogenic nucleic acid molecule to the subject.  
XX  
XX Claim 2; Page 35; 276pp; English.  
XX  
XX The invention relates to inhibiting angiogenesis in a subject, comprising  
XX administering at least one antiangiogenic nucleic acid molecule. Also  
XX included is a kit comprising a first container housing the antiangiogenic  
XX nucleic acids and instructions for administering them to a subject  
XX having a condition characterised by unwanted angiogenesis. The method is  
XX useful for inhibiting angiogenesis associated with solid tumour growth,  
XX tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,  
XX diabetic retinopathy, retinopathy of prematurity, macular degeneration,  
XX corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,  
XX rubeosis, Osler-Weber Syndrome, myocardial angiogenesis, plaque  
XX neovascularisation, telangiectasia, haemophilic joints, angiofibroma,  
XX wound granulation, intestinal adhesions, atherosclerosis, scleroderma and  
XX hypertrophic scars. The present sequence is an antiangiogenic nucleic  
XX acid of the invention  
XX  
XX Sequence 21 BP; 0 A; 0 C; 10 G; 11 T; 0 U; 0 Other;  
XX  
XX Query Match 2.0%; Score 21; DB 1; Length 21;  
XX Best Local Similarity 100.0%; Pred.No. 47;  
XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0  
XX  
XX QY 1793 TGTGTGTGTGTGTGTGTGTGT 1813  
XX  
XX Db 1 TGTGTGTGTGTGTGTGTGTGT 21  
XX  
XX  
XX RESULT 64  
XX ABK87131/C  
XX ID ABK87131 standard; DNA; 21 BP.  
XX  
XX AC ABK87131;  
XX  
XX AC  
XX  
XX 07-OCT-2002 (first entry)  
XX  
XX Human connective tissue growth factor, RT-PCR primer #1.  
XX

KW	Human; endothelial cell-specific molecule 4; ECSM4; neovasculature;
KW	imaging vascular endothelium; proliferative disease; cancer; psoriasis;
KW	diabetic retinopathy; atherosclerosis; menorrhagia; endothelial damage;
KW	tumour neovasculature; cardiac disease; endometriosis; hypoxic condition;
KW	angiogenesis; cytostatic; RT-PCR; connective tissue growth factor;
KW	reverse transcription-PCR; primer; ss.
OS	Homo sapiens.
PN	WO200236771-A2.
PN	10-MAY-2002.
PD	06-NOV-2001; 2001WO-GB004906.
PF	06-NOV-2000; 2000US-0245566P.
PR	07-MAR-2001; 2001US-0273682P.
PR	(IMCR ) IMPERIAL CANCER RES TECHNOLOGY LTD.
XX	Bicknell R, Huminiecki L;
XX	WPI; 2002-508120/54.
XX	Novel endothelial cell-specific molecule polypeptide 1 or 4, useful for
PT	imaging, diagnosing and treating a condition involving vascular
PT	endothelium e.g. cancer, cardiac disease, endometriosis, diabetes.
XX	Example 1; Page 165; 248pp; English.
PS	The present invention relates to endothelial cell-specific molecule 4
CC	(ECSM4), and the polynucleotide sequences encoding it. The ECSM4 proteins
CC	are useful for imaging vascular endothelium in the body of an individual,
CC	and for diagnosing and treating a proliferative disease or condition
CC	involving the vascular endothelium (preferably, neovasculature) such as
CC	cancer, psoriasis, diabetic retinopathy, atherosclerosis or menorrhagia.
CC	The ECSM4 proteins are also useful in the manufacture of diagnostic or
CC	prognostic agent for such conditions. The proteins are also useful for
CC	detecting endothelial damage or activation, detecting a tumour or tumour
CC	neovasculature, cardiac disease, or endometriosis by detecting the amount
CC	of ECSM4 present in a sample. The polynucleotide sequences encoding ECSM4
CC	are useful in gene therapy for treating a hypoxic condition such as
CC	cancer, cardiac disease, endometriosis or atherosclerosis and in the
CC	manufacture of medicaments for treating the above disease. The sequences
CC	are useful for modulating angiogenesis in an individual. The present
CC	sequence represents a RT-PCR primer for RNA encoding human connective
CC	tissue growth factor
XX	
XX	Sequence 21 BP; 9 A; 4 C; 4 G; 4 T; 0 U; 0 Other;
QY	Query Match 2.0%; Score 21; DB 1; Length 21;
DB	Best Local Similarity 100.0%; Pred. No. 47;
DB	Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY	2148 TTTTTCACCTGGAGCATTG 2168
DB	21 TTTTTCACCTGGAGCATTG 1
RESULT 65	
ACH03241	
ID	ACH03241 standard; DNA; 21 BP.
XX	ACH03241;
XX	25-SEP-2003 (first entry)
DT	
XX	Immunostimulatory nucleic acid #876.
DE	
XX	Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;
KW	antiulcer; gene therapy; vaccine; non-allergic inflammatory disease;
KW	psoriasis; eczema; allergic contact dermatitis; latex dermatitis;
KW	inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.

XX OS Synthetic.  
XX PN US2003050268-A1.  
XX PD 13-MAR-2003.  
XX PF 29-MAR-2002; 2002US-00112653.  
XX PR 29-MAR-2001; 2001US-0279642P.  
XX PA (KRIE/) KRIEG A M.  
XX PA (BERG/) BERG D J.  
XX PI Krieg AM, Berg DJ;  
XX PW 2003-521815/49.  
XX PT Treating non-allergic inflammatory diseases, such as psoriasis, eczema,  
XX PT allergic contact dermatitis, latex dermatitis or inflammatory bowel  
XX PT disease by administering an immunostimulatory nucleic acid.  
XX PS Disclosure; Page 32; 229pp; English.  
XX CC The invention describes a method of treating non-allergic inflammatory  
XX CC disease comprising administering to a subject having or at risk of  
XX CC developing a non-allergic inflammatory disease an immunostimulatory  
XX CC nucleic acid for prevention or treatment of the disease. The method is  
XX CC useful for treating non-allergic inflammatory diseases, such as  
XX CC psoriasis, eczema, allergic contact dermatitis, latex dermatitis or  
XX CC inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.  
XX CC This sequence represents an immunostimulatory nucleic acid  
XX CC  
XX SQ Sequence 21 BP; 0 A; 0 C; 10 G; 11 T; 0 U; 0 Other;  
Query Match 2.0%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 47;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1793 TGTGTGTGTGTGTGTGTGTGT 1813  
DB 1 TGTGTGTGTGTGTGTGTGTGT 21  
RESULT 66  
ADB37204  
ID ADB37204 standard; DNA; 21 BP.  
XX AC ADB37204;  
XX DT 04-DEC-2003 (first entry)  
XX DE Immunostimulatory nucleic acid #818.  
XX KW ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;  
XX KW hypo-responsive subject; immunostimulatory.  
XX OS Synthetic.  
XX PN US2003087848-A1.  
XX PD 08-MAY-2003.  
XX PF 02-FEB-2001; 2001US-00776479.  
XX PR 03-FEB-2000; 2000US-0179991P.  
XX PA (BRAT/) BRATZLER R L.  
XX PA (PETE/) PETERSEN D M.  
XX PA (FOUR/) FOURON Y.  
XX PI Bratzler RL, Petersen DM, Fouron Y;

DR WPI; 2003-657977/62.  
XX Treating and/or preventing allergy or asthma using an immunostimulatory  
XX nucleic acid alone or in combination with an asthma/allergy medicament.  
XX PS Disclosure; Page 17; 221pp; English.  
XX CC The invention relates to a method of treating or preventing allergy or  
XX CC asthma which comprises administering to a subject a poly-G nucleic acid  
XX CC in an aerosol formulation. The methods and compositions of the present  
XX CC invention are useful for diagnosing and/or treating asthma and allergy  
XX CC especially in a hypo-responsive subject. The present sequence represents  
XX CC an immunostimulatory nucleic acid of the invention.  
XX SQ Sequence 21 BP; 0 A; 0 C; 10 G; 11 T; 0 U; 0 Other;  
Query Match 2.0%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 47;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1793 TGTGTGTGTGTGTGTGTGTGT 1813  
DB 1 TGTGTGTGTGTGTGTGTGTGT 21  
RESULT 67  
AAQ33810  
ID AAQ33810 standard; DNA; 22 BP.  
XX AC AAQ33810;  
XX DT 25-MAR-2003 (revised)  
XX DT 02-FEB-1993 (first entry)  
XX DE Microsatellite sequence from clone TGLA214.  
XX KW PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;  
XX KW Genetic mapping; traits; amplification; ss.  
XX OS Bos taurus.  
XX PN WO9213102-A1.  
XX PD 06-AUG-1992.  
XX PF 15-JAN-1992; 92WO-US000340.  
XX PR 15-JAN-1991; 91US-00642342.  
XX PA (GENM-) GENMARK.  
XX PI Georges M, Massey JM;  
XX PW 1992-284684/34.  
XX PT Polymorphic bovine DNA markers - used in genetic identification, gene  
XX PT mapping, and selective breeding.  
XX PS Table 7; Page 253; 517pp; English.  
XX CC The sequence is that of a bovine microsatellite sequence obtd. by  
XX CC screening a library of bovine MboI DNA fragments of between 250 and 500  
XX CC bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50  
XX CC clones cross-hybridised. Assuming independent distribution of  
XX CC microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites  
XX CC in the bovine genome is estimated at >100,000. The sequence information  
XX CC for ca. 230 such bovine microsatellites is summarised in the  
XX CC specification and indexed herein (see below). The sequences upstream and  
XX CC downstream of the microsatellite sequence were used to generate the  
XX CC required PCR primers for in vitro amplification of the corresp.  
XX CC microsatellite (using the program OPTIPRIM). The microsatellites may be  
XX CC used to identify individuals, for parentage testing, and in the genetic  
XX CC mapping of economic trait loci, or genes involved in the determination of

CC economically important traits esp. in cattle, to allow selective  
CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN  
CC field.)  
XX  
SQ Sequence 22 BP; 0 A; 0 C; 11 G; 11 T; 0 U; 0 Other;  
  
Query Match 2.0%; Score 21; DB 1; Length 22;  
Best Local Similarity 100.0%; Pred. No. 49;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1793 TGTGTGTGTGTGTGTGTGTGTGTGTGT 1813  
DB 2 TGTGTGTGTGTGTGTGTGTGTGTGTGT 22  
  
RESULT 68  
AAQ33675  
ID AAQ33675 standard; DNA; 22 BP.  
XX  
AC AAQ33675;  
XX  
DT 25-MAR-2003 (revised)  
DT 02-FEB-1993 (first entry)  
XX  
DE Microsatellite sequence from clone TGLA117.  
XX  
XX PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;  
KW genetic mapping; traits; amplification; ss.  
KW  
XX Bos taurus.  
OS  
XX WO9213102-A1.  
FN  
XX 06-AUG-1992.  
PD  
XX 15-JAN-1992; 92WO-US000340.  
PF  
XX 15-JAN-1991; 91US-00642342.  
PR  
XX (GENM-) GENMARK.  
PA  
XX Georges M, Massey JM;  
PI  
XX WPI; 1992-284684/34.  
DR  
XX Polymorphic bovine DNA markers - used in genetic identification, gene  
PT mapping, and selective breeding.  
PT  
XX Table 7; Page 199; 517pp; English.  
PS  
XX The sequence is that of a bovine microsatellite sequence obtd. by  
CC screening a library of bovine MboI DNA fragments of between 250 and 500  
CC bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50  
CC clones cross-hybridised. Assuming independent distribution of  
CC microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites  
CC in the bovine genome is estimated at >100, 000. The sequence information  
CC for ca 230 such bovine microsatellites is summarised in the  
CC specification and indexed herein (see below). The sequences upstream and  
CC downstream of the microsatellite sequence were used to generate the  
CC required PCR primers for in vitro amplification of the corresp.  
CC microsatellite (using the program OPTIPRIM). The microsatellites may be  
CC used to identify individuals, for parentage testing, and in the genetic  
CC mapping of economic trait loci, or genes involved the determinism of  
CC economically important traits esp. in cattle, to allow selective  
CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN  
CC field.)  
XX  
SQ Sequence 22 BP; 0 A; 0 C; 11 G; 11 T; 0 U; 0 Other;  
  
Query Match 2.0%; Score 21; DB 1; Length 22;  
Best Local Similarity 100.0%; Pred. No. 49;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTGTGTGTGT 1813  
DB 1 TGTGTGTGTGTGTGTGTGTGTGTGTGT 21  
  
RESULT 69  
AAQ34038  
ID AAQ34038 standard; DNA; 22 BP.  
XX  
AC AAQ34038;  
XX  
DT 25-MAR-2003 (revised)  
DT 02-FEB-1993 (first entry)  
XX  
DE Microsatellite sequence from clone TGLA432.  
XX  
KW PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;  
KW genetic mapping; traits; amplification; ss.  
XX  
OS Bos taurus.  
XX  
FN WO9213102-A1.  
XX  
PD 06-AUG-1992.  
PD  
XX 15-JAN-1992; 92WO-US000340.  
PF  
XX 15-JAN-1991; 91US-00642342.  
PR  
XX (GENM-) GENMARK.  
PA  
XX Georges M, Massey JM;  
PI  
XX WPI; 1992-284684/34.  
DR  
XX Polymorphic bovine DNA markers - used in genetic identification, gene  
PT mapping, and selective breeding.  
PT  
XX Table 7; Page 346; 517pp; English.  
PS  
XX The sequence is that of a bovine microsatellite sequence obtd. by  
CC screening a library of bovine MboI DNA fragments of between 250 and 500  
CC bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50  
CC clones cross-hybridised. Assuming independent distribution of  
CC microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites  
CC in the bovine genome is estimated at >100, 000. The sequence information  
CC for ca 230 such bovine microsatellites is summarised in the  
CC specification and indexed herein (see below). The sequences upstream and  
CC downstream of the microsatellite sequence were used to generate the  
CC required PCR primers for in vitro amplification of the corresp.  
CC microsatellite (using the program OPTIPRIM). The microsatellites may be  
CC used to identify individuals, for parentage testing, and in the genetic  
CC mapping of economic trait loci, or genes involved the determinism of  
CC economically important traits esp. in cattle, to allow selective  
CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN  
CC field.)  
XX  
SQ Sequence 22 BP; 0 A; 0 C; 11 G; 11 T; 0 U; 0 Other;  
  
Query Match 2.0%; Score 21; DB 1; Length 22;  
Best Local Similarity 100.0%; Pred. No. 49;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1793 TGTGTGTGTGTGTGTGTGTGTGTGTGT 1813  
DB 1 TGTGTGTGTGTGTGTGTGTGTGTGTGT 21  
  
RESULT 70  
AAQ34080  
ID AAQ34080 standard; DNA; 22 BP.  
XX  
AC AAQ34080;

XX 25-MAR-2003 (revised)  
 DT 02-FEB-1993 (first entry)  
 XX  
 DE Microsatellite sequence from clone TGLA48.  
 XX  
 KW PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;  
 KW genetic mapping; traits; amplification; ss.  
 XX  
 OS Bos taurus.  
 XX  
 FN W09213102-A1.  
 XX  
 PD 06-AUG-1992.  
 XX  
 PF 15-JAN-1992; 92WO-US000340.  
 XX  
 PR 15-JAN-1991; 91US-00642342.  
 XX  
 XX (GENM-) GENMARK.  
 XX  
 XX Georges M, Massey JM;  
 XX  
 DR WPI; 1992-284684/34.  
 XX  
 XX Polymorphic bovine DNA markers - used in genetic identification, gene  
 PT mapping, and selective breeding.  
 XX  
 PS Table 7; Page 363; 517pp; English.  
 XX  
 CC The sequence is that of a bovine microsatellite sequence obt'd. by  
 CC screening a library of bovine MboI DNA fragments of between 250 and 500  
 CC bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50  
 CC clones cross-hybridised. Assuming independent distribution of  
 CC microsatellites and MboI sites, the frequency of (TC)n > 9 microsatellites  
 CC in the bovine genome is estimated at >100, 000. The sequence information  
 CC for ca. 230 such bovine microsatellites is summarised in the  
 CC specification and indexed herein (see below). The sequences upstream and  
 CC downstream of the microsatellite sequence were used to generate the  
 CC required PCR primers for in vitro amplification of the corresp.  
 CC microsatellite (using the program OPTIPRIM). The microsatellites may be  
 CC used to identify individuals, for parentage testing, and in the genetic  
 CC mapping of economic trait loci, or genes involved in the determination of  
 CC economically important traits esp. in cattle, to allow selective  
 CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN  
 CC field.)  
 XX  
 SQ Sequence 22 BP; 0 A; 0 C; 11 G; 11 T; 0 U; 0 Other;  
 Query Match 2.0%; Score 21; DB 1; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 49;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1793 TGTGTGTGTGTGTGTGTGTGT 1813  
 DB 1 TGTGTGTGTGTGTGTGTGTGT 21  
 RESULT 71  
 AAQ33991  
 ID AAQ33991 standard; DNA; 22 BP.  
 XX  
 AC AAQ33991;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 02-FEB-1993 (first entry)  
 XX  
 DE Microsatellite sequence from clone TGLA39.  
 XX  
 KW PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;  
 KW genetic mapping; traits; amplification; ss.  
 XX  
 OS Bos taurus.

XX W09213102-A1.  
 XX  
 PD 06-AUG-1992.  
 XX  
 PF 15-JAN-1992; 92WO-US000340.  
 XX  
 PR 15-JAN-1991; 91US-00642342.  
 XX  
 XX (GENM-) GENMARK.  
 XX  
 XX Georges M, Massey JM;  
 XX  
 DR WPI; 1992-284684/34.  
 XX  
 XX Polymorphic bovine DNA markers - used in genetic identification, gene  
 PT mapping, and selective breeding.  
 XX  
 PS Table 7; Page 327; 517pp; English.  
 XX  
 CC The sequence is that of a bovine microsatellite sequence obt'd. by  
 CC screening a library of bovine MboI DNA fragments of between 250 and 500  
 CC bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50  
 CC clones cross-hybridised. Assuming independent distribution of  
 CC microsatellites and MboI sites, the frequency of (TC)n > 9 microsatellites  
 CC in the bovine genome is estimated at >100, 000. The sequence information  
 CC for ca. 230 such bovine microsatellites is summarised in the  
 CC specification and indexed herein (see below). The sequences upstream and  
 CC downstream of the microsatellite sequence were used to generate the  
 CC required PCR primers for in vitro amplification of the corresp.  
 CC microsatellite (using the program OPTIPRIM). The microsatellites may be  
 CC used to identify individuals, for parentage testing, and in the genetic  
 CC mapping of economic trait loci, or genes involved in the determination of  
 CC economically important traits esp. in cattle, to allow selective  
 CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN  
 CC field.)  
 XX  
 SQ Sequence 22 BP; 0 A; 0 C; 11 G; 11 T; 0 U; 0 Other;  
 Query Match 2.0%; Score 21; DB 1; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 49;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1793 TGTGTGTGTGTGTGTGTGTGT 1813  
 DB 1 TGTGTGTGTGTGTGTGTGTGT 21  
 RESULT 72  
 AAQ83952/c  
 ID AAQ83952 standard; DNA; 22 BP.  
 XX  
 AC AAQ83952;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 04-OCT-1995 (first entry)  
 XX  
 DE Oligonucleotide clamp n, for producing comb-type brached polymer.  
 XX  
 KW HIV; pol; nef; oligonucleotide clamp; branched; macromolecule; ss.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_base 1  
 FT /\*tag= a  
 FT /note= "Modified with BrCH2(=O)CNH-"  
 FT modified\_base 8..9  
 FT /\*tag= b  
 FT /note= "C(pnp)A, pnp = a linkage or monomer containing a  
 FT bromoacetyl amino functionality, and p = phosphodiester  
 FT linkage"  
 FT modified\_base 14..15

OS	Homo sapiens.
PN	US5582979-A.
XX	
PD	10-DEC-1996.
XX	
PF	04-APR-1994; 94US-00222177.
XX	
PR	21-APR-1989; 89US-00341562.
XX	
PR	05-SEP-1991; 91US-00754351.
XX	
PA	(MARS-) MARSHFIELD CLINIC.
XX	
PI	Weber JL;
XX	
DR	WPI; 1997-042299/04.
XX	
PT	Detection of polymorphic genetic markers of the form (GC-dA)n(dG-dT)n -
XX	
PT	using novel nucleic acid mois. as primers.
XX	
PS	Disclosure; Col 9-10; 186pp; English.
XX	
CC	The invention relates to the isolation of polymorphic repeat sequences
CC	having the sequence (GC-dA)n.(dG-dT)n which can be used as genetic
CC	markers. Primers based on these sequences can be used to detect these
CC	repeats, especially for use in e.g. paternity or maternity testing, human
CC	genetic analysis such as linkage analysis of genetic disease, commercial
CC	animal or plant breeding or pedigree analysis. Clones containing the
CC	repeat sequences were isolated by hybridisation of chromosome-specific
CC	phage libraries with a synthetic poly(dC-dA).(dG-dT) probe. Over 100
CC	repeat blocks were isolated. The inserts from the clones were amplified
CC	by primers AAT65798-T66047. Those clones where the repeat sequence has
CC	been determined are shown in AAT65704-797. This repeat sequence is from
CC	the marker clone Maf25 which contains the repeat sequence having the
CC	formula: (AC)11. (Updated on 25-MAR-2003 to correct PF field.)
XX	
SQ	Sequence 22 BP; 11 A; 11 C; 0 G; 0 T; 0 U; 0 Other;
	Query Match 2.0%; Score 21; DB 1; Length 22;
	Best Local Similarity 100.0%; Pred. No. 49;
	Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	1793 TGTGTGTGTGTGTGTGTGTGT 1813
Db	21 TGTGTGTGTGTGTGTGTGTGT 1
RESULT 74	
AAI64448	
ID	AAI64448 standard; DNA; 22 BP.
XX	
AC	AAI64448;
XX	
DT	23-NOV-2001 (first entry)
XX	
DE	SSR motif #8.
XX	
KW	Simple Sequence Repeat; SSR; clover; microsatellite; genome mapping;
KW	trait mapping; marker-assisted selection; gene selection; legume;
KW	DNA profiling; breeding; ds.
XX	
OS	Unidentified.
XX	
PN	NZ509194-A.
XX	
PD	25-MAY-2001.
XX	
PF	03-JAN-2001; 2001NZ-00509194.
XX	
PR	24-DEC-1999; 99AU-00004307.
XX	
PR	28-MAR-2000; 2000AU-00006520.
XX	
PA	(AGRI-) AGRIC VICTORIA SERVICES PTY LTD.



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XX
PI Koelliker R, Forster JW;
XX
DR WPI; 2001-431058/46.
XX
PT Novel simple sequence repeats in clover species useful for selection of
PT Genes in legume breeding, for profiling legume species varieties and for
XX testing the purity of legume seed batches.
XX
PS Claim 6; Page 35; 52pp; English.
XX
CC The present invention relates to Simple Sequence Repeats (SSRs) from
CC clover species. SSRs, also called microsatellites, are based on a 1-7
CC nucleotide core element which is tandemly repeated. The SSR array is
CC embedded in complex flanking DNA. SSRs are ideal markers for genome
CC mapping, trait mapping and marker-assisted selection. The SSRs may be
CC used in methods for selecting genes in clover/ legume breeding. The SSRs
CC are also useful for DNA profiling of clover varieties and for testing the
CC purity of legume seed batches. The present sequence is a SSR motif, which
CC was used in the present invention
XX
SQ Sequence 22 BP; 0 A; 0 C; 11 G; 11 T; 0 U; 0 Other;
      Query Match      2.0%; Score 21; DB 1; Length 22;
      Best Local Similarity 100.0%; Pred. No. 49;
      Matches 21; Conservative 0; Mismatches 0; Gaps 0;
      Indels 0;
      Y 1793 TGTGTGTGTGTGTGTGTGTGT 1813
      Db 1 TGTGTGTGTGTGTGTGTGTGT 21

RESULT 75
AAF60472/c
ID AAF60472 standard; DNA; 23 BP.
XX
AC AAF60472;
XX
DT 27-APR-2001 (first entry)
XX
DE Oligonucleotide clamp #17.
XX
XX Oligonucleotide clamp; ds.
XX
XX Unidentified.
XX
XX US6180777-B1.
XX
XX 30-JAN-2001.
XX
XX 03-JAN-1997; 97US-00787321.
XX
XX 12-JAN-1996; 96US-0009918P.
XX
XX (FARB ) BAYER CORP.
XX
XX Horn T;
XX
XX WPI; 2001-201911/20.
XX
PT Synthesizing branched nucleic acids useful as diagnostic and molecular
PT probes, involves combining first units having haloalkylamino groups and
PT second units having thiol or phosphorothioate groups.
XX
XX Example 7; Col 19; 20pp; English.
XX
CC The present invention relates to a method for synthesising a branched or
CC multiply connected macromolecular structure, comprising oligonucleotide
CC clamps (OC). The macromolecular structure is capable of specifically
CC binding to a target molecule, and can therefore be used as probes. At
CC least one OC comprises a target binding sequence that binds specifically
CC and stably with the target molecule, and at least two OCs comprise signal
CC generation moieties capable of generating a detectable signal in the

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CC presence of the target molecule. In addition the OCs are connected to one
CC another by thioalkylamino, or thiophosphorylalkylamino bridges. The
CC present sequence is an OC used in the present invention
XX
SQ Sequence 23 BP; 11 A; 12 C; 0 G; 0 T; 0 U; 0 Other;
      Query Match      2.0%; Score 21; DB 1; Length 23;
      Best Local Similarity 100.0%; Pred. No. 51;
      Matches 21; Conservative 0; Mismatches 0; Gaps 0;
      Indels 0;
      Y 1793 TGTGTGTGTGTGTGTGTGTGT 1813
      Db 22 TGTGTGTGTGTGTGTGTGTGT 2

RESULT 76
AAH40155/c
ID AAH40155 standard; DNA; 25 BP.
XX
AC AAH40155;
XX
DT 14-AUG-2001 (first entry)
XX
DE SNP specific SNPE primer SEQ ID 2951.
XX
XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;
XX SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;
XX Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
XX polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
XX acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
XX inflammation; forensic investigation; paternity analysis; primer; ss.
XX
XX Homo sapiens.
XX
XX WO200129262-A2.
XX
XX 26-APR-2001.
XX
XX 13-OCT-2000; 2000WO-US028436.
XX
XX 15-OCT-1999; 99US-0160096P.
XX
XX (ORCH-) ORCHID BIOSCIENCES INC.
XX
XX Picoult-Newburg L, Pohl M;
XX
XX WPI; 2001-290930/30.
XX
XX New genotyping oligonucleotide, useful for detecting the presence,
XX absence or identity of single polynucleotide polymorphism in a nucleic
XX acid sample.
XX
XX Claim 1; Page 65; 63pp; English.
XX
CC Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
CC primer extension (SNPE) primers, and the sequences of regions flanking
CC sites of single nucleotide polymorphisms SNPs. The present invention
CC includes kits for determining the presence or absence of a SNP, using the
CC oligonucleotides of the invention. The PCR primers are used to amplify a
CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.
CC The oligonucleotides are useful for genotyping a nucleic acid sample by
CC performing a single-nucleotide primer extension reaction. The
CC oligonucleotides are useful for determining the presence, absence or
CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to
CC assess by association analysis the genotype of an individual or group of
CC individuals, having a pathological phenotypic trait suspected of being
CC caused by one or more SNPs. Phenotypic traits include diseases e.g.
CC agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
CC traits also include symptoms of or susceptibility to multifactorial
CC disease of which a component is or may be genetic such as autoimmune
CC diseases, including, rheumatoid arthritis, multiple sclerosis,

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RESULT 79
AAQ34170
ID AAQ34170 standard; DNA; 20 BP.
XX
AC AAQ34170;
XX
XX 25-MAR-2003 (revised)
DT 02-FEB-1993 (first entry)
XX
DE Sequence of a microsatellite from clone TGLA86.
XX
XX PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
KW genetic mapping; traits; amplification; ss.
XX
OS Bos taurus.
XX
XX WO9213102-A1.
PN
XX 06-AUG-1992.
PD
XX 15-JAN-1992; 92WO-US000340.
PF
XX 15-JAN-1991; 91US-00642342.
PR
XX (GENM-) GENMARK.
PA
XX Georges M, Massey JM;
PI
XX WPI; 1992-284684/34.
DR
XX Polymorphic bovine DNA markers - used in genetic identification, gene
PT mapping, and selective breeding.
PT
XX Table 7; Page 397; 517pp; English.
PS
XX The sequence is that of a bovine microsatellite sequence obtd. by
CC screening a library of bovine MboI DNA fragments of between 250 and 500
CC bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
CC clones cross-hybridised. Assuming independent distribution of
CC microsatellites and MboI sites, the frequency of (T6)n > 9 microsatellites
CC in the bovine genome is estimated at >100,000. The sequence information
CC for ca. 230 such bovine microsatellites is summarised in the
CC specification and indexed herein (see below). The sequences upstream and
CC downstream of the microsatellite sequence were used to generate the
CC required PCR primers for in vitro amplification of the corresp.
CC microsatellite (using the program OPTIPRIM). The microsatellites may be
CC used to identify individuals, for parentage testing, and in the genetic
CC mapping of economically important traits esp. in cattle, to allow selective
CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
SQ Sequence 20 BP; 0 A; 0 C; 10 G; 10 T; 0 U; 0 Other;
Query Match 1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTG 1812
DB 1 TGTGTGTGTGTGTGTGTGTG 20

RESULT 80
AAQ33816
ID AAQ33816 standard; DNA; 20 BP.
XX
AC AAQ33816;
XX
XX 25-MAR-2003 (revised)
DT 02-FEB-1993 (first entry)
XX
DE Microsatellite sequence from clone TGLA22.

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XX
KW PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
KW genetic mapping; traits; amplification; ss.
XX
OS Bos taurus.
XX
XX WO9213102-A1.
PN
XX 06-AUG-1992.
PD
XX 15-JAN-1992; 92WO-US000340.
PF
XX 15-JAN-1991; 91US-00642342.
PR
XX (GENM-) GENMARK.
PA
XX Georges M, Massey JM;
PI
XX WPI; 1992-284684/34.
DR
XX Polymorphic bovine DNA markers - used in genetic identification, gene
PT mapping, and selective breeding.
PT
XX Table 7; Page 256; 517pp; English.
PS
XX The sequence is that of a bovine microsatellite sequence obtd. by
CC screening a library of bovine MboI DNA fragments of between 250 and 500
CC bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
CC clones cross-hybridised. Assuming independent distribution of
CC microsatellites and MboI sites, the frequency of (T6)n > 9 microsatellites
CC in the bovine genome is estimated at >100,000. The sequence information
CC for ca. 230 such bovine microsatellites is summarised in the
CC specification and indexed herein (see below). The sequences upstream and
CC downstream of the microsatellite sequence were used to generate the
CC required PCR primers for in vitro amplification of the corresp.
CC microsatellite (using the program OPTIPRIM). The microsatellites may be
CC used to identify individuals, for parentage testing, and in the genetic
CC mapping of economically important traits esp. in cattle, to allow selective
CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
SQ Sequence 20 BP; 0 A; 0 C; 10 G; 10 T; 0 U; 0 Other;
Query Match 1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTG 1812
DB 1 TGTGTGTGTGTGTGTGTGTG 20

RESULT 81
AAQ33672
ID AAQ33672 standard; DNA; 20 BP.
XX
AC AAQ33672;
XX
XX 25-MAR-2003 (revised)
DT 02-FEB-1993 (first entry)
XX
DE Microsatellite sequence from clone TGLA116.
XX
KW PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
KW genetic mapping; traits; amplification; ss.
XX
OS Bos taurus.
XX
XX WO9213102-A1.
PN
XX 06-AUG-1992.

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PF 15-JAN-1992; 92WO-US000340.  
 XX  
 PR 15-JAN-1991; 91US-00642342.  
 XX  
 PA (GENM-) GENMARK.  
 XX  
 PI Georges M, Massey JM;  
 XX  
 DR WPI; 1992-284684/34.  
 XX

XX  
 DR Polymorphic bovine DNA markers - used in genetic identification, gene  
 XX mapping, and selective breeding.  
 PT  
 PT  
 XX  
 PS Table 7; Page 198; 517pp; English.  
 XX

XX The sequence is that of a bovine microsatellite sequence obtd. by  
 CC screening a library of bovine MboI DNA fragments of between 250 and 500  
 CC bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50  
 CC clones cross-hybridised. Assuming independent distribution of  
 CC microsatellites and MboI sites, the frequency of (16)n > 9 microsatellites  
 CC in the bovine genome is estimated at >100, 000. The sequence information  
 CC for ca. 230 such bovine microsatellites is summarised in the  
 CC specification and indexed herein (see below). The sequences upstream and  
 CC downstream of the microsatellite sequence were used to generate the  
 CC required PCR primers for in vitro amplification of the corresp.  
 CC microsatellite (using the program OPTIPRIM). The microsatellites may be  
 CC used to identify individuals, for parentage testing, and in the genetic  
 CC mapping of economic trait loci, or genes involved in the determination of  
 CC economically important traits esp. in cattle, to allow selective  
 CC breeding, for example this microsatellite is a marker for the Weaver  
 CC condition and the QTL trait of enhanced milk prodn. in Brown Swiss  
 CC cattle. See also AAQ33501-34442. (Updated on 25-MAR-2003 to correct PN  
 CC field.)  
 XX

XX Sequence 20 BP; 0 A; 0 C; 10 G; 10 T; 0 U; 0 Other;  
 XX  
 Query Match 1.9%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 60;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1794 GTGTGTGTGTGTGTGTGTGT 1813  
 DB 1 GTGTGTGTGTGTGTGTGTGT 20  
 RESULT 82  
 AAT30427/C  
 ID AAT30427 standard; DNA; 20 BP.  
 XX  
 AC AAT30427;  
 XX  
 DT 28-JAN-1997 (first entry)  
 XX  
 DE Compound simple sequence repeat primer (CA)4.5(TA)7.5.  
 XX  
 KW Detection; polymorphism; perfect compound simple sequence repeat;  
 KW adaptor directed primer; genome; genetic; fingerprinting;  
 KW amplified fragment length polymorphism assay; microsatellite region;  
 KW genetic trait marking; germplasm comparisons; compound; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9617082-A2.  
 XX  
 PD 06-JUN-1996.  
 XX  
 PF 21-NOV-1995; 95WO-US015150.  
 XX  
 PR 28-NOV-1994; 94US-00346456.  
 XX  
 PA (DUPO) DU PONT DE NEMOURS & CO E I.  
 XX  
 PI Morgante M, Vogel JM;  
 XX

XX WPI; 1996-277795/28.  
 XX  
 DR Modified amplified fragment length polymorphism assay - for detection of  
 XX polymorphism esp. in micro:satellite regions.  
 PT  
 PT  
 XX  
 PS Disclosure; Fig 1c; 173pp; English.  
 XX

XX Detecting polymorphisms between 2 nucleic acid samples, esp. in  
 CC microsatellite regions, comprises digesting the nucleic acid to generate  
 CC fragments, ligating adaptor segments to their ends, amplifying them using  
 CC primer directed amplification and comparing the prods. to detect  
 CC differences. The primers used in the amplification comprise a primer  
 CC consisting of a perfect cpd. simple sequence repeat (SSR), and an adaptor  
 CC directed primer, comprising a sequence complementary to an adaptor  
 CC segment. The present sequence is an example of a compound SSR primer. The  
 CC method represents a modified amplified fragment length polymorphism  
 CC assay, which is partic. useful for genome fingerprinting, i.e. for  
 CC genetic trait marking and germplasm comparisons  
 XX

SQ Sequence 20 BP; 10 A; 7 C; 0 G; 3 T; 0 U; 0 Other;  
 XX

Query Match 1.9%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 60;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1799 TGCTGTGTGTGTGTATATA 1818  
 DB 20 TGCTGTGTGTGTGTATATA 1

RESULT 83  
 AAT93829  
 ID AAT93829 standard; DNA; 20 BP.  
 XX  
 AC AAT93829;  
 XX

DT 25-MAR-2003 (revised)  
 DT 24-FEB-1998 (first entry)  
 XX  
 DE Antitumoural phosphodiester oligonucleotide 19 with cytotoxic activity.  
 XX  
 KW Phosphodiester; selective binding; cell viability; growth;  
 KW tumoural cell line; cytotoxic activity; tumour cell; lymphoma;  
 KW lymphoblastic tumour; ss.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_base 1..20  
 FT /\*tag= a  
 FT /note= "phosphodiester oligonucleotide"  
 XX  
 PN WO9720924-A1.  
 XX  
 PD 12-JUN-1997.  
 XX  
 PF 04-DEC-1996; 96WO-EP005388.  
 XX  
 PR 04-DEC-1995; 95IT-MI002539.  
 XX  
 PA (SAIC-) SAICOM SRL.  
 XX  
 PI Scaggiante B, Quadrifoglio F;  
 XX  
 DR WPI; 1997-319771/29.  
 XX  
 PT New phospho:di:esteric oligo:nucleotide(s) - which exert a specific and  
 PT selective cytotoxic effect on tumour cells, for treating both solid and  
 PT liquid tumours.  
 XX  
 PS Claim 11; Page 4; 38pp; English.  
 XX

CC The present phosphodiesteric oligonucleotide is based on the generic  
CC formula, in the 3'-5' or 5'-3' direction: (GaTa')a''-(GbTb')b''-  
CC (GcTc')c''-(GdTd')d''-(GeTe')e''-(GfTf')f''-(GgTg')g''-N', where: N and  
CC N' = T or G, equal or different from each other; x = 0-8, equal or  
CC different from each other; a, b, c, d, e, f, and g = 0-10, equal or  
CC different from each other; a', b', c', d', e', f', and g' = 1-  
CC 16, equal or different from each other; a'', b'', c'', d'', e'', f'', and g'' = 1-  
CC 16, equal or different from each other; Oligonucleotides of this generic  
CC sequence (see also AAT93811-27) are believed to selectively bind and  
CC sequester some proteins which are essential to the viability and growth  
CC of tumoural cell line. They have specific and selective cytotoxic  
CC activity against tumour cells, and can be used for treating tumours of  
CC the liquid type, in particular of lymphoblastic origin, and of solid  
CC type, in particular lymphomas. The present oligonucleotide is known, but  
CC no biological activity has been reported until the reported cytotoxic  
CC antitumour activity. (Updated on 25-MAR-2003 to correct PR field.)  
XX  
SQ Sequence 20 BP; 0 A; 0 C; 10 G; 10 T; 0 U; 0 Other;

Query Match 1.9%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 60;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTGTGTGTGTGT 1813  
Db 1 GTGTGTGTGTGTGTGTGTGTGTGTGT 20

RESULT 84  
AAV06824  
ID AAV06824 standard; DNA; 20 BP.  
AC AAV06824;  
XX  
DT 01-JUL-1998 (first entry)  
XX  
DE Oligonucleotide which binds retroviral nucleocapsid protein.  
XX  
KW Retroviral nucleocapsid protein; NC; high affinity; viral replication;  
KW gene therapy; retroviral infection; HIV; transduced cell; ss.  
XX  
OS Synthetic.  
XX  
PN WO9744064-A2.  
XX  
PD 27-NOV-1997.  
XX  
PF 19-MAY-1997; 97WO-US008936.  
XX  
PR 20-MAY-1996; 96US-0017128P.  
XX  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX  
PI Rein A, Casas-Finet J, Fisher R, Fivash M, Henderson LE;  
XX  
DR WPT; 1998-018230/02.  
XX  
PT Oligo:nucleotide which binds to retroviral nucleocapsid protein with high  
PT affinity - used in targeted molecules, transduced cells and gene therapy  
PT vectors for treatment of retroviral infections such as those caused by  
PT HIV.  
XX  
PS Claim 7; Page 56; 70pp; English.  
XX  
CC This sequence represents an oligonucleotide which binds to a retroviral  
CC nucleocapsid (NC) protein with high affinity. The invention relates to a  
CC targeted molecule which binds to a retroviral nucleocapsid protein with  
CC high affinity and comprises the oligonucleotide and a fusion partner.  
CC Retroviral nucleocapsid proteins, such as NC and the Gag precursors, bind  
CC to specific nucleic acid sequences with high affinity. This binding is  
CC dependent upon the zinc fingers of the NC protein and has a strong  
CC hydrophobic component. The specific nucleic acid sequences which bind NC  
CC are useful as molecular decoys for retroviral NC proteins, for making

CC fusion proteins which inactivate retroviral NC proteins, in screening  
CC assays for detecting molecules which inactivate retroviral NC proteins  
CC nucleic acid binding, and for purification of retroviral NC proteins. In  
CC particular, the targeted molecules, the transduced cells and gene therapy  
CC vectors based on the oligonucleotides can be used for treatment and  
CC prevention of retroviral infections such as those caused by HIV  
XX  
SQ Sequence 20 BP; 0 A; 0 C; 10 G; 10 T; 0 U; 0 Other;

Query Match 1.9%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 60;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTGTGTGTGT 1812  
Db 1 TGTGTGTGTGTGTGTGTGTGTGTGTGT 20

RESULT 85  
AAA39091  
ID AAA39091 standard; DNA; 20 BP.  
XX  
AC AAA39091;  
XX  
DT 30-AUG-2000 (first entry)  
XX  
DE 20-mer oligonucleotide sequence.  
XX  
KW Displacement chromatography; purification; separation; ss.  
XX  
OS Unidentified.  
XX  
PN WO200023798-A1.  
XX  
PD 27-APR-2000.  
XX  
PF 20-OCT-1999; 99WO-GB003463.  
XX  
PR 20-OCT-1998; 98GB-00022963.  
XX  
PA (MARS/) MARSDEN J C.  
PA (AGNE/) AGNER E.  
XX  
PI Agner E;  
XX  
DR WPI; 2000-339759/29.  
XX  
PT Displacement chromatography for purification of peptide samples by non-  
PT homogeneous application of sample components to chromatography bed.  
XX  
PS Example 2; Page 22; 37pp; English.  
XX  
CC The present invention describes a method (I) for sample displacement  
CC chromatography separation. The method comprises applying a multicomponent  
CC sample to one end of a chromatography bed, distributing the sample along  
CC the bed by passing non-eluting mobile solvent phase over the bed, and  
CC recovering a desired component of the sample from at least portion of the  
CC bed. The sample components are applied in a non-homogeneous manner to  
CC enhance concentration of at least one component with relatively low  
CC and/or high affinity for the stationary phase material, respectively,  
CC during an earlier and later part of the sample application. The method is  
CC useful for chromatographic separation of samples. The method permits  
CC recovery of sample components at significantly higher concentrations and  
CC generally makes more efficient use of the stationary phase material. The  
CC method allows ten-fold greater loading than comparable gradient elution  
CC separation, it involves minimal use of costly HPLC solvents and fraction  
CC analysis, avoids the use of displacer solution during actual separation  
CC and operating costs are lower. The present sequence represents a 20-mer  
CC oligonucleotide which is used in an example from the present invention  
CC for the purification of an oligonucleotide by sample displacement  
CC chromatography  
XX  
SQ Sequence 20 BP; 0 A; 0 C; 10 G; 10 T; 0 U; 0 Other;

Query Match

XXI

XX Treating systemic lupus erythematosus in individual comprises e.g.  
PT administering conjugate comprising non-immunogenic valency platform  
PT molecule and double stranded DNA epitopes which specifically bind to  
PT antibody from individual.

XX Claim 4; Page 57; 87pp; English.

XX The present invention describes a method of treating systemic lupus  
CC erythematosus and lupus nephritis, involving administering a conjugate  
CC comprising a non-immunogenic valency platform molecule and 2 double  
CC stranded DNA epitopes which specifically bind to dsDNA-binding  
CC antibodies. Affinity of the epitopes for the antibody is used as a basis  
CC for selecting individuals to receive treatment. The present sequence is  
CC an antibody binding dsDNA sequence described in the exemplification of  
CC the invention

XX Sequence 20 BP; 0 A; 0 C; 10 G; 10 T; 0 U; 0 Other;  
SQ Query Match 1.9%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 60;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTGTGTGTGTGTGT 1813  
DB 1 GTGTGTGTGTGTGTGTGTGTGTGTGTGT 20

RESULT 92  
AAH64445/C  
ID AAH64445 standard; DNA; 20 BP.  
AC AAH64445;  
XX XX  
DT 23-NOV-2001 (first entry)  
XX XX  
DE SSR motif #5.  
XX Simple Sequence Repeat; SSR; clover; microsatellite; genome mapping;  
KW trait mapping; marker-assisted selection; gene selection; legume;  
XX DNA profiling; breeding; ds.  
XX Unidentified.  
OS OS  
PN NZ509194-A.  
XX XX  
PD 25-MAY-2001.  
XX 03-JAN-2001; 2001NZ-00509194.  
XX 24-DEC-1999; 99AU-00004907.  
PR 28-MAR-2000; 2000AU-00006520.  
XX XX  
PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
XX Koelliker R, Forster JW;  
PI WPI; 2001-431058/46.  
XX Novel simple sequence repeats in clover species useful for selection of  
PT genes in legume breeding, for profiling legume species varieties and for  
PT testing the purity of legume seed batches.

XX Claim 6; Page 35; 52pp; English.

XX The present invention relates to Simple Sequence Repeats (SSRs) from  
CC clover species. SSRs, also called microsatellites, are based on a 1-7  
CC nucleotide core element which is tandemly repeated. The SSR array is  
CC embedded in complex flanking DNA. SSRs are ideal markers for genome  
CC mapping, trait mapping and marker-assisted selection. The SSRs may be  
CC used in methods for selecting genes in clover/legume breeding. The SSRs  
CC are also useful for DNA profiling of clover varieties and for testing the  
CC purity of legume seed batches. The present sequence is a SSR motif, which

XX Treating systemic lupus erythematosus in individual comprises e.g.  
PT administering conjugate comprising non-immunogenic valency platform  
PT molecule and double stranded DNA epitopes which specifically bind to  
PT antibody from individual.

XX Claim 4; Page 57; 87pp; English.

XX The present invention describes a method of treating systemic lupus  
CC erythematosus and lupus nephritis, involving administering a conjugate  
CC comprising a non-immunogenic valency platform molecule and 2 double  
CC stranded DNA epitopes which specifically bind to dsDNA-binding  
CC antibodies. Affinity of the epitopes for the antibody is used as a basis  
CC for selecting individuals to receive treatment. The present sequence is  
CC an antibody binding dsDNA sequence described in the exemplification of  
CC the invention

XX Sequence 20 BP; 0 A; 0 C; 10 G; 10 T; 0 U; 0 Other;  
SQ Query Match 1.9%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 60;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTGTGTGTGTGTGT 1813  
DB 1 GTGTGTGTGTGTGTGTGTGTGTGTGTGT 20

RESULT 92  
AAH64445/C  
ID AAH64445 standard; DNA; 20 BP.  
AC AAH64445;  
XX XX  
DT 23-NOV-2001 (first entry)  
XX XX  
DE SSR motif #5.  
XX Simple Sequence Repeat; SSR; clover; microsatellite; genome mapping;  
KW trait mapping; marker-assisted selection; gene selection; legume;  
XX DNA profiling; breeding; ds.  
XX Unidentified.  
OS OS  
PN NZ509194-A.  
XX XX  
PD 25-MAY-2001.  
XX 03-JAN-2001; 2001NZ-00509194.  
XX 24-DEC-1999; 99AU-00004907.  
PR 28-MAR-2000; 2000AU-00006520.  
XX XX  
PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
XX Koelliker R, Forster JW;  
PI WPI; 2001-431058/46.  
XX Novel simple sequence repeats in clover species useful for selection of  
PT genes in legume breeding, for profiling legume species varieties and for  
PT testing the purity of legume seed batches.

XX Claim 6; Page 35; 52pp; English.

XX The present invention relates to Simple Sequence Repeats (SSRs) from  
CC clover species. SSRs, also called microsatellites, are based on a 1-7  
CC nucleotide core element which is tandemly repeated. The SSR array is  
CC embedded in complex flanking DNA. SSRs are ideal markers for genome  
CC mapping, trait mapping and marker-assisted selection. The SSRs may be  
CC used in methods for selecting genes in clover/legume breeding. The SSRs  
CC are also useful for DNA profiling of clover varieties and for testing the  
CC purity of legume seed batches. The present sequence is a SSR motif, which

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02-JUL-1998; 98US-0091481P.
11-DEC-1998; 98US-0111800P.
02-JUL-1999; 99US-00347443.
(REGC ) UNIV CALIFORNIA.
Dev AP, Bruice TC;
WPI; 2001-122276/13.
Preparing novel deoxynucleic alkyl thiourea oligonucleotide for use in
antisense therapy, by synthesizing oligonucleotides comprising backbone
of alkyl or alkoxy thiourea linkages in solution or on solid phase.
Example 7; Fig 16; 48pp; English.
The present sequence was used to demonstrate the ability of deoxynucleic
S-methylthiourea (DMt) compounds to form triplexes with DNA oligomers. An
increase in the C content of the oligos resulted in a large decrease in
binding. This experiment was performed as an example of a method for
preparing oligonucleotides comprising a backbone of alkyl or alkoxy
thiourea linkages. The method is useful for preparing oligonucleotides
for use in antisense or antigen therapy, to inhibit production of
proteins associated with genetic diseases, cardiovascular, inflammatory
and neurocellular diseases, and for antiviral therapy, e.g. to treat
human immunodeficiency virus, human-cytomegalovirus, influenza and herpes
infections. The compounds are also useful as diagnostic reagents to
detect the presence or absence of the target DNA or RNA sequences to
which they specifically bind and by antagonising the normal biological
activity of a target protein, they can be used in the manipulation of
tissue e.g. tissue differentiation, both in vivo and in ex vivo tissue
cultures. The method provides an efficient and rapid solid-phase method
for the synthesis of thiourea and S-methylthiourea
XX
SQ Sequence 20 BP; 10 A; 10 C; 0 G; 0 T; 0 U; 0 Other;
Query Match 1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred.No.60;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1793 TGTGTGTGTGTGTGTGTG 1812
DB 20 TGTGTGTGTGTGTGTG 1
RESULT 91
AAH48201
ID AAH48201 standard; DNA; 20 BP.
XX AC AAH48201;
XX AC
XX AC
DT 20-SEP-2001 (first entry)
XX XX
XX XX
DE Antibody binding oligonucleotide.
XX XX
XX Antibody affinity; DNA epitope; anti-DNA antibody; lupus nephritis;
XX KW systemic lupus erythematosus; immunotolerance; ds.
XX OS Synthetic.
XX OS
XX WO200141813-A2.
XX FN
XX PN
XX 14-JUN-2001.
XX PD
XX 28-NOV-2000; 2000WO-US042307.
XX PF
XX 28-NOV-1999; 99US-0167716P.
XX PR
XX (LJOL-) LA JOLLA PHARM CO.
XX PA
XX Linnik MD, Mcnealy PA;
XX FI
XX WPI; 2001-451501/48.
XX DR

```



CC was used in the present invention

XX Sequence 20 BP; 10 A; 10 C; 0 G; 0 T; 0 U; 0 Other;

SQ Query Match 1.9%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 60;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTGT 1813

Db 20 GTGTGTGTGTGTGTGTGT 1

RESULT 93

AAI64449

ID AAI64449 standard; DNA; 20 BP.

XX AAI64449;

DT 23-NOV-2001 (first entry)

DE SSR motif #9.

XX Simple Sequence Repeat; SSR; clover; microsatellite; genome mapping;  
KW trait mapping; marker-assisted selection; gene selection; legume;  
KW DNA profiling; breeding; ds.

XX Unidentified.

OS NZ509194-A.

PN 25-MAY-2001.

PD 03-JAN-2001; 2001NZ-00509194.

PF 24-DEC-1999; 99AU-00004907.

PR 28-MAR-2000; 2000AU-00006520.

XX (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.

XX Koelliker R, Forster JW;

PI WPI; 2001-431058/46.

XX Novel simple sequence repeats in clover species useful for selection of  
PT genes in legume breeding, for profiling legume species varieties and for  
PT testing the purity of legume seed batches.

XX Claim 6; Page 35; 52pp; English.

XX The present invention relates to Simple Sequence Repeats (SSRs) from  
CC clover species. SSRs, also called microsatellites, are based on a 1-7  
CC nucleotide core element which is tandemly repeated. The SSR array is  
CC embedded in complex flanking DNA. SSRs are ideal markers for genome  
CC mapping, trait mapping and marker-assisted selection. The SSRs may be  
CC used in methods for selecting genes in clover/ legume breeding. The SSRs  
CC are also useful for DNA profiling of clover varieties and for testing the  
CC purity of legume seed batches. The present sequence is a SSR motif, which  
CC was used in the present invention

XX Sequence 20 BP; 0 A; 0 C; 10 G; 10 T; 0 U; 0 Other;

Query Match 1.9%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 60;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTGT 1813

Db 1 GTGTGTGTGTGTGTGTGT 20

RESULT 94

ABK87132

ID ABK87132 standard; DNA; 20 BP.

XX ABK87132;

AC 07-OCT-2002 (first entry)

XX Human connective tissue growth factor, RT-PCR primer #2.

XX Human, endothelial cell-specific molecule 4; ECSM4; neovasculature;  
KW imaging vascular endothelium; proliferative disease; cancer; psoriasis;  
KW diabetic retinopathy; atherosclerosis; menorrhagia; endothelial damage;  
KW tumour neovasculature; cardiac disease; endometriosis; hypoxic condition;  
KW angiogenesis; cytostatic; RT-PCR; connective tissue growth factor;  
KW reverse transcription-PCR; primer; ss.

XX Homo sapiens.

OS W0200236771-A2.

PN 10-MAY-2002.

PD 06-NOV-2001; 2001WO-GB004906.

PF 06-NOV-2000; 2000US-0245566P.

PP 07-MAR-2001; 2001US-0273662P.

XX (IMCR ) IMPERIAL CANCER RES TECHNOLOGY LTD.

PI Bicknell R, Huminiecki L;

PN WPI; 2002-508120/54.

XX Novel endothelial cell-specific molecule polypeptide 1 or 4, useful for  
PT imaging, diagnosing and treating a condition involving vascular  
PT endothelium e.g. cancer, cardiac disease, endometriosis, diabetes.

XX Example 1; Page 165; 248pp; English.

XX The present invention relates to endothelial cell-specific molecule 4  
CC (ECSM4), and the polynucleotide sequences encoding it. The ECSM4 proteins  
CC are useful for imaging vascular endothelium in the body of an individual,  
CC and for diagnosing and treating a proliferative disease or condition  
CC involving the vascular endothelium (preferably, neovasculature) such as  
CC cancer, psoriasis, diabetic retinopathy, atherosclerosis or menorrhagia.  
CC The ECSM4 proteins are also useful in the manufacture of diagnostic or  
CC prognostic agent for such conditions. The proteins are also useful for  
CC detecting endothelial damage or activation, detecting a tumour or tumour  
CC neovasculature, cardiac disease, or endometriosis by detecting the amount  
CC of ECSM4 present in a sample. The polynucleotide sequences encoding ECSM4  
CC are useful in gene therapy for treating a hypoxic condition such as  
CC cancer, cardiac disease, endometriosis or atherosclerosis and in the  
CC manufacture of medicaments for treating the above disease. The sequences  
CC are useful for modulating angiogenesis in an individual. The present  
CC sequence represents a RT-PCR primer for RNA encoding human connective  
CC tissue growth factor

SQ Sequence 20 BP; 8 A; 3 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 1.9%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 60;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1951 CGTTCAAAGCATGAATGGA 1970

Db 1 CGTTCAAAGCATGAATGGA 20

RESULT 95

AAI45125

ID AAI45125 standard; DNA; 20 BP.

XX AAI45125;

AC AAI45125;

XX

DT 24-MAY-2002 (first entry)  
XX Oligonucleotide synthesis method related DNA #4.  
DE  
XX Oligonucleotide synthesis; polynucleotide array; protecting group;  
KW oxidation; ss.  
XX  
OS Synthetic.  
XX  
XX EP1176151-A1.  
XX  
XX 30-JAN-2002.  
PD  
XX  
XX 27-JUL-2001; 2001EP-00118360.  
PF  
XX 28-JUL-2000; 2000US-00627249.  
XX  
XX (AGIL-) AGILENT TECHNOLOGIES INC.  
PA  
XX Dellinger DJ, Perbost MCM, Betley JR, Caruthers M;  
PI WPI; 2002-156732/21.  
XX  
XX  
XX Synthesis of polynucleotide useful during fabrication of an array  
PT involves coupling nucleoside phosphoramidite and a solid-supported  
PT nucleoside and treating the product with an oxidation/deprotection  
PT composition.  
XX  
XX Example 1; Page 15; 36pp; English.  
PS  
XX The present invention relates to a method for the synthesis of a  
CC polynucleotide which involves coupling a second nucleoside to a first  
CC nucleoside through a phosphite linkage, where the second nucleoside has a  
CC non-carbonate protecting group protecting a hydroxyl, and exposing the  
CC product to a composition which concurrently oxidizes the phosphite formed  
CC to a phosphate and deprotects the protected hydroxyl of the second  
CC nucleoside. The method is useful for synthesizing the polynucleotides,  
CC for carrying out either 3' to 5' or 5' to 3' synthesis and for  
CC fabricating an addressable array of polynucleotides on a substrate. The  
CC present sequence is an oligonucleotide produced to demonstrate the method  
CC of the invention  
XX  
XX Sequence 20 BP; 0 A; 0 C; 10 G; 10 T; 0 U; 0 Other;  
SQ

Query Match 1.9%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 60;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1793 TGTGTGTGTGTGTGTGTGTG 1812  
DB 1 TGTGTGTGTGTGTGTGTGTG 20

RESULT 96  
ABA96307/c  
ID ABA96307 standard; DNA; 20 BP.  
AC ABA96307;  
XX  
XX 18-MAR-2002 (first entry)  
DT  
XX Oligonucleotide SEQ ID NO 2.  
DE  
XX Immobilisation; Diels-Alder reaction; ss.  
KW  
XX Synthetic.  
OS  
XX Key Location/Qualifiers  
FH 1  
FT /\*tag= a  
FT /mod base= OTHER  
FT /note= "5, fluorescein label"  
XX

PN WO200184234-A1.  
XX  
PD 08-NOV-2001.  
XX  
XX 01-MAY-2001; 2001WO-US013956.  
PF  
XX 01-MAY-2000; 2000US-0201561P.  
PR  
XX 30-JAN-2001; 2001US-0265020P.  
PR  
XX (PROL-) PROLIGO LLC.  
PA  
XX Picken W, Wolter A, Sebesta DP, Leuck M, Latham-Timmons HA;  
PI Pilon J, Husar GM;  
XX  
XX WPI; 2002-114155/15.  
DR  
XX  
XX New method for immobilizing a molecule on a support comprises reacting a  
PT derivatized molecule with a derivatized support via a cycloaddition  
PT reaction, shows high selectivity and efficiency.  
XX  
XX Example 6; Page 31; 86pp; English.  
PS  
XX The invention relates to a method for immobilising a molecule on a  
CC support comparing reacting a derivatised molecule with a derivatised  
CC support capable of reacting with the molecule via a cycloaddition  
CC reaction. The method is used for immobilising molecules on a support  
CC using cycloaddition reactions such as the Diels-Alder reaction. The  
CC method shows better chemoselectivity, functional groups do not need to be  
CC protected and it is highly efficient for immobilising molecules compared  
CC to other methods. The present sequence is that of an oligonucleotide,  
CC useful to the invention  
XX  
XX Sequence 20 BP; 10 A; 10 C; 0 G; 0 T; 0 U; 0 Other;  
SQ

Query Match 1.9%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 60;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1793 TGTGTGTGTGTGTGTGTGTG 1812  
DB 20 TGTGTGTGTGTGTGTGTGTG 1

RESULT 97  
ABA96306  
ID ABA96306 standard; DNA; 20 BP.  
XX  
XX ABA96306;  
AC  
XX 18-MAR-2002 (first entry)  
DT  
XX Oligonucleotide SEQ ID NO 1.  
DE  
XX Immobilisation; Diels-Alder reaction; ss.  
KW  
XX Synthetic.  
OS  
XX WO200184234-A1.  
PN  
XX 08-NOV-2001.  
PD  
XX  
XX 01-MAY-2001; 2001WO-US013956.  
PF  
XX 01-MAY-2000; 2000US-0201561P.  
PR  
XX 30-JAN-2001; 2001US-0265020P.  
PR  
XX (PROL-) PROLIGO LLC.  
PA  
XX Picken W, Wolter A, Sebesta DP, Leuck M, Latham-Timmons HA;  
PI Pilon J, Husar GM;  
XX  
XX WPI; 2002-114155/15.  
DR  
XX

PT New method for immobilizing a molecule on a support comprises reacting a  
PT derivatized molecule with a derivatized support via a cycloaddition  
PT reaction, shows high selectivity and efficiency.  
XX  
PS  
XX Example 6; Page 31; 86pp; English.  
XX  
XX The invention relates to a method for immobilising a molecule on a  
XX support comprising reacting a derivatised molecule with a derivatised  
XX support capable of reacting with the molecule via a cycloaddition  
XX reaction. The method is used for immobilising molecules on a support  
XX using cycloaddition reactions such as the Diels-Alder reaction. The  
XX method shows better chemoselectivity, functional groups do not need to be  
XX protected and it is highly efficient for immobilising molecules compared  
XX to other methods. The present sequence is that of an oligonucleotide,  
XX useful to the invention  
XX  
SQ Sequence 20 BP; 0 A; 0 C; 10 G; 10 T; 0 U; 0 Other;  
Query Match 1.9%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 60;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1793 TGTGTGTGTGTGTGTGTG 1812  
Db 1 TGTGTGTGTGTGTGTGTG 20  
RESULT 98  
ID ABZ24438/c  
XX ABZ24438 standard; DNA; 20 BP.  
XX  
AC ABZ24438;  
XX  
XX 18-MAR-2003 (first entry)  
XX  
XX Oligonucleotide (CA)10 used in nucleic acid hybridisation.  
XX  
XX Nucleic acid detection; hybridisation; microarray; thermistor;  
XX microcalorimetry; ss.  
XX Synthetic.  
XX WO200299386-A2.  
XX 07-JUN-2002; 2002WO-US018200.  
XX 12-DEC-2002.  
XX  
XX 07-JUN-2002; 2002WO-US018200.  
XX  
XX 07-JUN-2001; 2001US-0296685P.  
XX  
XX (PROL-) PROLIGO LLC.  
XX  
XX Roach JS, Wolter A;  
XX  
XX WPI; 2003-148685/14.  
XX  
XX  
XX Detection device useful for detecting binding between members of specific  
XX binding pair, and for multiparallel thermal analysis of samples, has an  
XX array of addressable thermistors.  
XX  
XX Example 2; Page 36; 60pp; English.  
XX  
XX The present sequence is that of a (CA)10 oligonucleotide used to  
XX illustrate the method of the invention. The invention provides methods  
XX for detecting specific binding interactions through measuring the heat of  
XX binding generated when members of specific binding pairs interact with  
XX each other. The invention also provides methods to detect analytes in a  
XX solution through measurement of the heat of binding or reaction generated  
XX from the interaction of the analytes with binding or reaction partners.  
XX Detection devices are provided that consist of spatially addressable  
XX arrays of thermistors, which are useful in the multiparallel thermal  
XX analysis of samples. The methods and devices are particularly in the  
XX analysis of nucleic acids, especially DNA/DNA, DNA/RNA, DNA/LNA (linear

CC nucleic acid), DNA/siRNA (short interfering RNA) and DNA/PNA (peptide  
CC nucleic acid). The binding between the analyte and its binding partner  
CC comprises part of an enzymatic amplification reaction, especially PCR or  
CC primer extension reaction. The detection device provides a real time,  
CC digital profile of the binding or reaction between the analyte and its  
CC binding or reaction partner. An example from the invention, using the  
CC present oligonucleotide, showed that the thermal detection technique is  
CC able to distinguish between perfectly matched and mismatched DNA  
CC sequences  
XX  
SQ Sequence 20 BP; 10 A; 10 C; 0 G; 0 T; 0 U; 0 Other;  
Query Match 1.9%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 60;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1793 TGTGTGTGTGTGTGTGTG 1812  
Db 20 TGTGTGTGTGTGTGTGTG 1  
RESULT 99  
ID ABZ24439  
XX ABZ24439 standard; DNA; 20 BP.  
XX  
AC ABZ24439;  
XX  
XX 18-MAR-2003 (first entry)  
XX  
XX Oligonucleotide (TG)10 used in nucleic acid hybridisation.  
XX  
XX Nucleic acid detection; hybridisation; microarray; thermistor;  
XX microcalorimetry; ss.  
XX Synthetic.  
XX WO200299386-A2.  
XX 12-DEC-2002.  
XX  
XX 07-JUN-2002; 2002WO-US018200.  
XX  
XX 07-JUN-2001; 2001US-0296685P.  
XX  
XX (PROL-) PROLIGO LLC.  
XX  
XX Roach JS, Wolter A;  
XX  
XX WPI; 2003-148685/14.  
XX  
XX  
XX Detection device useful for detecting binding between members of specific  
XX binding pair, and for multiparallel thermal analysis of samples, has an  
XX array of addressable thermistors.  
XX  
XX Example 2; Page 36; 60pp; English.  
XX  
XX The present sequence is that of a (TG)10 oligonucleotide used to  
XX illustrate the method of the invention. The invention provides methods  
XX for detecting specific binding interactions through measuring the heat of  
XX binding generated when members of specific binding pairs interact with  
XX each other. The invention also provides methods to detect analytes in a  
XX solution through measurement of the heat of binding or reaction generated  
XX from the interaction of the analytes with binding or reaction partners.  
XX Detection devices are provided that consist of spatially addressable  
XX arrays of thermistors, which are useful in the multiparallel thermal  
XX analysis of samples. The methods and devices are particularly in the  
XX analysis of nucleic acids, especially DNA/DNA, DNA/RNA, DNA/LNA (linear

CC present oligonucleotide, showed that the thermal detection technique is  
CC able to distinguish between perfectly matched and mismatched DNA  
CC sequences  
SQ Sequence 20 BP; 0 A; 0 C; 10 G; 10 T; 0 U; 0 Other;  
Query Match 1.9%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 60;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1793 TGTGTGTGTGTGTGTGTG 1812  
DB 1 TGTGTGTGTGTGTGTGTG 20  
RESULT 100  
ADB25647/C  
ID ADB25647 standard; DNA; 20 BP.  
XX AC  
XX ADB25647;  
XX 20-NOV-2003 (first entry)  
XX Human connective tissue growth factor antisense oligo DNA (SeqID 40).  
DE antisense; human; ss; connective tissue growth factor; CTGF;  
KW chromosome 6q23.1; ctgrofact; fibroblast inducible secreted protein;  
KW fisp-12; NOV2;  
KW insulin-like growth factor binding protein-related protein 2; IGFBP-rp2;  
KW IGFBP-8; Hcs24; ecogenin; acute lymphoblastic leukaemia; gene therapy;  
KW hyperproliferative disorder; cancer; pulmonary fibrosis; renal fibrosis;  
KW scleroderma; atherosclerosis; cytostatic; dermatological;  
KW antiarteriosclerotic.  
XX Homo sapiens.  
XX Key Location/Qualifiers  
PH modified\_base 1..20  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "OTHER= phosphorothioate backbone, where 1-5 and  
FT 16-20 are 2' methoxyethyl nucleotides. All cytidines are  
FT 5-methylcytidines"  
XX WC2003053340-A2.  
XX 03-JUL-2003.  
XX 09-DEC-2002; 2002WO-US038618.  
XX 10-DEC-2001; 2001US-00006191.  
XX (ISIS-) ISIS PHARM INC.  
XX Gaarde WA, Watt AT;  
XX WPI; 2003-559091/52.  
XX New antisense oligonucleotides for modulating connective tissue growth  
PT factor expression, particularly useful for treating cancers (e.g. breast  
PT or prostate cancer), pulmonary or renal fibrosis, scleroderma or  
PT atherosclerosis.  
XX Claim 3; Page 85; 139pp; English.  
XX This invention relates to novel methods for modulating the expression of  
CC connective tissue growth factor (CTGF) by antisense oligonucleotides.  
CC CTGF has been mapped to human chromosome region 6q23.1, and is also known  
CC as ctgrofact, fibroblast inducible secreted protein, fisp-12, NOV2,  
CC insulin-like growth factor binding protein-related protein 2, IGFBP-rp2,  
CC IGFBP-8, Hcs24 and ecogenin. It is known to stimulate DNA synthesis and  
CC promote chemotaxis of fibroblasts, however, it is also upregulated in  
CC acute lymphoblastic leukaemia and in tumour or endothelial cells

CC associated with the vasculature. Accordingly, antisense oligonucleotides  
CC that inhibit the expression of CTGF in cells or tissues can be used in  
CC gene therapy to treat various conditions including hyperproliferative  
CC disorders (particularly cancer, e.g. breast, prostate or renal cancer),  
CC pulmonary fibrosis, renal fibrosis, scleroderma and atherosclerosis. As  
CC such, the present invention describes these antisense oligos as having  
CC cytotatic, dermatological and antiarteriosclerotic activities. This  
CC oligonucleotide sequence is a chimeric phosphorothioate antisense oligo  
CC with 2' MOE wings and a deoxy gap, which is used to inhibit expression of  
CC human CTGF of the invention.  
XX SQ Sequence 20 BP; 5 A; 7 C; 4 G; 4 T; 0 U; 0 Other;  
Query Match 1.9%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 60;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1724 CTGCACAGCTTGCGCAAGT 1743  
DB 20 CTGCACAGCTTGCGCAAGT 1  
RESULT 101  
ADB25669/C  
ID ADB25669 standard; DNA; 20 BP.  
XX AC  
XX ADB25669;  
XX 20-NOV-2003 (first entry)  
XX Human connective tissue growth factor antisense oligo DNA (SeqID 62).  
DE antisense; human; ss; connective tissue growth factor; CTGF;  
KW chromosome 6q23.1; ctgrofact; fibroblast inducible secreted protein;  
KW fisp-12; NOV2;  
KW insulin-like growth factor binding protein-related protein 2; IGFBP-rp2;  
KW IGFBP-8; Hcs24; ecogenin; acute lymphoblastic leukaemia; gene therapy;  
KW hyperproliferative disorder; cancer; pulmonary fibrosis; renal fibrosis;  
KW scleroderma; atherosclerosis; cytostatic; dermatological;  
KW antiarteriosclerotic.  
XX Homo sapiens.  
XX Key Location/Qualifiers  
PH modified\_base 1..20  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "OTHER= phosphorothioate backbone, where 1-5 and  
FT 16-20 are 2' methoxyethyl nucleotides. All cytidines are  
FT 5-methylcytidines"  
XX WO2003053340-A2.  
XX 03-JUL-2003.  
XX 09-DEC-2002; 2002WO-US038618.  
XX 10-DEC-2001; 2001US-00006191.  
XX (ISIS-) ISIS PHARM INC.  
XX Gaarde WA, Watt AT;  
XX WPI; 2003-559091/52.  
XX New antisense oligonucleotides for modulating connective tissue growth  
PT factor expression, particularly useful for treating cancers (e.g. breast  
PT or prostate cancer), pulmonary or renal fibrosis, scleroderma or  
PT atherosclerosis.  
XX Claim 3; Page 85; 139pp; English.  
XX This invention relates to novel methods for modulating the expression of

CC connective tissue growth factor (CTGF) by antisense oligonucleotides.  
 CC CTGF has been mapped to human chromosome region 6q23.1, and is also known  
 CC as ctgfact, fibroblast inducible secreted protein, fisp-12, NOV2,  
 CC insulin-like growth factor binding protein-related protein 2, IGFBP-rp2,  
 CC IGFBP-8, Hcs24 and ecogenin. It is known to stimulate DNA synthesis and  
 CC promote chemotaxis of fibroblasts, however, it is also upregulated in  
 CC acute lymphoblastic leukaemia and in tumour or endothelial cells  
 CC associated with the vasculature. Accordingly, antisense oligonucleotides  
 CC that inhibit the expression of CTGF in cells or tissues can be used in  
 CC gene therapy to treat various conditions including hyperproliferative  
 CC disorders (particularly cancer, e.g. breast, prostate or renal cancer),  
 CC pulmonary fibrosis, renal fibrosis, scleroderma and atherosclerosis. As  
 CC such, the present invention describes these antisense oligos as having  
 CC cytosstatic, dermatological and antiarteriosclerotic activities. This  
 CC oligonucleotide sequence is a chimeric phosphorothioate antisense oligo  
 CC with 2' MOE wings and a deoxy gap, which is used to inhibit expression of  
 CC human CTGF of the invention.  
 XX  
 SQ Sequence 20 BP; 6 A; 6 C; 2 G; 6 T; 0 U; 0 Other;  
 Query Match 1.9%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 60;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2206 TTGTTGAGAGTGTGACCAA 2225  
 Db 20 TTGTTGAGAGTGTGACCAA 1  
 RESULT 102  
 ADB25654/C  
 ID ADB25654 standard; DNA; 20 BP.  
 AC ADB25654;  
 XX  
 DT 20-NOV-2003 (first entry)  
 DE Human connective tissue growth factor antisense oligo DNA (SeqID 47).  
 KW antisense; human; ss; connective tissue growth factor; CTGF;  
 KW chromosome 6q23.1; ctgfact; fibroblast inducible secreted protein;  
 KW fisp-12; NOV2;  
 KW insulin-like growth factor binding protein-related protein 2; IGFBP-rp2;  
 KW IGFBP-8; Hcs24; ecogenin; acute lymphoblastic leukaemia; gene therapy;  
 KW hyperproliferative disorder; cancer; pulmonary fibrosis; renal fibrosis;  
 KW scleroderma; atherosclerosis; cytostatic; dermatological;  
 KW antiarteriosclerotic.  
 XX Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_base 1..20  
 FT /\*tag= a  
 FT /mod\_base= OTHER  
 FT /note= "OTHER= phosphorothioate backbone, where 1-5 and  
 FT 16-20 are 2' methoxyethyl nucleotides. All cytidines are  
 FT 5-methylcytidines"  
 XX WO2003053340-A2.  
 XX  
 XX 03-JUL-2003.  
 XX  
 XX 09-DEC-2002; 2002WO-US038618.  
 XX  
 XX 10-DEC-2001; 2001US-00006191.  
 XX  
 XX (ISIS-) ISIS PHARM INC.  
 XX  
 XX Gaarde WA, Watt AT;  
 XX  
 XX WPI; 2003-559091/52.  
 XX  
 XX New antisense oligonucleotides for modulating connective tissue growth

PT factor expression, particularly useful for treating cancers (e.g. breast  
 PT or prostate cancer), pulmonary or renal fibrosis, scleroderma or  
 PT atherosclerosis.  
 XX  
 PS Claim 3; Page 85; 139pp; English.  
 XX  
 CC This invention relates to novel methods for modulating the expression of  
 CC connective tissue growth factor (CTGF) by antisense oligonucleotides.  
 CC CTGF has been mapped to human chromosome region 6q23.1, and is also known  
 CC as ctgfact, fibroblast inducible secreted protein, fisp-12, NOV2,  
 CC insulin-like growth factor binding protein-related protein 2, IGFBP-rp2,  
 CC IGFBP-8, Hcs24 and ecogenin. It is known to stimulate DNA synthesis and  
 CC promote chemotaxis of fibroblasts, however, it is also upregulated in  
 CC acute lymphoblastic leukaemia and in tumour or endothelial cells  
 CC associated with the vasculature. Accordingly, antisense oligonucleotides  
 CC that inhibit the expression of CTGF in cells or tissues can be used in  
 CC gene therapy to treat various conditions including hyperproliferative  
 CC disorders (particularly cancer, e.g. breast, prostate or renal cancer),  
 CC pulmonary fibrosis, renal fibrosis, scleroderma and atherosclerosis. As  
 CC such, the present invention describes these antisense oligos as having  
 CC cytosstatic, dermatological and antiarteriosclerotic activities. This  
 CC oligonucleotide sequence is a chimeric phosphorothioate antisense oligo  
 CC with 2' MOE wings and a deoxy gap, which is used to inhibit expression of  
 CC human CTGF of the invention.  
 XX  
 SQ Sequence 20 BP; 4 A; 5 C; 3 G; 8 T; 0 U; 0 Other;  
 Query Match 1.9%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 60;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2213 GAGTGTGACCAAAAGTTACA 2232  
 Db 20 GAGTGTGACCAAAAGTTACA 1  
 RESULT 103  
 ADB25649/C  
 ID ADB25649 standard; DNA; 20 BP.  
 AC ADB25649;  
 XX  
 DT 20-NOV-2003 (first entry)  
 DE Human connective tissue growth factor antisense oligo DNA (SeqID 42).  
 KW antisense; human; ss; connective tissue growth factor; CTGF;  
 KW chromosome 6q23.1; ctgfact; fibroblast inducible secreted protein;  
 KW fisp-12; NOV2;  
 KW insulin-like growth factor binding protein-related protein 2; IGFBP-rp2;  
 KW IGFBP-8; Hcs24; ecogenin; acute lymphoblastic leukaemia; gene therapy;  
 KW hyperproliferative disorder; cancer; pulmonary fibrosis; renal fibrosis;  
 KW scleroderma; atherosclerosis; cytostatic; dermatological;  
 KW antiarteriosclerotic.  
 XX Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_base 1..20  
 FT /\*tag= a  
 FT /mod\_base= OTHER  
 FT /note= "OTHER= phosphorothioate backbone, where 1-5 and  
 FT 16-20 are 2' methoxyethyl nucleotides. All cytidines are  
 FT 5-methylcytidines"  
 XX WO2003053340-A2.  
 XX  
 XX 03-JUL-2003.  
 XX  
 XX 09-DEC-2002; 2002WO-US038618.  
 XX  
 XX 10-DEC-2001; 2001US-00006191.  
 XX  
 XX

(ISIS-) ISIS PHARM INC.  
Gaarde WA, Watt AT;  
WPI; 2003-559091/52.  
New antisense oligonucleotides for modulating connective tissue growth factor expression, particularly useful for treating cancers (e.g. breast or prostate cancer), pulmonary or renal fibrosis, scleroderma or atherosclerosis.  
Claim 3; Page 85; 139pp; English.  
This invention relates to novel methods for modulating the expression of connective tissue growth factor (CTGF) by antisense oligonucleotides. CTGF has been mapped to human chromosome region 6q23.1, and is also known as ctgrofact, fibroblast inducible secreted protein, fisp-12, NOV2, insulin-like growth factor binding protein-related protein 2, IGFBP-rp2, IGFBP-8, Hcs24 and ecogenin. It is known to stimulate DNA synthesis and promote chemotaxis of fibroblasts, however, it is also upregulated in acute lymphoblastic leukemia and in tumour or endothelial cells associated with the vasculature. Accordingly, antisense oligonucleotides that inhibit the expression of CTGF in cells or tissues can be used in gene therapy to treat various conditions including hyperproliferative disorders (particularly cancer, e.g. breast, prostate or renal cancer), pulmonary fibrosis, renal fibrosis, scleroderma and atherosclerosis. As such, the present invention describes these antisense oligos as having cytostatic, dermatological and antiarteriosclerotic activities. This oligonucleotide sequence is a chimeric phosphorothioate antisense oligo with 2' MOE wings and a deoxy gap, which is used to inhibit expression of human CTGF of the invention.  
Sequence 20 BP; 9 A; 2 C; 1 G; 8 T; 0 U; 0 Other;  
Query Match 1.9%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 60;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1832 AGTTATCTAAGTTAAATTAA 1851  
DB 20 AGTTATCTAAGTTAAATTAA 1  
RESULT 104  
ADB25648/c  
ID ADB25648 standard; DNA; 20 BP.  
XX AC ADB25648;  
XX AC ADB25648;  
XX 20-NOV-2003 (first entry)  
XX Human connective tissue growth factor antisense oligo DNA (SeqID 41).  
XX antisense; human; ss; connective tissue growth factor; CTGF;  
XX chromosome 6q23.1; ctgrofact; fibroblast inducible secreted protein;  
XX fisp-12; NOV2;  
XX insulin-like growth factor binding protein-related protein 2; IGFBP-rp2;  
XX IGFBP-8; Hcs24; ecogenin; acute lymphoblastic leukaemia; gene therapy;  
XX hyperproliferative disorder; cancer; pulmonary fibrosis; renal fibrosis;  
XX scleroderma; atherosclerosis; cytostatic; dermatological;  
XX antiarteriosclerotic.  
XX Homo sapiens.  
XX  
XX Key Location/Qualifiers  
XX modified\_base 1..20  
XX /mod\_base= a  
XX /note= "OTHER= phosphorothioate backbone, where 1-5 and  
XX 16-20 are 2' methoxyethyl nucleotides. All cytidines are  
XX 5-methylcytidines"  
XX  
XX WO2003053340-A2.

XX	03-JUL-2003.
PD	
XX	09-DEC-2002; 2002WO-US038618.
XX	PF
XX	10-DEC-2001; 2001US-00006191.
XX	PR
PA	(ISIS-) ISIS PHARM INC.
XX	
XX	Gaarde WA, Watt AT;
PI	
XX	WPI; 2003-559091/52.
XX	
XX	New antisense oligonucleotides for modulating connective tissue growth
PT	factor expression, particularly useful for treating cancers (e.g. breast
PT	or prostate cancer), pulmonary or renal fibrosis, scleroderma or
PT	atherosclerosis.
XX	
XX	Claim 3; Page 85; 139pp; English.
PS	
XX	
XX	This invention relates to novel methods for modulating the expression of
CC	connective tissue growth factor (CTGF) by antisense oligonucleotides.
CC	CTGF has been mapped to human chromosome region 6q23.1, and is also known
CC	as ctgfract, fibroblast inducible secreted protein, fisp-12, NOV2,
CC	insulin-like growth factor binding protein-related protein 2, IGFBP-rp2,
CC	IGFBP-8, Hcs24 and ecogenin. It is known to stimulate DNA synthesis and
CC	promote chemotaxis of fibroblasts, however, it is also upregulated in
CC	acute lymphoblastic leukaemia and in tumour or endothelial cells
CC	associated with the vasculature. Accordingly, antisense oligonucleotides
CC	that inhibit the expression of CTGF in cells or tissues can be used in
CC	gene therapy to treat various conditions including hyperproliferative
CC	disorders (particularly cancer, e.g. breast, prostate or renal cancer),
CC	pulmonary fibrosis, renal fibrosis, scleroderma and atherosclerosis. As
CC	such, the present invention describes these antisense oligos as having
CC	cytostatic, dermatological and antiarteriosclerotic activities. This
CC	oligonucleotide sequence is a chimeric phosphorothioate antisense oligo
CC	with 2' MOE wings and a deoxy gap, which is used to inhibit expression of
CC	human CTGF of the invention.
XX	
XX	Sequence 20 BP; 8 A; 3 C; 2 G; 7 T; 0 U; 0 Other;
XX	
QY	Query Match 1.9%; Score 20; DB 1; Length 20;
	Best Local Similarity 100.0%; Pred. No. 60;
DB	Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1927 TGTACAGTTATCTAGTTAA 1846
DB	20 TGTACAGTTATCTAGTTAA 1
RESULT 105	
ADB25653/c	
ID	ADB25653 standard; DNA; 20 BP.
XX	
AC	ADB25653;
XX	
XX	20-NOV-2003 (first entry)
DT	
XX	
DE	Human connective tissue growth factor antisense oligo DNA (SeqID 46).
XX	
KW	antisense; human; ss; connective tissue growth factor; CTGF;
KW	chromosome 6q23.1; ctgfract; fibroblast inducible secreted protein;
KW	fisp-12; NOV2;
KW	insulin-like growth factor binding protein-related protein 2; IGFBP-rp2;
KW	IGFBP-8; Hcs24; ecogenin; acute lymphoblastic leukaemia; gene therapy;
KW	hyperproliferative disorder; cancer; pulmonary fibrosis; renal fibrosis;
KW	scleroderma; atherosclerosis; cytostatic; dermatological;
KW	antiarteriosclerotic.
XX	
OS	Homc sapiens.
XX	
PH	Key Location/Qualifiers
FT	modified_base 1..20

FT FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "OTHER= phosphorothioate backbone, where 1-5 and  
FT 16-20 are 2' methoxyethyl nucleotides. All cytidines are  
FT 5-methylcytidines"  
XX WO2003053340-A2.  
PN 03-JUL-2003.  
XX 09-DEC-2002; 2002WO-US038618.  
XX 10-DEC-2001; 2001US-00006191.  
XX (ISIS-) ISIS PHARM INC.  
XX Gaarde WA, Watt AT;  
XX WPI; 2003-559091/52.  
XX  
XX New antisense oligonucleotides for modulating connective tissue growth  
PT factor expression, particularly useful for treating cancers (e.g. breast  
PT or prostate cancer), pulmonary or renal fibrosis, scleroderma or  
PT atherosclerosis.  
XX  
XX Claim 3; Page 85; 139pp; English.  
XX  
XX This invention relates to novel methods for modulating the expression of  
CC connective tissue growth factor (CTGF) by antisense oligonucleotides.  
CC CTGF has been mapped to human chromosome region 6q23.1, and is also known  
CC as ctgrofact, fibroblast inducible secreted protein, fisp-12, NOV2,  
CC insulin-like growth factor binding protein-related protein 2, IGFBP-rp2,  
CC IGFBP-8, Hcs24 and ecogenin. It is known to stimulate DNA synthesis and  
CC promote chemotaxis of fibroblasts, however, it is also upregulated in  
CC acute lymphoblastic leukaemia and in tumour or endothelial cells  
CC associated with the vasculature. Accordingly, antisense oligonucleotides  
CC that inhibit the expression of CTGF in cells or tissues can be used in  
CC gene therapy to treat various conditions including hyperproliferative  
CC disorders (particularly cancer, e.g. breast, prostate or renal cancer),  
CC pulmonary fibrosis, renal fibrosis, scleroderma and atherosclerosis. As  
CC such, the present invention describes these antisense oligos as having  
CC cytostatic, dermatological and antiarteriosclerotic activities. This  
CC oligonucleotide sequence is a chimeric phosphorothioate antisense oligo  
CC with 2' MOE wings and a deoxy gap, which is used to inhibit expression of  
CC human CTGF of the invention.  
XX  
XX Sequence 20 BP; 4 A; 7 C; 2 G; 7 T; 0 U; 0 Other;  
Query Match 1.9%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 60;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2208 GTTGAGAGTGTGACCAAAAG 2227  
Db 20 GTTGAGAGTGTGACCAAAAG 1  
RESULT 106  
ADB25656/c  
ID ADB25656 standard; DNA; 20 BP.  
XX ADB25656;  
XX  
XX 20-NOV-2003 (first entry)  
XX  
XX Human connective tissue growth factor antisense oligo DNA (seqID 49).  
XX  
XX antisense; human; ss; connective tissue growth factor; CTGF;  
XX chromosome 6q23.1; ctgrofact; fibroblast inducible secreted protein;  
XX fisp-12; NOV2;  
XX insulin-like growth factor binding protein-related protein 2; IGFBP-rp2;  
XX IGFBP-8; Hcs24; ecogenin; acute lymphoblastic leukaemia; gene therapy;  
XX hyperproliferative disorder; cancer; pulmonary fibrosis; renal fibrosis;  
KW

KW scleroderma; atherosclerosis; cytostatic; dermatological;  
KW antiarteriosclerotic.  
XX  
XX Homo sapiens.  
OS  
FH Key Location/Qualifiers  
FT modified\_base 1..20  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "OTHER= phosphorothioate backbone, where 1-5 and  
FT 16-20 are 2' methoxyethyl nucleotides. All cytidines are  
XX 5-methylcytidines"  
PN WO2003053340-A2.  
XX  
XX 03-JUL-2003.  
XX 09-DEC-2002; 2002WO-US038618.  
XX 10-DEC-2001; 2001US-00006191.  
XX (ISIS-) ISIS PHARM INC.  
XX Gaarde WA, Watt AT;  
XX WPI; 2003-559091/52.  
XX  
XX New antisense oligonucleotides for modulating connective tissue growth  
PT factor expression, particularly useful for treating cancers (e.g. breast  
PT or prostate cancer), pulmonary or renal fibrosis, scleroderma or  
PT atherosclerosis.  
XX  
XX Example 15; Page 85; 139pp; English.  
XX  
XX This invention relates to novel methods for modulating the expression of  
CC connective tissue growth factor (CTGF) by antisense oligonucleotides.  
CC CTGF has been mapped to human chromosome region 6q23.1, and is also known  
CC as ctgrofact, fibroblast inducible secreted protein, fisp-12, NOV2,  
CC insulin-like growth factor binding protein-related protein 2, IGFBP-rp2,  
CC IGFBP-8, Hcs24 and ecogenin. It is known to stimulate DNA synthesis and  
CC promote chemotaxis of fibroblasts, however, it is also upregulated in  
CC acute lymphoblastic leukaemia and in tumour or endothelial cells  
CC associated with the vasculature. Accordingly, antisense oligonucleotides  
CC that inhibit the expression of CTGF in cells or tissues can be used in  
CC gene therapy to treat various conditions including hyperproliferative  
CC disorders (particularly cancer, e.g. breast, prostate or renal cancer),  
CC pulmonary fibrosis, renal fibrosis, scleroderma and atherosclerosis. As  
CC such, the present invention describes these antisense oligos as having  
CC cytostatic, dermatological and antiarteriosclerotic activities. This  
CC oligonucleotide sequence is a chimeric phosphorothioate antisense oligo  
CC with 2' MOE wings and a deoxy gap, which is used to inhibit expression of  
CC human CTGF of the invention.  
XX  
XX Sequence 20 BP; 7 A; 3 C; 2 G; 8 T; 0 U; 0 Other;  
Query Match 1.9%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 60;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2242 CTTTCTAGTTGAAATAAAG 2261  
Db 20 CTTTCTAGTTGAAATAAAG 1  
RESULT 107  
ADB25671/c  
ID ADB25671 standard; DNA; 20 BP.  
XX ADB25671;  
XX  
XX 20-NOV-2003 (first entry)  
XX  
XX Human connective tissue growth factor antisense oligo DNA (seqID 64).  
DE

XX antisense; human; ss; connective tissue growth factor; CTGF;  
KW chromosome 6q23.1; ctgfract; fibroblast inducible secreted protein;  
KW fisp-12; NOV2;  
KW insulin-like growth factor binding protein-related protein 2; IGFBP-rp2;  
KW IGFBP-8; Hcs24; ecogenin; acute lymphoblastic leukaemia; gene therapy;  
KW hyperproliferative disorder; cancer; pulmonary fibrosis; renal fibrosis;  
KW scleroderma; atherosclerosis; cystostatic; dermatological;  
KW antiarteriosclerotic.  
XX  
OS Homo sapiens.  
XX  
XX  
XX Key Location/Qualifiers  
FH modified\_base 1..20 /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "OTHER= phosphorothioate backbone, where 1-5 and  
FT 16-20 are 2' methoxyethyl nucleotides. All cytidines are  
FT 5-methylcytidines"  
XX  
XX WO2003053340-A2.  
XX  
XX  
XX 03-JUL-2003.  
XX  
XX 09-DEC-2002; 2002WO-US038618.  
XX  
XX 10-DEC-2001; 2001US-00006191.  
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XX (ISIS-) ISIS PHARM INC.  
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XX Gaarde WA, Watt AT;  
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XX WPI; 2003-559091/52.  
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PT factor expression, particularly useful for treating cancers (e.g. breast  
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PT atherosclerosis.  
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CC IGFBP-8, Hcs24 and ecogenin. It is known to stimulate DNA synthesis and  
CC promote chemotaxis of fibroblasts, however, it is also upregulated in  
CC acute lymphoblastic leukaemia and in tumour or endothelial cells  
CC associated with the vasculature. Accordingly, antisense oligonucleotides  
CC that inhibit the expression of CTGF in cells or tissues can be used in  
CC gene therapy to treat various conditions including hyperproliferative  
CC disorders (particularly cancer, e.g. breast, prostate or renal cancer),  
CC pulmonary fibrosis, renal fibrosis, scleroderma and atherosclerosis. As  
CC such, the present invention describes these antisense oligos as having  
CC cystostatic, dermatological and antiarteriosclerotic activities. This  
CC oligonucleotide sequence is a chimeric phosphorothioate antisense oligo  
CC with 2' MOE wings and a deoxy gap, which is used to inhibit expression of  
CC human CTGF of the invention.  
XX  
XX Sequence 20 BP; 6 A; 4 C; 3 G; 7 T; 0 U; 0 Other;  
XX  
XX Query Match 1.9%; Score 20; DB 1; Length 20;  
XX Best Local Similarity 100.0%; Pred. No. 60;  
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 2219 GACCAAAAGTTACATGTTG 2238  
Db 20 GACCAAAAGTTACATGTTG 1  
RESULT 108  
ADB25666/c

ID ADB25666 standard; DNA; 20 BP.  
XX  
XX ADB25666;  
XX  
XX 20-NOV-2003 (first entry)  
XX  
XX Human connective tissue growth factor antisense oligo DNA (SeqID 59).  
XX  
XX antisense; human; ss; connective tissue growth factor; CTGF;  
KW chromosome 6q23.1; ctgfract; fibroblast inducible secreted protein;  
KW fisp-12; NOV2;  
KW insulin-like growth factor binding protein-related protein 2; IGFBP-rp2;  
KW IGFBP-8; Hcs24; ecogenin; acute lymphoblastic leukaemia; gene therapy;  
KW hyperproliferative disorder; cancer; pulmonary fibrosis; renal fibrosis;  
KW scleroderma; atherosclerosis; cystostatic; dermatological;  
KW antiarteriosclerotic.  
XX  
XX Homo sapiens.  
XX  
XX Key Location/Qualifiers  
FH modified\_base 1..20 /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "OTHER= phosphorothioate backbone, where 1-5 and  
FT 16-20 are 2' methoxyethyl nucleotides. All cytidines are  
FT 5-methylcytidines"  
XX  
XX WO2003053340-A2.  
XX  
XX 03-JUL-2003.  
XX  
XX 09-DEC-2002; 2002WO-US038618.  
XX  
XX 10-DEC-2001; 2001US-00006191.  
XX  
XX (ISIS-) ISIS PHARM INC.  
XX  
XX Gaarde WA, Watt AT;  
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XX WPI; 2003-559091/52.  
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PT factor expression, particularly useful for treating cancers (e.g. breast  
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CC as ctgfract, fibroblast inducible secreted protein, fisp-12, NOV2,  
CC insulin-like growth factor binding protein-related protein 2, IGFBP-rp2,  
CC IGFBP-8, Hcs24 and ecogenin. It is known to stimulate DNA synthesis and  
CC promote chemotaxis of fibroblasts, however, it is also upregulated in  
CC acute lymphoblastic leukaemia and in tumour or endothelial cells  
CC associated with the vasculature. Accordingly, antisense oligonucleotides  
CC that inhibit the expression of CTGF in cells or tissues can be used in  
CC gene therapy to treat various conditions including hyperproliferative  
CC disorders (particularly cancer, e.g. breast, prostate or renal cancer),  
CC pulmonary fibrosis, renal fibrosis, scleroderma and atherosclerosis. As  
CC such, the present invention describes these antisense oligos as having  
CC cystostatic, dermatological and antiarteriosclerotic activities. This  
CC oligonucleotide sequence is a chimeric phosphorothioate antisense oligo  
CC with 2' MOE wings and a deoxy gap, which is used to inhibit expression of  
CC human CTGF of the invention.  
XX  
XX Sequence 20 BP; 4 A; 7 C; 4 G; 5 T; 0 U; 0 Other;  
XX  
XX Query Match 1.9%; Score 20; DB 1; Length 20;  
XX Best Local Similarity 100.0%; Pred. No. 60;  
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



```
OY 1723 ACTGCACAGCTTGCGCAAG 1742
Db 20 ACTGCACAGCTTGCGCAAG 1

RESULT 109
ADB25702/c
ID ADB25702 standard; DNA; 20 BP.
XX
XX
XX ADB25702;
AC
XX
XX 20-NOV-2003 (first entry)
DT
DE Human connective tissue growth factor antisense oligo DNA (SeqID 95).
XX
XX antisense; human; ss; connective tissue growth factor; CTGF;
KW chromosome 6q23.1; ctgrofact; fibroblast inducible secreted protein;
KW fisp-12; NOV2;
KW insulin-like growth factor binding protein-related protein 2; IGFBP-rp2;
KW IGFBP-8; Hcs24; ecogenin; acute lymphoblastic leukaemia; gene therapy;
KW hyperproliferative disorder; cancer; pulmonary fibrosis; renal fibrosis;
KW scleroderma; atherosclerosis; cytostatic; dermatological;
KW antiarteriosclerotic.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER= phosphorothioate backbone, where 1-5 and
FT 16-20 are 2' methoxyethyl nucleotides. All cytidines are
FT 5-methylcytidines"
XX
XX WO2003053340-A2.
XX
XX 03-JUL-2003.
XX
XX 09-DEC-2002; 2002WO-US038618.
XX
XX 10-DEC-2001; 2001US-00006191.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Gaarde WA, Watt AT;
XX
XX WPI; 2003-559091/52.
XX
XX Claim 3; Page 86; 139pp; English.
XX
XX This invention relates to novel methods for modulating the expression of
XX connective tissue growth factor (CTGF) by antisense oligonucleotides.
XX CTGF has been mapped to human chromosome region 6q23.1, and is also known
XX as ctgrofact, fibroblast inducible secreted protein, fisp-12, NOV2,
XX insulin-like growth factor binding protein-related protein 2, IGFBP-rp2,
XX IGFBP-8, Hcs24 and ecogenin. It is known to stimulate DNA synthesis and
XX promote chemotaxis of fibroblasts, however, it is also upregulated in
XX acute lymphoblastic leukaemia and in tumour or endothelial cells
XX associated with the vasculature. Accordingly, antisense oligonucleotides
XX that inhibit the expression of CTGF in cells or tissues can be used in
XX gene therapy to treat various conditions including hyperproliferative
XX disorders (particularly cancer, e.g. breast, prostate or renal cancer),
XX pulmonary fibrosis, renal fibrosis, scleroderma and atherosclerosis. As
XX such, the present invention describes these antisense oligos as having
XX cytostatic, dermatological and antiarteriosclerotic activities. This
XX oligonucleotide sequence is a chimeric phosphorothioate antisense oligo
XX with 2' MOE wings and a deoxy gap, which is used to inhibit expression of
XX human CTGF of the invention.
```

```
XX Sequence 20 BP; 7 A; 4 C; 4 G; 5 T; 0 U; 0 Other;
SQ Query Match 1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1553 AAATTTTACGCTGCTCAGTG 1572
Db 20 AAATTTTACGCTGCTCAGTG 1

RESULT 110
ADB25652/c
ID ADB25652 standard; DNA; 20 BP.
XX
XX ADB25652;
AC
XX
XX 20-NOV-2003 (first entry)
DT
DE Human connective tissue growth factor antisense oligo DNA (SeqID 45).
XX
XX antisense; human; ss; connective tissue growth factor; CTGF;
KW chromosome 6q23.1; ctgrofact; fibroblast inducible secreted protein;
KW fisp-12; NOV2;
KW insulin-like growth factor binding protein-related protein 2; IGFBP-rp2;
KW IGFBP-8; Hcs24; ecogenin; acute lymphoblastic leukaemia; gene therapy;
KW hyperproliferative disorder; cancer; pulmonary fibrosis; renal fibrosis;
KW scleroderma; atherosclerosis; cytostatic; dermatological;
KW antiarteriosclerotic.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER= phosphorothioate backbone, where 1-5 and
FT 16-20 are 2' methoxyethyl nucleotides. All cytidines are
FT 5-methylcytidines"
XX
XX WO2003053340-A2.
XX
XX 03-JUL-2003.
XX
XX 09-DEC-2002; 2002WO-US038618.
XX
XX 10-DEC-2001; 2001US-00006191.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Gaarde WA, Watt AT;
XX
XX WPI; 2003-559091/52.
XX
XX New antisense oligonucleotides for modulating connective tissue growth
XX factor expression, particularly useful for treating cancers (e.g. breast
XX or prostate cancer), pulmonary or renal fibrosis, scleroderma or
XX atherosclerosis.
XX
XX Claim 3; Page 85; 139pp; English.
XX
XX This invention relates to novel methods for modulating the expression of
XX connective tissue growth factor (CTGF) by antisense oligonucleotides.
XX CTGF has been mapped to human chromosome region 6q23.1, and is also known
XX as ctgrofact, fibroblast inducible secreted protein, fisp-12, NOV2,
XX insulin-like growth factor binding protein-related protein 2, IGFBP-rp2,
XX IGFBP-8, Hcs24 and ecogenin. It is known to stimulate DNA synthesis and
XX promote chemotaxis of fibroblasts, however, it is also upregulated in
XX acute lymphoblastic leukaemia and in tumour or endothelial cells
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XX that inhibit the expression of CTGF in cells or tissues can be used in
XX gene therapy to treat various conditions including hyperproliferative
```

CC disorders (particularly cancer, e.g. breast, prostate or renal cancer),  
 CC pulmonary fibrosis, renal fibrosis, scleroderma and atherosclerosis. As  
 CC such, the present invention describes these antisense oligos as having  
 CC cystostatic, dermatological and antiarteriosclerotic activities. This  
 CC oligonucleotide sequence is a chimeric phosphorothioate antisense oligo  
 CC with 2' MOE wings and a deoxy gap, which is used to inhibit expression of  
 CC human CTGF of the invention.

XX Sequence 20 BP; 8 A; 6 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 1.9%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 60;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2203 TATTGTTGAGAGTGTGACC 2222

DB 20 TATTGTTGAGAGTGTGACC 1

RESULT 111  
 ADB25703/C  
 ID ADB25703 standard; DNA; 20 BP.

XX ADB25703;

XX 20-NOV-2003 (first entry)

DE Human connective tissue growth factor antisense oligo DNA (SeqID 96).

XX antisense; human; ss; connective tissue growth factor; CTGF;  
 KW chromosome 6q23.1; ctgrofact; fibroblast inducible secreted protein;  
 KW fisp-12; NOV2;  
 KW insulin-like growth factor binding protein-related protein 2; IGFBP-rp2;  
 KW IGFBP-8; Hcs24; ecogenin; acute lymphoblastic leukaemia; gene therapy;  
 KW hyperproliferative disorder; cancer; pulmonary fibrosis; renal fibrosis;  
 KW scleroderma; atherosclerosis; cytostatic; dermatological;  
 KW antiarteriosclerotic.

XX Homo sapiens.

XX Key Location/Qualifiers

FT modified\_base 1..20  
 FT /\*tag= a  
 FT /mod\_base= OTHER  
 FT /note= "OTHER= phosphorothioate backbone, where 1-5 and  
 FT 16-20 are 2' methoxyethyl nucleotides. All cytidines are  
 FT 5-methylcytidines"

XX WO2003053340-A2.

XX 03-JUL-2003.

XX 09-DEC-2002; 2002WO-US038618.

XX 10-DEC-2001; 2001US-00006191.

XX (ISIS-) ISIS PHARM INC.

XX Gaarde WA, Watt AT;

XX WPI; 2003-559091/52.

XX New antisense oligonucleotides for modulating connective tissue growth  
 PT factor expression, particularly useful for treating cancers (e.g. breast  
 PT or prostate cancer), pulmonary or renal fibrosis, scleroderma or  
 PT atherosclerosis.

XX Example 15; Page 86; 139pp; English.

XX This invention relates to novel methods for modulating the expression of  
 CC connective tissue growth factor (CTGF) by antisense oligonucleotides.  
 CC CTGF has been mapped to human chromosome region 6q23.1, and is also known  
 CC as ctgrofact, fibroblast inducible secreted protein, fisp-12, NOV2,

CC insulin-like growth factor binding protein-related protein 2; IGFBP-rp2,  
 CC IGFBP-8, Hcs24 and ecogenin. It is known to stimulate DNA synthesis and  
 CC promote chemotaxis of fibroblasts, however, it is also upregulated in  
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 CC associated with the vasculature. Accordingly, antisense oligonucleotides  
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 CC disorders (particularly cancer, e.g. breast, prostate or renal cancer),  
 CC pulmonary fibrosis, renal fibrosis, scleroderma and atherosclerosis. As  
 CC such, the present invention describes these antisense oligos as having  
 CC cytostatic, dermatological and antiarteriosclerotic activities. This  
 CC oligonucleotide sequence is a chimeric phosphorothioate antisense oligo  
 CC with 2' MOE wings and a deoxy gap, which is used to inhibit expression of  
 CC human CTGF of the invention.

XX Sequence 20 BP; 7 A; 4 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 1.9%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 60;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1637 GTTGTTCCTTAAGTCAGAAC 1656

DB 20 GTTGTTCCTTAAGTCAGAAC 1

RESULT 112

ID ADB25655/C

ADB25655 standard; DNA; 20 BP.

XX ADB25655;

XX 20-NOV-2003 (first entry)

DE Human connective tissue growth factor antisense oligo DNA (SeqID 48).

XX antisense; human; ss; connective tissue growth factor; CTGF;  
 KW chromosome 6q23.1; ctgrofact; fibroblast inducible secreted protein;  
 KW fisp-12; NOV2;  
 KW insulin-like growth factor binding protein-related protein 2; IGFBP-rp2;  
 KW IGFBP-8; Hcs24; ecogenin; acute lymphoblastic leukaemia; gene therapy;  
 KW hyperproliferative disorder; cancer; pulmonary fibrosis; renal fibrosis;  
 KW scleroderma; atherosclerosis; cytostatic; dermatological;  
 KW antiarteriosclerotic.

XX Homo sapiens.

XX Key Location/Qualifiers

FT modified\_base 1..20  
 FT /\*tag= a  
 FT /mod\_base= OTHER  
 FT /note= "OTHER= phosphorothioate backbone, where 1-5 and  
 FT 16-20 are 2' methoxyethyl nucleotides. All cytidines are  
 FT 5-methylcytidines"

XX WO2003053340-A2.

XX 03-JUL-2003.

XX 09-DEC-2002; 2002WO-US038618.

XX 10-DEC-2001; 2001US-00006191.

XX (ISIS-) ISIS PHARM INC.

XX Gaarde WA, Watt AT;

XX WPI; 2003-559091/52.

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 PT factor expression, particularly useful for treating cancers (e.g. breast  
 PT or prostate cancer), pulmonary or renal fibrosis, scleroderma or  
 PT atherosclerosis.

```

XX PS Claim 3; Page 85; 139pp; English.
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XX CC connective tissue growth factor (CTGF) by antisense oligonucleotides.
XX CC CTGF has been mapped to human chromosome region 6q23.1, and is also known
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XX CC promote chemotaxis of fibroblasts, however, it is also upregulated in
XX CC acute lymphoblastic leukaemia and in tumour or endothelial cells
XX CC associated with the vasculature. Accordingly, antisense oligonucleotides
XX CC that inhibit the expression of CTGF in cells or tissues can be used in
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XX CC such, the present invention describes these antisense oligos as having
XX CC cytoskeletal, dermatological and antiarteriosclerotic activities. This
XX CC oligonucleotide sequence is a chimeric phosphorothioate antisense oligo
XX CC with 2' MOE wings and a deoxy gap, which is used to inhibit expression of
XX CC human CTGF of the invention.
XX SQ Sequence 20 BP; 7 A; 3 C; 3 G; 7 T; 0 U; 0 Other;
XX
XX Query Match 1.9%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 60;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 2218 TGACCAAAAGTTACATGTTT 2237
DB 20 TGACCAAAAGTTACATGTTT 1
XX
RESULT 113
ADB25650/C
ID ADB25650 standard; DNA; 20 BP.
XX AC
XX ADB25650;
XX
XX 20-NOV-2003 (first entry)
XX
XX Human connective tissue growth factor antisense oligo DNA (SeqID 43).
XX
XX antisense; human; ss; connective tissue growth factor; CTGF;
XX chromosome 6q23.1; ctgrofact; fibroblast inducible secreted protein;
XX fisp-12; NOV2;
XX insulin-like growth factor binding protein-related protein 2; IGFBP-rp2;
XX IGFBP-8; Hcs24; ecogenin; acute lymphoblastic leukaemia; gene therapy;
XX hyperproliferative disorder; cancer; pulmonary fibrosis; renal fibrosis;
XX scleroderma; atherosclerosis; cytoskeletal; dermatological;
XX antiarteriosclerotic.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX modified_base 1..20
XX /tag= a
XX /mod_base= OTHER
XX /note= "OTHER= phosphorothioate backbone, where 1-5 and
XX 16-20 are 2' methoxyethyl nucleotides. All cytidines are
XX 5-methylcytidines"
XX
XX WO2003053340-A2.
XX
XX 03-JUL-2003.
XX
XX 09-DEC-2002; 2002WO-US038618.
XX
XX 10-DEC-2001; 2001US-00006191.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Gaarde WA, Watt AT;

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XX WPI; 2003-559091/52.
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XX oligonucleotide sequence is a chimeric phosphorothioate antisense oligo
XX with 2' MOE wings and a deoxy gap, which is used to inhibit expression of
XX human CTGF of the invention.
XX
XX Sequence 20 BP; 6 A; 3 C; 3 G; 8 T; 0 U; 0 Other;
XX
XX Query Match 1.9%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 60;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 2098 GAACAAATGCCCTTTATTA 2117
DB 20 GAACAAATGCCCTTTATTA 1
XX
RESULT 114
ADB25651/C
ID ADB25651 standard; DNA; 20 BP.
XX AC
XX ADB25651;
XX
XX 20-NOV-2003 (first entry)
XX
XX Human connective tissue growth factor antisense oligo DNA (SeqID 44).
XX
XX antisense; human; ss; connective tissue growth factor; CTGF;
XX chromosome 6q23.1; ctgrofact; fibroblast inducible secreted protein;
XX fisp-12; NOV2;
XX insulin-like growth factor binding protein-related protein 2; IGFBP-rp2;
XX IGFBP-8; Hcs24; ecogenin; acute lymphoblastic leukaemia; gene therapy;
XX hyperproliferative disorder; cancer; pulmonary fibrosis; renal fibrosis;
XX scleroderma; atherosclerosis; cytoskeletal; dermatological;
XX antiarteriosclerotic.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX modified_base 1..20
XX /tag= a
XX /mod_base= OTHER
XX /note= "OTHER= phosphorothioate backbone, where 1-5 and
XX 16-20 are 2' methoxyethyl nucleotides. All cytidines are
XX 5-methylcytidines"
XX
XX WO2003053340-A2.
XX
XX 03-JUL-2003.
XX
XX
XX

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PF 09-DEC-2002; 2002WO-US038618.
XX
PR 10-DEC-2001; 2001US-00006191.
XX
PA (ISIS-) ISIS PHARM INC.
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PI Gaarde WA, Watt AT;
XX
DR WPI; 2003-559091/52.
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PT factor expression, particularly useful for treating cancers (e.g. breast
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XX
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XX IGFBP-8, Hcs24 and ecogenin. It is known to stimulate DNA synthesis and
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XX gene therapy to treat various conditions including hyperproliferative
XX disorders (particularly cancer, e.g. breast, prostate or renal cancer),
XX pulmonary fibrosis, renal fibrosis, scleroderma and atherosclerosis. As
XX such, the present invention describes these antisense oligos as having
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XX oligonucleotide sequence is a chimeric phosphorothioate antisense oligo
XX with 2' MOE wings and a deoxy gap, which is used to inhibit expression of
XX human CTGF of the invention.
XX
SQ Sequence 20 BP; 9 A; 6 C; 1 G; 4 T; 0 U; 0 Other;
Query Match 1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2198 CAGTTTATTGTTGAGAGTG 2217
DB 20 CAGTTTATTGTTGAGAGTG 1
RESULT 115
ADB25700/c
ID ADB25700 standard; DNA; 20 BP.
XX
AC ADB25700;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human connective tissue growth factor antisense oligo DNA (SeqID 93).
XX
XX antisense; human; ss; connective tissue growth factor; CTGF;
XX chromosome 6q23.1; ctgfract; fibroblast inducible secreted protein;
XX fisp-12; NOV2;
XX insulin-like growth factor binding protein-related protein 2; IGFBP-rp2;
XX IGFBP-8; Hcs24; ecogenin; acute lymphoblastic leukaemia; gene therapy;
XX hyperproliferative disorder; cancer; pulmonary fibrosis; renal fibrosis;
XX scleroderma; atherosclerosis; cytostatic; dermatological;
XX antiarteriosclerotic.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER= phosphorothioate backbone, where 1-5 and
```

```
FT 16-20 are 2' methoxyethyl nucleotides. All cytidines are
XX 5-methylcytidines"
XX
PN WC2003053340-A2.
XX
PD 03-JUL-2003.
XX
XX 09-DEC-2002; 2002WO-US038618.
XX
XX 10-DEC-2001; 2001US-00006191.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Gaarde WA, Watt AT;
XX
XX WPI; 2003-559091/52.
XX
XX New antisense oligonucleotides for modulating connective tissue growth
PT factor expression, particularly useful for treating cancers (e.g. breast
PT or prostate cancer), pulmonary or renal fibrosis, scleroderma or
PT atherosclerosis.
XX
PS Example 15; Page 86; 139pp; English.
XX
XX This invention relates to novel methods for modulating the expression of
XX connective tissue growth factor (CTGF) by antisense oligonucleotides.
XX CTGF has been mapped to human chromosome region 6q23.1, and is also known
XX as ctgfract, fibroblast inducible secreted protein, fisp-12, NOV2,
XX insulin-like growth factor binding protein-related protein 2, IGFBP-rp2,
XX IGFBP-8, Hcs24 and ecogenin. It is known to stimulate DNA synthesis and
XX promote chemotaxis of fibroblasts, however, it is also upregulated in
XX acute lymphoblastic leukaemia and in tumour or endothelial cells
XX associated with the vasculature. Accordingly, antisense oligonucleotides
XX that inhibit the expression of CTGF in cells or tissues can be used in
XX gene therapy to treat various conditions including hyperproliferative
XX disorders (particularly cancer, e.g. breast, prostate or renal cancer),
XX pulmonary fibrosis, renal fibrosis, scleroderma and atherosclerosis. As
XX such, the present invention describes these antisense oligos as having
XX cytostatic, dermatological and antiarteriosclerotic activities. This
XX oligonucleotide sequence is a chimeric phosphorothioate antisense oligo
XX with 2' MOE wings and a deoxy gap, which is used to inhibit expression of
XX human CTGF of the invention.
XX
SQ Sequence 20 BP; 7 A; 3 C; 2 G; 8 T; 0 U; 0 Other;
Query Match 1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1274 GTAGCACAGTTTATTAAT 1293
DB 20 GTAGCACAGTTTATTAAT 1
RESULT 116
ADB25704/c
ID ADB25704 standard; DNA; 20 BP.
XX
AC ADB25704;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human connective tissue growth factor antisense oligo DNA (SeqID 97).
XX
XX antisense; human; ss; connective tissue growth factor; CTGF;
XX chromosome 6q23.1; ctgfract; fibroblast inducible secreted protein;
XX fisp-12; NOV2;
XX insulin-like growth factor binding protein-related protein 2; IGFBP-rp2;
XX IGFBP-8; Hcs24; ecogenin; acute lymphoblastic leukaemia; gene therapy;
XX hyperproliferative disorder; cancer; pulmonary fibrosis; renal fibrosis;
XX scleroderma; atherosclerosis; cytostatic; dermatological;
XX antiarteriosclerotic.
XX
```

OS Homo sapiens.  
 XX Key Location/Qualifiers  
 FH modified\_base 1..20  
 FT /\*tag= a  
 FT /mod\_base= OTHER  
 FT /note= "OTHER= phosphorothioate backbone, where 1-5 and  
 FT 16-20 are 2' methoxyethyl nucleotides. All cytidines are  
 FT 5-methylcytidines"  
 XX  
 XX WO2003053340-A2.  
 XX  
 XX 03-JUL-2003.  
 XX  
 XX 09-DEC-2002; 2002WO-US038618.  
 XX  
 XX 10-DEC-2001; 2001US-00006191.  
 XX  
 XX (ISIS-) ISIS PHARM INC.  
 XX  
 XX Gaarde WA, Watt AT;  
 XX  
 XX WPI; 2003-559091/52.  
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 FT factor expression, particularly useful for treating cancers (e.g. breast  
 FT or prostate cancer), pulmonary or renal fibrosis, scleroderma or  
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 CC IGFBP-8, Hcs24 and ecogenin. It is known to stimulate DNA synthesis and  
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 CC associated with the vasculature. Accordingly, antisense oligonucleotides  
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 CC gene therapy to treat various conditions including hyperproliferative  
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 CC oligonucleotide sequence is a chimeric phosphorothioate antisense oligo  
 CC with 2' MOE wings and a deoxy gap, which is used to inhibit expression of  
 CC human CTGF of the invention.  
 XX  
 XX Sequence 20 BP; 5 A; 6 C; 4 G; 5 T; 0 U; 0 Other;  
 SQ  
 Query Match 1.9%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 60;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1713 TGTCGATTAGCTGGACGC 1732  
 DB 20 TGTCGATTAGCTGGACGC 1  
 RESULT 117  
 ADB25667/c  
 ID ADB25667 standard; DNA; 20 BP.  
 XX  
 XX ADB25667;  
 XX  
 XX 20-NOV-2003 (first entry)  
 XX  
 XX Human connective tissue growth factor antisense oligo DNA (SeqId 60).  
 DE  
 DE antisense; human; ss; connective tissue growth factor; CTGF;  
 KW chromosome 6q23.1; ctgfract; fibroblast inducible secreted protein;  
 KW

KW fisp-12; NOV2;  
 KW insulin-like growth factor binding protein-related protein 2; IGFBP-rp2;  
 KW IGFBP-8; Hcs24; ecogenin; acute lymphoblastic leukaemia; gene therapy;  
 KW hyperproliferative disorder; cancer; pulmonary fibrosis; renal fibrosis;  
 KW scleroderma; atherosclerosis; cytostatic; dermatological;  
 KW antiarteriosclerotic.  
 XX  
 XX Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 FH modified\_base 1..20  
 FT /\*tag= a  
 FT /mod\_base= OTHER  
 FT /note= "OTHER= phosphorothioate backbone, where 1-5 and  
 FT 16-20 are 2' methoxyethyl nucleotides. All cytidines are  
 FT 5-methylcytidines"  
 XX  
 XX WO2003053340-A2.  
 XX  
 XX 03-JUL-2003.  
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 XX 09-DEC-2002; 2002WO-US038618.  
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 XX WPI; 2003-559091/52.  
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 CC oligonucleotide sequence is a chimeric phosphorothioate antisense oligo  
 CC with 2' MOE wings and a deoxy gap, which is used to inhibit expression of  
 CC human CTGF of the invention.  
 XX  
 XX Sequence 20 BP; 7 A; 3 C; 4 G; 6 T; 0 U; 0 Other;  
 SQ  
 Query Match 1.9%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 60;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1752 CTGTAAACAAGCCAGATTTT 1771  
 DB 20 CTGTAAACAAGCCAGATTTT 1  
 RESULT 118  
 ADB25672/c  
 ID ADB25672 standard; DNA; 20 BP.  
 XX  
 XX ADB25672;  
 AC

XX DT 20-NOV-2003 (first entry)

XX DE Human connective tissue growth factor antisense oligo DNA (SeqID 65).

XX KW antisense; human; ss; connective tissue growth factor; CTGF;

XX KW chromosome 6q23.1; ctgofact; fibroblast inducible secreted protein;

XX KW fisp-12; NOV2;

XX KW insulin-like growth factor binding protein-related protein 2; IGFBP-rp2;

XX KW IGFBP-8; Hcs24; ecogenin; acute lymphoblastic leukaemia; gene therapy;

XX KW hyperproliferative disorder; cancer; pulmonary fibrosis; renal fibrosis;

XX KW scleroderma; atherosclerosis; cytostatic; dermatological;

XX KW antiarteriosclerotic.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT modified\_base 1..20

XX FT /\*tag= a

XX FT /mod\_base= OTHER

XX FT /note= "OTHER= phosphorothioate backbone, where 1-5 and

XX FT 16-20 are 2' methoxyethyl nucleotides. All cytidines are

XX FT 5-methylcytidines"

XX PN WO2003053340-A2.

XX XX 03-JUL-2003.

XX PF 09-DEC-2002; 2002WO-US038618.

XX PR 10-DEC-2001; 2001US-00006191.

XX PA (ISIS-) ISIS PHARM INC.

XX PI Gaarde WA, Watt AT;

XX PI WPI; 2003-559091/52.

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XX CC IGFBP-8, Hcs24 and ecogenin. It is known to stimulate DNA synthesis and

XX CC promote chemotaxis of fibroblasts, however, it is also upregulated in

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XX CC cytostatic, dermatological and antiarteriosclerotic activities. This

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XX CC with 2' MOE wings and a deoxy gap, which is used to inhibit expression of

XX CC human CTGF of the invention.

XX SQ Sequence 20 BP; 8 A; 3 C; 1 G; 8 T; 0 U; 0 Other;

Query Match 1.9%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 60;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2243 TTCTAGTTGAATAAAGT 2262

DB 20 TTCTAGTTGAATAAAGT 1

RESULT 119

ADB25699/C

XX ID ADB25699 standard; DNA; 20 BP.

XX AC ADB25699;

XX DT 20-NOV-2003 (first entry)

XX DE Human connective tissue growth factor antisense oligo DNA (SeqID 92).

XX KW antisense; human; ss; connective tissue growth factor; CTGF;

XX KW chromosome 6q23.1; ctgofact; fibroblast inducible secreted protein;

XX KW fisp-12; NOV2;

XX KW insulin-like growth factor binding protein-related protein 2; IGFBP-rp2;

XX KW IGFBP-8; Hcs24; ecogenin; acute lymphoblastic leukaemia; gene therapy;

XX KW hyperproliferative disorder; cancer; pulmonary fibrosis; renal fibrosis;

XX KW scleroderma; atherosclerosis; cytostatic; dermatological;

XX KW antiarteriosclerotic.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT modified\_base 1..20

XX FT /\*tag= a

XX FT /mod\_base= OTHER

XX FT /note= "OTHER= phosphorothioate backbone, where 1-5 and

XX FT 16-20 are 2' methoxyethyl nucleotides. All cytidines are

XX FT 5-methylcytidines"

XX PN WO2003053340-A2.

XX XX 03-JUL-2003.

XX PF 09-DEC-2002; 2002WO-US038618.

XX PR 10-DEC-2001; 2001US-00006191.

XX PA (ISIS-) ISIS PHARM INC.

XX PI Gaarde WA, Watt AT;

XX PI WPI; 2003-559091/52.

XX PS New antisense oligonucleotides for modulating connective tissue growth

XX PS factor expression, particularly useful for treating cancers (e.g. breast

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XX PS atherosclerosis.

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XX CC with 2' MOE wings and a deoxy gap, which is used to inhibit expression of

XX CC human CTGF of the invention.

XX SQ Sequence 20 BP; 9 A; 1 C; 6 G; 4 T; 0 U; 0 Other;

```
Query Match      1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 20; Conservative 0; Mismatches 0; Gaps 0;
Indels 0; Gaps 0;

QY 1242 TCACATCTCATTTTCGTA 1261
    20 TCACATCTCATTTTCGTA 1

Db
RESULT 120
ADB25701/c
ID ADB25701 standard; DNA; 20 BP.
XX
AC ADB25701;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human connective tissue growth factor antisense oligo DNA (SeqID 94).
XX
KW antisense; human; ss; connective tissue growth factor; CTGF;
KW chromosome 6q23.1; ctgofact; fibroblast inducible secreted protein;
KW fisp-12; NOV2;
KW insulin-like growth factor binding protein-related protein 2; IGFBP-rp2;
KW IGFBP-8; Hcs24; ecogenin; acute lymphoblastic leukaemia; gene therapy;
KW hyperproliferative disorder; cancer; pulmonary fibrosis; renal fibrosis;
KW scleroderma; atherosclerosis; cytostatic; dermatological;
KW antiarteriosclerotic.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1..20 /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER= phosphorothioate backbone, where 1-5 and
FT 16-20 are 2' methoxyethyl nucleotides. All cytidines are
FT 5-methylcytidines"
XX
PN WO2003053340-A2.
XX
PD 03-JUL-2003.
XX
PF 09-DEC-2002; 2002WO-US038618.
XX
PR 10-DEC-2001; 2001US-00006191.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Gaarde WA, Watt AT;
XX
DR WPI; 2003-559091/52.
XX
PS New antisense oligonucleotides for modulating connective tissue growth
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XX or prostate cancer), pulmonary or renal fibrosis, scleroderma or
XX atherosclerosis.
XX
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CC with 2' MOE wings and a deoxy gap, which is used to inhibit expression of
CC human CTGF of the invention.
XX
SQ Sequence 20 BP; 4 A; 5 C; 4 G; 7 T; 0 U; 0 Other;
Query Match      1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1371 CCAGACACTGCTTTGAAGAA 1390
    20 CCAGACACTGCTTTGAAGAA 1

Db
RESULT 121
ADB25646/c
ID ADB25646 standard; DNA; 20 BP.
XX
AC ADB25646;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human connective tissue growth factor antisense oligo DNA (SeqID 39).
XX
KW antisense; human; ss; connective tissue growth factor; CTGF;
KW chromosome 6q23.1; ctgofact; fibroblast inducible secreted protein;
KW fisp-12; NOV2;
KW insulin-like growth factor binding protein-related protein 2; IGFBP-rp2;
KW IGFBP-8; Hcs24; ecogenin; acute lymphoblastic leukaemia; gene therapy;
KW hyperproliferative disorder; cancer; pulmonary fibrosis; renal fibrosis;
KW scleroderma; atherosclerosis; cytostatic; dermatological;
KW antiarteriosclerotic.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1..20 /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER= phosphorothioate backbone, where 1-5 and
FT 16-20 are 2' methoxyethyl nucleotides. All cytidines are
FT 5-methylcytidines"
XX
PN WO2003053340-A2.
XX
PD 03-JUL-2003.
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PF 09-DEC-2002; 2002WO-US038618.
XX
PR 10-DEC-2001; 2001US-00006191.
XX
PA (ISIS-) ISIS PHARM INC.
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PI Gaarde WA, Watt AT;
XX
DR WPI; 2003-559091/52.
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XX
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```

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 CC human CTGF of the invention.

SQ Sequence 20 BP; 6 A; 7 C; 3 G; 4 T; 0 U; 0 Other;  
 Query Match 1.9%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 60;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1719 TTAGACTGGACAGCTGTGG 1738  
 DB 20 TTAGACTGGACAGCTGTGG 1

RESULT 122  
 ADB25668/C  
 ID ADB25668 standard; DNA; 20 BP.

XX ADB25668;

XX 20-NOV-2003 (first entry)

XX Human connective tissue growth factor antisense oligo DNA (SeqID 61).

XX antisense; human; ss; connective tissue growth factor; CTGF;  
 KW chromosome 6q23.1; ctgofact; fibroblast inducible secreted protein;  
 KW fisp-12; NOV2;  
 KW insulin-like growth factor binding protein-related protein 2; IGFBP-rp2;  
 KW IGFBP-8; Hcs24; ecogenin; acute lymphoblastic leukaemia; gene therapy;  
 KW hyperproliferative disorder; cancer; pulmonary fibrosis; renal fibrosis;  
 KW scleroderma; atherosclerosis; cytostatic; dermatological;  
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XX Homo sapiens.

XX Key Location/Qualifiers  
 FH modified\_base 1..20  
 FT /\*tag= a  
 FT /mod\_base= OTHER  
 FT /note= "OTHER= phosphorothioate backbone, where 1-5 and  
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XX WO2003053340-A2.

XX 03-JUL-2003.

XX 09-DEC-2002; 2002WO-US038618.

XX 10-DEC-2001; 2001US-00006191.

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XX Gaarde WA, Watt AT;

XX WPI; 2003-559091/52.

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SQ Sequence 20 BP; 9 A; 2 C; 1 G; 8 T; 0 U; 0 Other;

Query Match 1.9%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 60;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1834 TTATCTAAGTTAATTAAAG 1853

DB 20 TTATCTAAGTTAATTAAAG 1

RESULT 123

ADB25670/C

ID ADB25670 standard; DNA; 20 BP.

XX ADB25670;

XX 20-NOV-2003 (first entry)

XX Human connective tissue growth factor antisense oligo DNA (SeqID 63).

XX antisense; human; ss; connective tissue growth factor; CTGF;  
 KW chromosome 6q23.1; ctgofact; fibroblast inducible secreted protein;  
 KW fisp-12; NOV2;  
 KW insulin-like growth factor binding protein-related protein 2; IGFBP-rp2;  
 KW IGFBP-8; Hcs24; ecogenin; acute lymphoblastic leukaemia; gene therapy;  
 KW hyperproliferative disorder; cancer; pulmonary fibrosis; renal fibrosis;  
 KW scleroderma; atherosclerosis; cytostatic; dermatological;  
 KW antiarteriosclerotic.

XX Homo sapiens.

XX Key Location/Qualifiers  
 FH modified\_base 1..20  
 FT /\*tag= a  
 FT /mod\_base= OTHER  
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XX WO2003053340-A2.

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XX 10-DEC-2001; 2001US-00006191.

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XX Gaarde WA, Watt AT;

XX WPI; 2003-559091/52.



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CC associated with the vasculature. Accordingly, antisense oligonucleotides  
CC that inhibit the expression of CTGF in cells or tissues can be used in  
CC gene therapy to treat various conditions including hyperproliferative  
CC disorders (particularly cancer, e.g. breast, prostate or renal cancer),  
CC pulmonary fibrosis, renal fibrosis, scleroderma and atherosclerosis. As  
CC such, the present invention describes these antisense oligos as having  
CC cytostatic, dermatological and antiarteriosclerotic activities. This  
CC oligonucleotide sequence is a chimeric phosphorothioate antisense oligo  
CC with 2' MOE wings and a deoxy gap, which is used to inhibit expression of  
CC human CTGF of the invention.  
XX  
XX Sequence 20 BP; 4 A; 5 C; 3 G; 8 T; 0 U; 0 Other;  
SQ

Query Match 1.9%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 60;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2212 AGAGTGTGACCAAAAGTTAC 2231  
DB 20 AGAGTGTGACCAAAAGTTAC 1

RESULT 124  
ADD26665  
ID ADD26665 standard; DNA; 20 BP.  
XX  
XX ADD26665;  
XX

15-JAN-2004 (first entry)

Polynucleotide (dsDNA) used in treatment of SLE.

Systemic lupus erythematosus; SLE; impaired renal function;  
KW LJP 394 conjugate; dermatological; immunosuppressive; antiinflammatory;  
KW ds.  
XX

Unidentified.

US2003114405-A1.

19-JUN-2003.

13-AUG-2002; 2002US-00219238.

13-AUG-2001; 2001US-0311858P.

22-AUG-2001; 2001US-0314281P.

(LINN//) LINNIK M D.

(HEPB//) HEPBURN B.

Linnik MD, Hepburn B;

WPI; 2003-810915/76.

Treating systemic lupus erythematosus comprises selecting an individual  
PT having significantly impaired renal function and administering conjugate  
PT having non-immunogenic valency platform molecule and double stranded DNA  
PT epitopes.

XX Claim 3; Page 18; 22pp; English.  
XX The present invention relates to a method of treating systemic lupus  
CC erythematosus (SLE) in an individual. The method comprises selecting an  
CC individual having SLE, significantly impaired renal function, and  
CC antibodies with high affinity to a polynucleotide epitope by  
CC administering a conjugate comprising non-immunogenic valency platform  
CC molecules and two or more double stranded DNA (dsDNA) epitopes that are  
CC polynucleotides. Also disclosed is a kit comprising the conjugate, LJP  
CC 394. The conjugate is administered in an amount effective to reduce  
CC incidence of renal flares in the individual. A medication chosen from  
CC corticosteroids and cyclophosphamide is also administered to the  
CC individual. The conjugate is administered in an amount effective to  
CC reduce the amount of a corticosteroid or cyclophosphamide administered to  
CC the individual. The present sequence represents a polynucleotide (dsDNA)  
CC used in the treatment of SLE.

SQ Sequence 20 BP; 0 A; 0 C; 10 G; 10 T; 0 U; 0 Other;

Query Match 1.9%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 60;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTGT 1813  
DB 1 GTGTGTGTGTGTGTGTGT 20

RESULT 125  
AAQ34015  
ID AAQ34015 standard; DNA; 21 BP.  
XX  
XX AAQ34015;  
XX

25-MAR-2003 (revised)

02-FEB-1993 (first entry)

Microsatellite sequence from clone TGLA419.

PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;  
KW genetic mapping; traits; amplification; ss.  
XX Bos taurus.

WO9213102-A1.

06-AUG-1992.

15-JAN-1992; 92WO-US000340.

15-JAN-1991; 91US-00642342.

(GENM-) GENMARK.

Georges M, Massey JM;

WPI; 1992-284684/34.

Polymorphic bovine DNA markers - used in genetic identification, gene  
PT mapping, and selective breeding.

Table 7; Page 336; 517pp; English.

The sequence is that of a bovine microsatellite sequence obtd. by  
CC screening a library of bovine MboI DNA fragments of between 250 and 500  
CC bp with an (AC)<sub>15</sub> and a (TC)<sub>15</sub> oligonucleotide probe. One out of 50  
CC clones cross-hybridised. Assuming independent distribution of  
CC microsatellites and MboI sites, the frequency of (T6)<sub>n</sub> > 9 microsatellites  
CC in the bovine genome is estimated at >100,000. The sequence information  
CC for ca. 230 such bovine microsatellites is summarised in the  
CC specification and indexed herein (see below). The sequences upstream and  
CC downstream of the microsatellite sequence were used to generate the

CC required PCR primers for in vitro amplification of the corresp.  
CC microsatellite (using the program OPIPRIM). The microsatellites may be  
CC used to identify individuals, for parentage testing, and in the genetic  
CC mapping of economic trait loci, or genes involved the determinism of  
CC economically important traits esp. in cattle, to allow selective  
CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN  
CC field.)

```

Sequence 21 BP; 0 A; 0 C; 11 G; 10 T; 0 U; 0 Other;

Query Match      1.9%  Score 20;  DB 1;  Length 21;
Best Local Similarity 100.0%;  Pred.No. 62;
Matches 20;  Conservative 0;  Mismatches 0;  Gaps 0;

```

```

RESULT 126
AAx90296
ID   AAX90296 standard; DNA; 21 BP.
XX
XX
XX   AAX90296;
AC
XX
XX
24-SEP-1999 (first entry)
DT
XX
XX
XX
DE Oligonucleotide RNC05 used in an Example from US932556.

```

PT Oligo:nucleotide which reduces CD28 gene expression in T cells - for  
PT treating immune system diseases, e.g. graft vs. host disease, septic  
PT shock, psoriasis, etc.

xx The present invention describes a method for inhibiting the expression of CC CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method comprises CC subcutaneous administration of an oligonucleotide (OGN). AAX90288 to CC AAX90291 represent specifically claimed OGNs for use in the method. The CC OGNs are used for the treatment of immune system-mediated diseases. CC AAX90292 to AAX90323 represent oligonucleotides used in the CC exemplification of the present invention

```
Query Match      1.9%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

RESULT 127  
AAH46014  
ID AAH46014 standard; DNA; 21 BP.

xx Synthetic oligonucleotide; dinucleotide repeat;  
 KW cell cycle arrest; cell proliferation; caspase;  
 KW cytokine; interleukin;  
 KW tumour necrosis factor; TNF; cancer; carcinoma; sarcoma; leukemia;  
 KW lymphoma; ss.

XX Phillips NC, Filion MC;  
PI  
XX  
DR WPI: 2001-398150/42.

xx Composition comprising synthetic oligonucleotides which comprise multiple  
 pt repeats of dinucleotides such as GT, TG useful for treating cancer by  
 pt inducing cell cycle arrest, inhibiting proliferation, activating  
 pt caspases.

The present sequence is that of a synthetic oligonucleotide useful to the invention. The invention relates to a composition, comprising a 2 to 20 base 3'-OH, 5'-OH synthetic oligonucleotide which comprises multiple repeats of dinucleotides such as GT, TG, etc., according to specific formula and having cytostatic activity. The oligonucleotide compositions are useful for inducing cell cycle arrest, inhibition of proliferation, activation of caspases and induction of apoptosis or production of cytokines such as interleukin (IL)-1-beta, IL-6, IL-10, IL-12 and tumour necrosis factor (TNF)-alpha by immune system cells, in an animal having cancer such as primary carcinoma, secondary carcinoma, primary sarcoma and secondary sarcoma such as, leukemia, lymphoma, breast, prostate, colorectal, ovarian or bone cancer. The compositions induce apoptosis independent of Fas, p53/p21, p21/waf-1/Cip, p15(Ink4B), p16(Ink4), drug resistance, caspase 3, transforming growth factor (TGF)-beta 1 receptor and hormone dependence.

Query Match	1.9%	Score 20;	DB 1;	Length 21;
Best Local Similarity	100.0%	Pred. No. 62;		
Matches 20;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;

RESULT 128  
ABN88973  
ID ABN88973 standard; DNA; 21 BP.  
XX  
AC ABN88973;

```
DT 22-AUG-2002 (first entry)
XX Phosphorothioate 21mer oligonucleotide SEQ ID NO:2.
DE Phosphorothioate; oligonucleotide synthesis; phosphoramidite; ss.
XX Phosphorothioate; oligonucleotide synthesis; phosphoramidite; ss.
XX Synthetic.
XX Key Location/Qualifiers
FH modified_base 1..21
FT /*tag= a
FT /*mod_base= OTHER
FT /*note= "phosphorothioate linkages"
XX WO200220543-A2.
XX 14-MAR-2002.
XX 06-SEP-2001; 2001WO-CB003973.
XX 07-SEP-2000; 2000US-0230685P.
XX (AVEC-) AVECIA BIOTECHNOLOGY INC.
XX (AVEC-) AVECIA LTD.
XX Sinha N;
XX WPI; 2002-479457/51.
XX Novel phosphoramidite compound, useful for the synthesis of
PT oligonucleotides, comprising nucleoside moieties linked by one or more
PT internucleoside phosphorus atoms.
XX Example 4; Page 28; 67pp; English.
XX The present invention describes a phosphoramidite compound (I) comprising
CC two or more nucleoside moieties linked by one or more internucleoside
CC phosphorus atoms, where the internucleoside phosphorus atoms are
CC phosphorus (III) atoms. Also described: (1) preparing a trivalent
CC phosphorus multimer or its stereoisomer (I); (2) a trivalent phosphorus
CC multimer derivatised solid support (II); and (3) preparing (II). (I) or
CC (II) can be used for the synthesis of oligonucleotides. The present
CC sequence represents a phosphorothioate 21mer oligonucleotide which is
CC synthesised in an example from the present invention
XX Sequence 21 BP; 0 A; 0 C; 10 G; 11 T; 0 U; 0 Other;
XX
XX The present invention describes a phosphoramidite compound (I) comprising
CC two or more nucleoside moieties linked by one or more internucleoside
CC phosphorus atoms, where the internucleoside phosphorus atoms are
CC phosphorus (III) atoms. Also described: (1) preparing a trivalent
CC phosphorus multimer or its stereoisomer (I); (2) a trivalent phosphorus
CC multimer derivatised solid support (II); and (3) preparing (II). (I) or
CC (II) can be used for the synthesis of oligonucleotides. The present
CC sequence represents a phosphorothioate 21mer oligonucleotide which is
CC synthesised in an example from the present invention
XX Sequence 21 BP; 0 A; 0 C; 10 G; 11 T; 0 U; 0 Other;
XX
XX Query Match 1.9%; Score 20; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred.No. 62;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1794 GTGTGTGTGTGTGTGTGTGT 1813
DB 1 GTGTGTGTGTGTGTGTGTGT 20
RESULT 129
ABN88972/C
ID ABN88972 standard; DNA; 21 BP.
XX AC ABN88972;
XX AC ABN88972;
XX 22-AUG-2002 (first entry)
XX Phosphorothioate 21mer oligonucleotide SEQ ID NO:1.
DE Phosphorothioate; oligonucleotide synthesis; phosphoramidite; ss.
XX Phosphorothioate; oligonucleotide synthesis; phosphoramidite; ss.
XX Synthetic.
XX Key Location/Qualifiers
FH modified_base 1..21
FT /*tag= a
```

```
PT /mod_base= OTHER
FT /*note= "phosphorothioate linkages"
XX WO200220543-A2.
XX 14-MAR-2002.
XX 06-SEP-2001; 2001WO-CB003973.
XX 07-SEP-2000; 2000US-0230685P.
XX (AVEC-) AVECIA BIOTECHNOLOGY INC.
XX (AVEC-) AVECIA LTD.
XX Sinha N;
XX WPI; 2002-479457/51.
XX Novel phosphoramidite compound, useful for the synthesis of
PT oligonucleotides, comprising nucleoside moieties linked by one or more
PT internucleoside phosphorus atoms.
XX Example 4; Page 28; 67pp; English.
XX The present invention describes a phosphoramidite compound (I) comprising
CC two or more nucleoside moieties linked by one or more internucleoside
CC phosphorus atoms, where the internucleoside phosphorus atoms are
CC phosphorus (III) atoms. Also described: (1) preparing a trivalent
CC phosphorus multimer or its stereoisomer (I); (2) a trivalent phosphorus
CC multimer derivatised solid support (II); and (3) preparing (II). (I) or
CC (II) can be used for the synthesis of oligonucleotides. The present
CC sequence represents a phosphorothioate 21mer oligonucleotide which is
CC synthesised in an example from the present invention
XX Sequence 21 BP; 10 A; 10 C; 0 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 1.9%; Score 20; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred.No. 62;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1794 GTGTGTGTGTGTGTGTGTGT 1813
DB 20 GTGTGTGTGTGTGTGTGTGT 1
RESULT 130
ABZ57678
ID ABZ57678 standard; DNA; 24 BP.
XX AC ABZ57678;
XX AC ABZ57678;
XX 10-APR-2003 (first entry)
XX Human zinc finger protein 9.46 RT-PCR primer, SEQ ID NO:3.
DE Human; zinc finger protein 9.46; recombinant production; gene therapy;
KW malignant tumour; cancer; blood disease; human immunodeficiency virus;
KW HIV infection; immune disorder; inflammatory condition; cytostatic;
KW antiinflammatory; immunomodulator; reverse transcription-PCR; RT-PCR;
KW primer; ss.
XX Homo sapiens.
XX CNL361165-A.
XX 31-JUL-2002.
XX 26-DEC-2000; 2000CN-00136331.
XX 26-DEC-2000; 2000CN-00136331.
XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX
```

PI Mao Y, Xie Y;  
 DR WPI; 2003-000239/01.  
 XX  
 PT New polypeptide human zinc finger protein 9.46 and polynucleotides  
 PT encoding this polypeptide.  
 XX  
 PS Example 2; Page 16 (Disclosure); 31pp; Chinese.  
 XX  
 CC The invention relates to human zinc finger protein 9.46 (ABP59904) and  
 CC nucleic acids encoding it (ABZ57677). The protein has a molecular weight  
 CC of 9.46 kD. The invention also relates to a method for the recombinant  
 CC production of the protein, an antagonist of the protein, and the use of  
 CC the protein, gene and antagonist in therapeutic applications. Zinc finger  
 CC protein 9.46 can be used in the treatment of a variety of diseases such  
 CC as malignant tumours, blood diseases, HIV (human immunodeficiency virus)  
 CC infection, immune disorders and inflammatory conditions. Sequences  
 CC ABZ57678-ABZ57679 represent reverse transcription-PCR (RT-PCR) primers  
 CC used in an exemplification of the invention to isolate human zinc finger  
 CC protein 9.46 cDNA  
 XX  
 SQ Sequence 24 BP; 0 A; 0 C; 13 G; 11 T; 0 U; 0 Other;  
 CC  
 Query Match 1.9%; Score 19.8; DB 1; Length 24;  
 Best Local Similarity 91.3%; Pred. No. 73;  
 Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 XX  
 QY 1793 TGTGTGTGTGTGTGTGTGTAT 1815  
 DB 2 TGTGTGTGTGTGTGTGTGTGT 24  
 XX  
 RESULT 131  
 AAQ33789  
 ID AAQ33789 standard; DNA; 21 BP.  
 AC AAQ33789;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 02-FEB-1993 (first entry)  
 DE Microsatellite sequence from clone TGLA2.  
 XX  
 KW PCR; selection; primers; OPIPRIM; breeding; cattle; parentage;  
 KW Genetic mapping; traits; amplification; ss.  
 XX  
 OS Bos taurus.  
 XX  
 PN WO9213102-A1.  
 XX  
 PD 06-AUG-1992.  
 XX  
 PF 15-JAN-1992; 92MO-US000340.  
 XX  
 PR 15-JAN-1991; 91US-00642342.  
 XX  
 PA (GENM-) GENMARK.  
 XX  
 PI Georges M, Massey JM;  
 XX  
 DR WPI; 1992-284684/34.  
 XX  
 PT Polymorphic bovine DNA markers - used in genetic identification, gene  
 PT mapping, and selective breeding.  
 XX  
 PS Table 7; Page 245; 517pp; English.  
 XX  
 CC The sequence is that of a bovine microsatellite sequence obt'd. by  
 CC screening a library of bovine MboI DNA fragments of between 250 and 500  
 CC bp with an (AC)<sub>15</sub> and a (TC)<sub>15</sub> oligonucleotide probe. One out of 50  
 CC clones cross-hybridised. Assuming independent distribution of  
 CC microsatellites and MboI sites, the frequency of (T6)<sub>n</sub> > 9 microsatellites  
 CC in the bovine genome is estimated at >100, 000. The sequence information

CC for ca. 230 such bovine microsatellites is summarised in the  
 CC specification and indexed herein (see below). The sequences upstream and  
 CC downstream of the microsatellite sequence were used to generate the  
 CC required PCR primers for in vitro amplification of the corresp.  
 CC microsatellite (using the program OPIPRIM). The microsatellites may be  
 CC used to identify individuals, for parentage testing, and in the genetic  
 CC mapping of economic trait loci, or genes involved in the determination of  
 CC economically important traits esp. in cattle, to allow selective  
 CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN  
 CC field.)  
 XX  
 SQ Sequence 21 BP; 0 A; 1 C; 10 G; 10 T; 0 U; 0 Other;  
 CC  
 Query Match 1.8%; Score 19.4; DB 1; Length 21;  
 Best Local Similarity 95.2%; Pred. No. 73;  
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 XX  
 QY 1793 TGTGTGTGTGTGTGTGTGT 1813  
 DB 1 TGTGTGTGTGTGTGTGTGTGT 21  
 XX  
 RESULT 132  
 AAT58080/C  
 ID AAT58080 standard; DNA; 21 BP.  
 AC AAT58080;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 18-MAR-1997 (first entry)  
 XX  
 DE ICAM-1 antisense oligonucleotide #10.  
 XX  
 KW Antisense; pre-mRNA; mature mRNA; vascular defect; tissue defect;  
 KW human intercellular adhesion molecule-1; ICAM-1; inflammation;  
 KW adult respiratory distress syndrome; multiple organ failure; GM1594;  
 KW septic shock; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN USS580969-A.  
 XX  
 PD 03-DEC-1996.  
 XX  
 PF 12-OCT-1993; 93US-00136118.  
 XX  
 PR 24-JUL-1992; 92US-00918259.  
 XX  
 PA (USNA) US SEC OF NAVY.  
 XX  
 PI Lee C, Hoke GD, Bradley MO, Williams TU;  
 XX  
 DR WPI; 1997-033603/03.  
 XX  
 PT Anti-sense oligonucleotide(s) for blocking ICAM-1 mRNA translation - for  
 PT treating septic shock, adult respiratory distress syndrome etc.  
 XX  
 PS Claim 1; Col 21; 16pp; English.  
 XX  
 CC The sequences given in AAT58071-85 represent oligonucleotides which are  
 CC antisense to sequences contained in the pre-mRNA or mature mRNA  
 CC transcript of human intercellular adhesion molecule-1 (ICAM-1). These  
 CC oligonucleotides may be used for treating septic shock and the  
 CC manifestations of septic shock, e.g. inflammation, and vascular and  
 CC tissue defects. They are also useful in the treatment of septic shock  
 CC associated diseases, e.g. adult respiratory distress syndrome, multiple  
 CC organ failure etc. (Updated on 25-MAR-2003 to correct PF field.)  
 XX  
 SQ Sequence 21 BP; 11 A; 9 C; 0 G; 1 T; 0 U; 0 Other;  
 CC  
 Query Match 1.8%; Score 19.4; DB 1; Length 21;  
 Best Local Similarity 95.2%; Pred. No. 73;  
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTGTGTGT 1813  
 Db 21 TGTGTGTGTGTGTGTGTGTGTGTGT 1

RESULT 133  
 AAV38616/C  
 ID AAV38616 standard; DNA; 21 BP.  
 XX AAV38616;  
 AC AAV38616;  
 XX 13-OCT-1998 (first entry)  
 DT  
 DE Human ICAM-1, E-selectin, VCAM-1 antisense oligonucleotide.  
 XX ICAM-1; intracellular adhesion molecule-1; E-selectin; VCAM-1;  
 KW vascular cell adhesion molecule-1; antisense; inflammatory; disease;  
 KW treatment; septic shock; psoriasis; wounds; burns; acne; arthritis;  
 KW organ rejection; inhibition; expression; ss.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 PN WO9824797-A1.  
 XX  
 PD 11-JUN-1998.  
 XX  
 PF 02-DEC-1996; 96WO-US019194.  
 XX  
 PR 02-DEC-1996; 96WO-US019194.  
 XX  
 PA (DYAD-) DYAD PHARM CORP.  
 XX  
 XX Hoke GD, Bradley MO, Williams TJ, Lee C;  
 PI WPI; 1998-333253/29.  
 XX  
 DR Antisense oligonucleotides to ICAM-1, E-selectin or VCAM-1 - useful for  
 PT treating diseases having an inflammatory component, e.g. psoriasis,  
 FT wounds and septic shock.  
 PT  
 XX  
 PS Claim 8; Page 40; 48pp; English.  
 XX  
 CC The sequence is that of an antisense oligonucleotide which is  
 CC substantially complementary to at least a portion of the pre- or mature  
 CC RNA transcript of human intracellular adhesion molecule (ICAM), E-  
 CC selectin or vascular cell adhesion molecule (VCAM). It can be used to  
 CC inhibit expression of these proteins. Inhibition of these proteins forms  
 CC the basis for treatment of conditions and diseases that have an  
 CC inflammatory component, e.g. acne, psoriasis, arthritis, organ rejection,  
 CC wounds, burns, septic shock or inflammatory complications of septic shock  
 CC  
 XX Sequence 21 BP; 11 A; 9 C; 0 G; 1 T; 0 U; 0 Other;  
 SQ  
 Query Match 1.8%; Score 19.4; DB 1; Length 21;  
 Best Local Similarity 95.2%; Pred. No. 73;  
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTGTGTGT 1813  
 Db 21 TGTGTGTGTGTGTGTGTGTGTGTGT 1

RESULT 134  
 ABS97829/C  
 ID ABS97829 standard; DNA; 21 BP.  
 XX ABS97829;  
 AC ABS97829;  
 XX 23-DEC-2002 (first entry)  
 DT  
 DE Human NADPH quinone oxidoreductase 2 (NQO2) polymorphic sequence #37.

XX Human; ds; cytochrome P450 A1; CYP450A1; UGT2B4; MDR1;  
 KW cytochrome P450 A2; CYP450A2; cytochrome P450 02E; CYP45002E1; LTF;  
 KW adrenergic receptor beta1; ADRB1; aryl hydrocarbon; AHR; MRP3; NR1I2;  
 KW aryl hydrocarbon receptor nuclear translocator; ARNT; cathepsin S; CTSS;  
 KW cyclooxygenase 2; COX2; diazepam binding inhibitor; DBI; haematological;  
 KW epoxide hydroxylase 2; EPHX2; 5-lipoxygenase activating protein; FLAP;  
 KW glutathione-S-transferase 12; GSTI2; histamine-N-methyl transferase;  
 KW HNMT; kallikrein 2; KLK2; nicotinamide-N-methyl transferase; NNMT;  
 KW NADPH quinone oxidoreductase 2; NQO2; sulfoltransferase thermolabile; STM;  
 KW UDP-glucuronosyl transferase 2B4; UDP-glucuronosyl transferase 2B7;  
 KW UGT2B7; UDP-glucuronosyl transferase; UGT2B15; urokinase receptor; uPA;  
 KW multidrug resistance 1; lactotransferrin; orphan nuclear receptor;  
 KW multidrug resistance associated protein 3; cancer; prostate;  
 KW acetylcholine muscarinic receptor; CHMR1; CHMR2; CHMR3; CHMR4; CHMR5;  
 KW central nervous system; cardiovascular function; colorectal tumour;  
 KW altered drug metabolism; pulmonary; immunological; SNP;  
 XX single nucleotide polymorphism.  
 OS Homo sapiens.  
 XX WO200257410-A2.  
 XX 25-JUL-2002.  
 XX 28-NOV-2001; 2001WO-US044838.  
 XX 28-NOV-2000; 2000US-00724389.  
 XX (DNAS-) DNA SCI LAB INC.  
 XX Guida M, Hall J;  
 XX WPI; 2002-698522/75.  
 XX Isolated nucleic acid molecules having polymorphisms in known human genes  
 PT e.g. cytochrome P450 and cathepsin S useful as genetic linkage markers  
 PT for locating, identifying and characterizing the genes responsible for  
 PT disorder-related traits.  
 XX Example 16; Page 130; 714pp; English.  
 XX This invention relates to the sequence of an isolated nucleic acid  
 CC molecule comprising at least one base variation from that of a known  
 CC human cytochrome P450 A1 (CYP450A1), cytochrome P450 A2 (CYP450A2),  
 CC cytochrome P450 02E1 (CYP45002E1), adrenergic receptor beta1 (ADRB1),  
 CC aryl hydrocarbon (AHR), aryl hydrocarbon receptor nuclear translocator  
 CC (ARNT) cathepsin S (CTSS), cyclooxygenase 2 (COX2), diazepam binding  
 CC inhibitor (DBI), epoxide hydroxylase 2 (EPHX2), 5-lipoxygenase activating  
 CC protein (FLAP), glutathione-S-transferase 12 (GSTI2), histamine-N-methyl  
 CC transferase (HNMT), (kallikrein 2) KLK2, nicotinamide -N-methyl  
 CC transferase (NNMT), NADPH quinone oxidoreductase 2 (NQO2),  
 CC sulfoltransferase thermolabile (STM), UDP-glucuronosyl transferase 2B4  
 CC (UGT2B4), UDP-glucuronosyl transferase 2B7 (UGT2B7), UDP-glucuronosyl  
 CC transferase (UGT2B15), urokinase receptor (uPA), multidrug resistance 1  
 CC (MDR1), lactotransferrin (LTF), multidrug resistance associated protein 3  
 CC (MRP3), orphan nuclear receptor (NR1I2), or acetylcholine muscarinic  
 CC receptor 1, 2, 3, 4, or 5 (CHMR1, CHMR2, CHMR3, CHMR4 or CHMR5) sequence.  
 CC The polymorphisms in the human genes cited in the invention are useful as  
 CC genetic linkage markers for locating and characterizing the genes that  
 CC are responsible for specific traits within the genome and eventually  
 CC identifying the genes responsible for a variety of disorder-related  
 CC traits as a result of their e.g., overexpression, constitutive  
 CC expression, mutation or underexpression, which may be used in diagnosing  
 CC and/or treating the disorders. The nucleic acid molecules comprising the  
 CC polymorphic sequences contained in CYP450A1, CYP450A2, CYP4502E1,  
 CC ARNT, EPHX2, GSTI2, NNMT, NQO2, NR1I2, STM, UGT2B4, UGT2B7, UGT2B15, AHR,  
 CC MDR1 and/or MDR3 are useful for screening individuals for altered drug  
 CC metabolism. The polymorphic sequences contained in CYP450A1, CYP450A2,  
 CC AHR, MDR1 and/or MDR3 may also be used to screen individuals for  
 CC susceptibility to cancer. Polymorphic sequences in ADRB1 or CHMR2 are  
 CC used to screen for altered cardiovascular function, in COX2 for altered  
 CC susceptibility to colorectal tumours, in DBI or CHMR1 for altered central

nervous system function, in FLAP and HNMT for altered pulmonary, immunological or haematological function, in KXK2 for altered serine protease activity in the prostate, in LTF for altered immunological or haematological function, in CHMR3, CHMR4 or CHMR5 for altered central and peripheral nervous system function. The present sequence represents a polymorphic DNA sequence of the invention

Sequence 21 BP; 11 A; 9 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 1.8%; Score 19.4; DB 1; Length 21;  
Best Local Similarity 95.2%; Pred. No. 73;  
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1793 TGTGTGTGTGTGTGTGTGT 1813  
21 TATGTGTGTGTGTGTGTGT 1

RESULT 135  
ABS97831/C  
ID ABS97831 standard; DNA; 21 BP.  
AC ABS97831;  
XX  
XX  
23-DEC-2002 (first entry)  
XX  
XX  
DE Human NADPH quinone oxidoreductase 2 (NQO2) polymorphic sequence #39.  
XX  
KW Human; ds; cytochrome P450 A1; CYP450A1; UGT2B4; MDR1;  
KW cytochrome P450 A2; CYP450A2; cytochrome P450 02E; CYP45002E1; LTF;  
KW adrenergic receptor beta1; ADBR1; aryl hydrocarbon; AHR; MRP3; NR112;  
KW aryl hydrocarbon receptor nuclear translocator; ARNT; cathepsin S; CTSS;  
KW cyclooxygenase 2; COX2; diazepam binding inhibitor; DBI; haematological;  
KW epoxide hydroxylase 2; EPX2; 5-lipoxygenase activating protein; FLAP;  
KW glutathione-S-transferase 12; GST12; histamine-N-methyl transferase;  
KW HNMT; kallikrein 2; KUK2; nicotinamide-N-methyl transferase; NNMT;  
KW NADPH quinone oxidoreductase 2; NQO2; sulfoxyltransferase thermolabile; STM;  
KW UDP-glucuronosyl transferase 2B4; UDP-glucuronosyl transferase 2B7;  
KW UGT2B7; UDP-glucuronosyl transferase; UGT2B15; urokinase receptor; uPA;  
KW multidrug resistance 1; lactotransferrin; orphan nuclear receptor;  
KW multidrug resistance associated protein 3; cancer; prostate;  
KW acetylcholine muscarinic receptor; CHMR1; CHMR2; CHMR3; CHMR4; CHMR5;  
KW altered drug metabolism; cardiovascular function; colorectal tumour;  
KW central nervous system; pulmonary; immunological; SNP;  
KW single nucleotide polymorphism.  
XX  
OS Homo sapiens.  
XX  
XX W0200257410-A2.  
XX  
XX 25-JUL-2002.  
XX  
XX 28-NOV-2001; 2001WO-US044838.  
XX  
XX 28-NOV-2000; 2000US-00724389.  
XX  
XX (DNAS-) DNA SCI LAB INC.  
XX  
XX Guida M, Hall J;  
XX  
XX WPI; 2002-698522/75.  
XX  
XX Isolated nucleic acid molecules having polymorphisms in known human genes  
XX e.g. cytochrome P450 and cathepsin S useful as genetic linkage markers  
XX for locating, identifying and characterizing the genes responsible for  
XX disorder-related traits.  
XX  
XX Example 16; Page 131; 714pp; English.  
XX  
XX This invention relates to the sequence of an isolated nucleic acid  
XX molecule comprising at least one base variation from that of a known  
XX human cytochrome P450 A1 (CYP450A1), cytochrome P450 A2 (CYP450A2),  
XX cytochrome P450 02E1 (CYP45002E1), adrenergic receptor beta1 (ADBR1),

aryl hydrocarbon (AHR), aryl hydrocarbon receptor nuclear translocator (ARNT), cathepsin S (CTSS), cyclooxygenase 2 (COX2), diazepam binding inhibitor (DBI), epoxide hydroxylase 2 (EPX2), 5-lipoxygenase activating protein (FLAP), glutathione-S-transferase 12 (GST12), histamine-N-methyl transferase (HNMT), (kallikrein 2) KUK2, nicotinamide-N-methyl transferase (NNMT), NADPH quinone oxidoreductase 2 (NQO2), sulfoxyltransferase thermolabile (STM), UDP-glucuronosyl transferase 2B4 (UGT2B4), UDP-glucuronosyl transferase 2B7 (UGT2B7), UDP-glucuronosyl transferase (UGT2B15), urokinase receptor (uPA), multidrug resistance 1 (MDR1), lactotransferrin (LTF), multidrug resistance associated protein 3 (MRP3), orphan nuclear receptor (NR112), or acetylcholine muscarinic receptor 1, 2, 3, 4, or 5 (CHMR1, CHMR2, CHMR3, CHMR4 or CHMR5) sequence. The polymorphisms in the human genes cited in the invention are useful as genetic linkage markers for locating and characterizing the genes that are responsible for specific traits within the genome and eventually identifying the genes responsible for a variety of disorder-related traits as a result of their e.g., overexpression, constitutive expression, mutation or underexpression, which may be used in diagnosing and/or treating the disorders. The nucleic acid molecules comprising the polymorphic sequences contained in CYP450A1, CYP450A2, CYP45002E1, ARNT, EPX2, GST12, NNMT, NQO2, NR112, STM, UGT2B4, UGT2B7, UGT2B15, AHR, MDR1 and/or MDR3 are useful for screening individuals for altered drug metabolism. The polymorphic sequences contained in CYP450A1, CYP450A2, AHR, MDR1 and/or MDR3 may also be used to screen individuals for susceptibility to cancer. Polymorphic sequences in ADRB1 or CHMR2 are used to screen for altered cardiovascular function, in COX2 for altered central susceptibility to colorectal tumours, in DBI or CHMR1 for altered central nervous system function, in FLAP and HNMT for altered pulmonary, immunological or haematological function, in KXK2 for altered serine protease activity in the prostate, in LTF for altered immunological or haematological function, in CHMR3, CHMR4 or CHMR5 for altered central and peripheral nervous system function. The present sequence represents a polymorphic DNA sequence of the invention

Sequence 21 BP; 11 A; 9 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 1.8%; Score 19.4; DB 1; Length 21;  
Best Local Similarity 95.2%; Pred. No. 73;  
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1793 TGTGTGTGTGTGTGTGTGT 1813  
21 TGTATGTGTGTGTGTGTGT 1

RESULT 136  
AAQ33716  
ID AAQ33716 standard; DNA; 22 BP.  
XX  
XX AAQ33716;  
XX  
XX 25-MAR-2003 (revised)  
DT 02-FEB-1993 (first entry)  
XX  
XX Microsatellite sequence from clone TGLA135.  
XX  
XX PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;  
XX genetic mapping; traits; amplification; ss.  
XX  
XX Bos taurus.  
XX  
XX W09213102-A1.  
XX  
XX 06-AUG-1992.  
XX  
XX 15-JAN-1992; 92WO-US000340.  
XX  
XX 15-JAN-1991; 91US-00642342.  
XX  
XX (GENM-) GENMARK.  
XX  
XX Georges M, Massey JM;  
XX

DR WPI; 1992-284684/34.  
 XX Polymorphic bovine DNA markers - used in genetic identification, gene  
 PT mapping, and selective breeding.  
 XX Table 7; Page 216; 517pp; English.  
 XX The sequence is that of a bovine microsatellite sequence obtd. by  
 CC screening a library of bovine MbolI DNA fragments of between 250 and 500  
 CC bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50  
 CC clones cross-hybridised. Assuming independent distribution of  
 CC microsatellites and MbolI sites, the frequency of (Tf)n > 9 microsatellites  
 CC in the bovine genome is estimated at >100, 000. The sequence information  
 CC for ca. 230 such bovine microsatellites is summarised in the  
 CC specification and indexed herein (see below). The sequences upstream and  
 CC downstream of the microsatellite sequence were used to generate the  
 CC required PCR primers for in vitro amplification of the corresp.  
 CC microsatellite (using the program Optiprimer). The microsatellites may be  
 CC used to identify individuals, for parentage testing, and in the genetic  
 CC mapping of economic trait loci, or genes involved in the determination of  
 CC economically important traits esp. in cattle, to allow selective  
 CC breeding. See also AAQ39501-34437. (Updated on 25-MAR-2003 to correct PN  
 CC field.)  
 XX  
 XX Sequence 22 BP; 1 A; 0 C; 11 G; 10 T; 0 U; 0 Other;  
 SQ  
 Query Match 1.8%; Score 19.4; DB 1; Length 22;  
 Best Local Similarity 95.2%; Pred. No. 76;  
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1793 TGTGTGTGTGTGTGTGTGTGTGTGTGT 1813  
 Db 1 TGTGTGTGTGTGTGTGTGTGTGTGTGT 21  
 RESULT 137  
 AA16456/c  
 ID AA164456 standard; DNA; 22 BP.  
 XX  
 AC AA164456;  
 XX  
 DT 23-NOV-2001 (first entry)  
 XX  
 DE SSR motif #16.  
 XX  
 KW Simple Sequence Repeat; SSR; clover; microsatellite; genome mapping;  
 KW trait mapping; marker-assisted selection; gene selection; legume;  
 KW DNA profiling; breeding; ds.  
 XX  
 OS Unidentified.  
 XX  
 XX NZ509194-A.  
 XX  
 XX 25-MAY-2001.  
 XX  
 XX 03-JAN-2001; 2001NZ-00509194.  
 XX  
 XX 24-DEC-1999; 99AU-00004907.  
 PR  
 XX 28-MAR-2000; 2000AU-00006520.  
 XX  
 XX (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
 PA  
 XX  
 XX Koelliker R, Forster JW;  
 XX  
 XX WPI; 2001-431058/46.  
 DR  
 XX Novel simple sequence repeats in clover species useful for selection of  
 XX genes in legume breeding, for profiling legume species varieties and for  
 PT testing the purity of legume seed batches.  
 PT  
 XX  
 XX Claim 6; Page 35; 52pp; English.  
 PS  
 XX The present invention relates to Simple Sequence Repeats (SSRs) from

CC clover species. SSRs, also called microsatellites, are based on a 1-7  
 CC nucleotide core element which is tandemly repeated. The SSR array is  
 CC embedded in complex flanking DNA. SSRs are ideal markers for genome  
 CC mapping, trait mapping and marker-assisted selection. The SSRs may be  
 CC used in methods for selecting genes in clover/ legume breeding. The SSRs  
 CC are also useful for DNA profiling of clover varieties and for testing the  
 CC purity of legume seed batches. The present sequence is a SSR motif, which  
 CC was used in the present invention  
 XX  
 XX Sequence 22 BP; 10 A; 12 C; 0 G; 0 T; 0 U; 0 Other;  
 SQ  
 Query Match 1.8%; Score 19.4; DB 1; Length 22;  
 Best Local Similarity 95.2%; Pred. No. 76;  
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1793 TGTGTGTGTGTGTGTGTGTGTGTGTGT 1813  
 Db 22 TGTGTGTGTGTGTGTGTGTGTGTGTGT 2  
 RESULT 138  
 ADD69447  
 ID ADD69447 standard; DNA; 23 BP.  
 XX  
 AC ADD69447;  
 XX  
 DT 15-JAN-2004 (first entry)  
 XX  
 DE 5' anchored (ISSR)-PCR primer - SEQ ID 5.  
 XX  
 KW inter-simple sequence repeat; ISSR; SSR; PCR; primer; genotyping; plant;  
 KW animal; Basmati rice; ss.  
 XX  
 OS Synthetic.  
 XX  
 XX WO2003085133-A2.  
 PN  
 XX 16-OCT-2003.  
 PD  
 XX 09-JAN-2003; 2003WO-IB000041.  
 PF  
 XX 08-APR-2002; 2002IN-CH000260.  
 PR  
 XX (DNAP-) CENT DNA FINGERPRINTING & DIAGNOSTICS.  
 PA  
 XX  
 XX NagaraJu JG;  
 PI  
 XX WPI; 2003-804317/75.  
 DR  
 XX  
 XX New set of inter-simple sequence repeats (ISSR)-PCR primers for  
 PT genotyping eukaryotes, useful for genotyping diverse genomes of plant and  
 PT animal systems.  
 PT  
 XX Claim 1; SEQ ID NO 5; 60pp; English.  
 PS  
 XX  
 XX The invention relates to a novel set of inter-simple sequence repeats  
 CC (ISSR)-PCR primers for genotyping eukaryotes. The primers of the  
 CC invention may be useful for genotyping diverse genomes of plant and  
 CC animal systems, in particular for distinguishing Basmati rice varieties  
 CC from non-Basmati rice varieties and traditional Basmati rice varieties  
 CC from evolved Basmati rice varieties. The current sequence is that of the  
 CC 5' anchored (ISSR)-PCR primer of the invention.  
 CC  
 XX Sequence 23 BP; 1 A; 1 C; 10 G; 11 T; 0 U; 0 Other;  
 SQ  
 Query Match 1.8%; Score 19.4; DB 1; Length 23;  
 Best Local Similarity 95.2%; Pred. No. 78;  
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1793 TGTGTGTGTGTGTGTGTGTGTGTGTGT 1813  
 Db 3 TATGTGTGTGTGTGTGTGTGTGTGTGT 23

RESULT 140	
ABZ70239/c	
ID	ABZ70239 standard; DNA; 24 BP.
XX	XX
XX	AC AC
XX	XX
DT	DT
25-APR-2003	(first entry)
DE	Murine tricarboxylic acid carrier 13.53 PCR primer #1.
DE	
XX	Murine; tricarboxylic acid carrier 13.53; tumour; cytostatic; haemopathy;
KW	HIV infection; anti-HIV; immunological disease; inflammation; PCR;
KW	primer; ss.
XX	XX
OS	Mus sp.
XX	XX
PN	CN1361126-A.
XX	XX
PD	31-JUL-2002.
XX	XX
PF	26-DEC-2000; 2000CN-00136313.
XX	XX
PR	26-DEC-2000; 2000CN-00136313.
XX	XX
PA	(BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX	XX
FI	Mao Y, Xie Y;
XX	XX
XX	WPI; 2002-751545/82.
XX	XX
PT	New polypeptide murine tricarboxylic acid carrier 13.53 and
XX	polynucleotides encoding this polypeptide.
DS	Example 2; Page 17 (Disclosure); 33pp; Chinese.
XX	XX
CC	The present invention relates to murine tricarboxylic acid carrier 13.53
CC	(see ABP59163). The protein is useful for treating various diseases, such
CC	as malignant tumours, haemopathy, HIV infection, immunological diseases
CC	and various inflammations. The present sequence is a PCR primer, which
CC	was used in an example from the invention
XX	XX
SQ	Sequence 24 BP; 10 A; 12 C; 2 G; 0 T; 0 U; 0 Other;
Query Match	1.8%; Score 19.4; DB 1; Length 24;
Best Local Similarity	95.2%; Pred. NO. 81;
Matches	20; Conservative 0; Mismatches 1; Indels 0; Gaps 0
QY	1793 TGCTGTGCTGTGTGTGTGTGT 1813
Dd	22 TGCTGTGCTGTGTGTGTGTGT 2
RESULT 141	
AAQ33728	
ID	AAQ33728 standard; DNA; 19 BP.
XX	XX
AC	AAQ33728;
XX	XX
DT	25-MAR-2003 (revised)
DT	02-FEB-1993 (first entry)
XX	XX
DE	Microsatellite sequence from clone TGLA147.
XX	XX
KW	PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
KW	genetic mapping; traits; amplification; ss.
XX	XX
OS	Bos taurus.
XX	XX
PN	WO9213102-A1.
PD	06-AUG-1992.



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XX PF 15-JAN-1992; 92WO-US000340.
XX PR 15-JAN-1991; 91US-00642342.
XX XX (GENM-) GENMARK.
XX PA
XX PI Georges M, Massey JM;
XX PR WPI; 1992-284684/34.
XX PS Polymorphic bovine DNA markers - used in genetic identification, gene
XX PT mapping, and selective breeding.
XX PT Table 7; Page 221; 517pp; English.
XX CC The sequence is that of a bovine microsatellite sequence obt'd. by
XX CC screening a library of bovine MboI DNA fragments of between 250 and 500
XX CC bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
XX CC clones cross-hybridised. Assuming independent distribution of
XX CC microsatellites and MboI sites, the frequency of (76)n > 9 microsatellites
XX CC in the bovine genome is estimated at >100,000. The sequence information
XX CC for ca. 230 such bovine microsatellites is summarised in the
XX CC specification and indexed herein (see below). The sequences upstream and
XX CC downstream of the microsatellite sequence were used to generate the
XX CC required PCR primers for in vitro amplification of the corresp.
XX CC microsatellite (using the program OPIPRIM). The microsatellites may be
XX CC used to identify individuals, for parentage testing, and in the genetic
XX CC mapping of economic trait loci, or genes involved the determinism of
XX CC economically important traits esp. in cattle, to allow selective
XX CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
XX CC field.)
XX SQ Sequence 19 BP; 0 A; 0 C; 9 G; 10 T; 0 U; 0 Other;

Query Match 1.8%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGT 1811
Db 1 TGTGTGTGTGTGTGTGTGT 19

RESULT 142
AAT30412
ID AAT30412 standard; DNA; 19 BP.
XX AC AAT30412;
XX DT 28-JAN-1997 (first entry)
XX DE Compound simple sequence repeat primer (GT)7.5(AT)2.
XX KW Detection; polymorphism; perfect compound simple sequence repeat;
XX KW adaptor directed primer; genome; genetic; fingerprinting;
XX KW amplified fragment length polymorphism assay; microsatellite region;
XX KW genetic trait marking; germplasm comparisons; compound; ss.
XX OS Synthetic.
XX XX WO9617082-A2.
XX PN 06-JUN-1996.
XX PD 21-NOV-1995; 95WO-US015150.
XX PF 28-NOV-1994; 94US-00346456.
XX PR (DUPO) DU PONT DE NEMOURS & CO E I.
XX PA Morgante M, Vogel JM;
XX PI
XX XX

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DR WPI; 1996-277795/28.
XX Modified amplified fragment length polymorphism assay - for detection of
XX PT polymorphism esp. in microsatellite regions.
XX PS Example 2; Page 84; 173pp; English.
XX CC Detecting polymorphisms between 2 nucleic acid samples, esp. in
XX CC microsatellite regions, comprises digesting the nucleic acid to generate
XX CC fragments, ligating adaptor segments to their ends, amplifying them using
XX CC primer directed amplification and comparing the prods. to detect
XX CC differences. The primers used in the amplification comprise a primer
XX CC consisting of a perfect cpd. simple sequence complementary to an adaptor
XX CC segment. The present sequence is an example of a compound SSR primer. The
XX CC method represents a modified amplified fragment length polymorphism
XX CC assay which is partic. useful for genome fingerprinting, i.e. for
XX CC genetic trait marking and germplasm comparisons
XX SQ Sequence 19 BP; 2 A; 0 C; 7 G; 10 T; 0 U; 0 Other;

Query Match 1.8%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1799 TGTGTGTGTGTGTGTATAT 1817
Db 1 TGTGTGTGTGTGTGTATAT 19

RESULT 143
AAT66093/c
ID AAT66093 standard; DNA; 19 BP.
XX AC AAT66093;
XX DT 25-MAR-2003 (revised)
XX DT 18-JUN-1997 (first entry)
XX DE Repeat sequence found in the haemoglobin gamma G gene.
XX KW Polymorphism; repeat sequence; genetic marker; primer; amplification;
XX KW PCR; polymerase chain reaction; paternity; maternity; human; pedigree;
XX KW linkage analysis; genetic disease; animal; plant; breeding; locus;
XX KW hybridisation; chromosome; ds.
XX OS Homo sapiens.
XX PN US5582379-A.
XX PD 10-DEC-1996.
XX PF 04-APR-1994; 94US-00222177.
XX PR 21-APR-1989; 89US-00341562.
XX PR 05-SEP-1991; 91US-00754351.
XX PA (MARS-) MARSHFIELD CLINIC.
XX PI Weber JL;
XX XX WPI; 1997-042299/04.
XX PT Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n -
XX PT using novel nucleic acid mols. as primers.
XX PS Example 9; Col 59-60; 186pp; English.
XX CC The invention relates to the isolation of polymorphic repeat sequences
XX CC having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic
XX CC markers. Primers based on these sequences can be used to detect these
XX CC repeats, especially for use in e.g. paternity or maternity testing, human
XX CC genetic analysis such as linkage analysis of genetic disease, commercial

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CC animal or plant breeding or pedigree analysis. The sequences AAT66084-  
CC T66107 represent repeat sequences of low informativeness found in  
CC specific human genes. This repeat sequence is found in the haemoglobin  
CC gamma G gene located at chromosomal position 11p15.5. The sequence is  
CC amplified by primers AAT66094-5. (Updated on 25-MAR-2003 to correct PF  
CC field.)  
XX  
SQ Sequence 19 BP; 10 A; 9 C; 0 G; 0 T; 0 U; 0 Other;  
Query Match 1.8%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 75;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1793 TGTGTGTGTGTGTGTGTGT 1811  
DB 19 TGTGTGTGTGTGTGTGTGT 1  
RESULT 144  
AAZ89471/C  
ID AAZ89471 standard; DNA; 19 BP.  
XX  
AC AAZ89471;  
XX  
DT 16-JUN-2000 (first entry)  
XX  
DE SSA primer 3 for amplifying A. thaliana and Z. mays DNA.  
XX  
KW Simple sequence repeat; SSR; single site amplification; SSA; disease;  
KW primer; ss.  
XX  
OS Arabidopsis thaliana.  
OS Zea mays.  
XX  
PN US6054300-A.  
XX  
PD 25-APR-2000.  
XX  
PF 21-AUG-1997; 97US-00915609.  
XX  
PR 21-AUG-1997; 97US-00915609.  
XX  
PA (USDA ) US SEC OF AGRIC.  
PI Mckendree WL;  
XX  
DR WPI; 2000-328353/28.  
XX  
PT Obtaining unknown DNA sequence flanking a single known sequence for use  
PT as PCR templates, involves single site amplification with polymerase  
PT having strand displacement capability.  
XX  
PS Example 1; Col 9-10; 11pp; English.  
XX  
CC This invention describes a novel method for obtaining DNA of unknown  
CC sequence flanking a single site of known sequence involves single site  
CC amplification of circular DNA template flanking a target DNA of known  
CC sequence using a polymerase having strand displacement capability. The  
CC method is used for obtaining a particular target DNA sequence that can be  
CC useful as templates that contain entire simple sequence repeat (SSR)  
CC alleles for amplification (SSA) procedures e.g. PCR or can be employed as  
CC molecular markers, e.g. in distinguishing between species, strains or  
CC varieties within species or identifying the presence of a disease  
CC condition. It also provides a marker for use in areas such as import and  
CC export regulation, variety and ecotype identification, marker  
CC development, forensic DNA fingerprinting, etc. The method can also be  
CC used to generate a linear DNA molecule containing two target sequences  
CC from one sequence within a single stranded DNA template and flanking  
CC regions for these target sequences. It can also be used for e.g. for  
CC cloning cDNA or genomic DNA which flanks any known short target sequence.  
CC The present method can also be used to obtain entire coding regions of  
CC genes based upon a known nucleic acid sequence or by using a degenerate  
CC nucleic acid sequence derived from amino acid sequence back translation

CC using a polymerase having strand displacement capability which can  
CC synthesize up to 10 kb fragments. This is especially useful for obtaining  
CC plant genes which are usually less than 10 kb in length. The method  
CC allows accelerated development of high resolution DNA markers that may be  
CC used for fingerprinting, mapping etc., using small amounts of tissue  
CC (less than 1 mug). It also allows the production of a PCR template with  
CC knowledge of only one region of target DNA sequence, the size of which is  
CC regulated only by the primer design. The present method also eliminates  
CC genomic DNA library preparation and screening which are the most time  
CC consuming steps, typically requiring no less than three months, with  
CC total time for target DNA development being between 4-6 months. AAZ89469-  
CC Z89474 represent primers used to illustrate the method of the invention  
XX  
SQ Sequence 19 BP; 9 A; 10 C; 0 G; 0 T; 0 U; 0 Other;  
Query Match 1.8%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 75;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1794 GTGTGTGTGTGTGTGTGTGT 1812  
DB 19 GTGTGTGTGTGTGTGTGTGT 1  
RESULT 145  
AAZ89472  
ID AAZ89472 standard; DNA; 19 BP.  
XX  
AC AAZ89472;  
XX  
DT 16-JUN-2000 (first entry)  
XX  
DE SSA primer 4 for amplifying A. thaliana and Z. mays DNA.  
XX  
KW Simple sequence repeat; SSR; single site amplification; SSA; disease;  
KW primer; ss.  
XX  
OS Arabidopsis thaliana.  
OS Zea mays.  
XX  
PN US6054300-A.  
XX  
PD 25-APR-2000.  
XX  
PF 21-AUG-1997; 97US-00915609.  
XX  
PR 21-AUG-1997; 97US-00915609.  
XX  
PA (USDA ) US SEC OF AGRIC.  
PI Mckendree WL;  
XX  
DR WPI; 2000-328353/28.  
XX  
PT Obtaining unknown DNA sequence flanking a single known sequence for use  
PT as PCR templates, involves single site amplification with polymerase  
PT having strand displacement capability.  
XX  
PS Example 1; Col 9-10; 11pp; English.  
XX  
CC This invention describes a novel method for obtaining DNA of unknown  
CC sequence flanking a single site of known sequence involves single site  
CC amplification of circular DNA template flanking a target DNA of known  
CC sequence using a polymerase having strand displacement capability. The  
CC method is used for obtaining a particular target DNA sequence that can be  
CC useful as templates that contain entire simple sequence repeat (SSR)  
CC alleles for amplification (SSA) procedures e.g. PCR or can be employed as  
CC molecular markers, e.g. in distinguishing between species, strains or  
CC varieties within species or identifying the presence of a disease  
CC condition. It also provides a marker for use in areas such as import and  
CC export regulation, variety and ecotype identification, marker  
CC development, forensic DNA fingerprinting, etc. The method can also be  
CC used to generate a linear DNA molecule containing two target sequences  
CC from one sequence within a single stranded DNA template and flanking  
CC regions for these target sequences. It can also be used for e.g. for  
CC cloning cDNA or genomic DNA which flanks any known short target sequence.  
CC The present method can also be used to obtain entire coding regions of  
CC genes based upon a known nucleic acid sequence or by using a degenerate  
CC nucleic acid sequence derived from amino acid sequence back translation

CC from one sequence within a single stranded DNA template and flanking  
CC regions for these target sequences. It can also be used for e.g. for  
CC cloning cDNA or genomic DNA which flanks any known short target sequence.  
CC The present method can also be used to obtain entire coding regions of  
CC genes based upon a known nucleic acid sequence or by using a degenerate  
CC nucleic acid sequence derived from amino acid sequence back translation  
CC using a polymerase having strand displacement capability which can  
CC synthesize up to 10 kb fragments. This is especially useful for obtaining  
CC plant genes which are usually less than 10 kb in length. The method  
CC allows accelerated development of high resolution DNA markers that may be  
CC used for fingerprinting, mapping etc., using small amounts of tissue  
CC (less than 1 mug). It also allows the production of a PCR template with  
CC knowledge of only one region of target DNA sequence, the size of which is  
CC regulated only by the primer design. The present method also eliminates  
CC genomic DNA library preparation and screening which are the most time  
CC consuming steps, typically requiring no less than three months, with  
CC total time for target DNA development being between 4-6 months. AA289469-  
CC 289474 represent primers used to illustrate the method of the invention  
XX  
XX  
SQ Sequence 19 BP; 0 A; 0 C; 10 G; 9 T; 0 U; 0 Other;

Query Match 1.8%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 75;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTGTG 1812  
Db 1 GTGTGTGTGTGTGTGTGTG 19

RESULT 146  
AAC66739  
ID AAC66739 standard; DNA; 19 BP.

AC AAC66739;  
DT 15-FEB-2001 (first entry)  
DE Heterologous insert sequence #2.  
KW Probe; cytostatic; antiviral; gene therapy; ss.  
OS Unidentified.

XX WO200063365-A1.  
XX 26-OCT-2000.  
XX 21-APR-2000; 2000WO-US010909.  
XX 21-APR-1999; 99US-0130345P.  
XX (PANG-) PANGENE CORP.

XX Belotserkovskii B, Reddy G, Zarling D;  
XX WPI; 2000-647516/62.  
XX

XX Composition for modulating transcription or replication of a pre-selected  
PT target sequence and for treating a plant or animal disease, comprises a  
PT recombinase and two probes, each containing a homology clamp and an  
PT anchoring sequence.

XX Disclosure; Fig 9; 103pp; English.

XX The present invention relates to a composition comprising a recombinase  
CC and two complementary single stranded probes each containing at least one  
CC homology clamp corresponding or complementary to a preselected target  
CC nucleic acid sequence and at least one anchoring sequence. The present  
CC sequence is a heterologous insert sequence used to generate the probes  
CC that can be used in the present invention. The composition of the present  
CC invention can be used to modulate transcription or replication of a pre-  
CC selected target sequence, treat a disease state of a plant or animal

CC caused by expression of a disease gene, detect a double stranded nucleic  
CC acid target sequence, isolate either strand of a double stranded target  
CC sequence, isolate either strand of a member of a gene family, produce a  
CC transgenic non-human organism or plant, determine the function of a  
CC double stranded nucleic acid target sequence and inhibit double stranded  
CC nucleic acid rotation or branch migration. In addition, the composition  
CC may be used to produce animal models for genetic defects

XX Sequence 19 BP; 0 A; 0 C; 9 G; 10 T; 0 U; 0 Other;

Query Match 1.8%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 75; 0; Gaps 0;  
Matches 19; Conservative 0; Mismatches 0; Indels 0;

QY 1793 TGTGTGTGTGTGTGTGTGT 1811  
Db 1 TGTGTGTGTGTGTGTGTGT 19

RESULT 147  
AAC66738/C  
ID AAC66738 standard; DNA; 19 BP.

AC AAC66738;  
DT 15-FEB-2001 (first entry)  
DE Heterologous insert sequence #1.  
KW Probe; cytostatic; antiviral; gene therapy; ss.

OS Unidentified.  
XX WO200063365-A1.  
XX 26-OCT-2000.  
XX 21-APR-2000; 2000WO-US010909.  
XX 21-APR-1999; 99US-0130345P.

XX (PANG-) PANGENE CORP.  
XX Belotserkovskii B, Reddy G, Zarling D;  
XX WPI; 2000-647516/62.  
XX

XX Composition for modulating transcription or replication of a pre-selected  
PT target sequence and for treating a plant or animal disease, comprises a  
PT recombinase and two probes, each containing a homology clamp and an  
PT anchoring sequence.

XX Disclosure; Fig 9; 103pp; English.

XX The present invention relates to a composition comprising a recombinase  
CC and two complementary single stranded probes each containing at least one  
CC homology clamp corresponding or complementary to a preselected target  
CC nucleic acid sequence and at least one anchoring sequence. The present  
CC sequence is a heterologous insert sequence used to generate the probes  
CC that can be used in the present invention. The composition of the present  
CC invention can be used to modulate transcription or replication of a pre-  
CC selected target sequence, treat a disease state of a plant or animal  
CC caused by expression of a disease gene, detect a double stranded nucleic  
CC acid target sequence, isolate either strand of a double stranded target  
CC sequence, isolate either strand of a member of a gene family, produce a  
CC transgenic non-human organism or plant, determine the function of a  
CC double stranded nucleic acid target sequence and inhibit double stranded  
CC nucleic acid rotation or branch migration. In addition, the composition  
CC may be used to produce animal models for genetic defects

XX Sequence 19 BP; 10 A; 9 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.8%; Score 19; DB 1; Length 19;

Best Local Similarity 100.0%; Pred. No. 75;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGT 1811  
Db 19 TGTGTGTGTGTGTGTGTGT 1

RESULT 148  
ADD69517  
ID ADD69517 standard; DNA; 19 BP.  
XX  
XX AC ADD69517;  
XX DT 15-JAN-2004 (first entry)  
XX DE ISSR-related PCR primer 4.  
XX inter-simple sequence repeat; ISSR; SSR; PCR; primer; genotyping; plant;  
KW animal; Basmati rice; ss.  
XX Unidentified.  
XX WO2003085133-A2.  
PN 16-OCT-2003.  
PD  
XX  
XX 09-JAN-2003; 2003WO-IB000041.  
XX  
XX 08-APR-2002; 2002IN-CH000260.  
PR  
XX (DNAP-) CENT DNA FINGERPRINTING & DIAGNOSTICS.  
XX  
XX Nagaraaju JG;  
XX WPI; 2003-804317/75.  
XX  
XX New set of inter-simple sequence repeats (ISSR)-PCR primers for  
PT genotyping eukaryotes, useful for genotyping diverse genomes of plant and  
PT animal systems.  
XX  
XX Disclosure; Page 19; 60pp; English.  
XX  
XX The invention relates to a novel set of inter-simple sequence repeats  
CC (ISSR)-PCR primers for genotyping eukaryotes. The primers of the  
CC invention may be useful for genotyping diverse genomes of plant and  
CC animal systems, in particular for distinguishing Basmati rice varieties  
CC from non-Basmati rice varieties and traditional Basmati rice varieties  
CC from evolved Basmati rice varieties. The current sequence is that of the  
CC ISSR-related PCR primer of the invention.  
XX  
XX Sequence 19 BP; 0 A; 0 C; 9 G; 10 T; 0 U; 0 Other;

Query Match 1.8%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 75;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGT 1811  
Db 1 TGTGTGTGTGTGTGTGTGT 19

RESULT 149  
AAF85976  
ID AAF85976 standard; DNA; 21 BP.  
XX  
XX AC AAF85976;  
XX DT 20-JUN-2001 (first entry)  
XX DE CA repeat fluorogenic probe.  
XX Probe; Fluorescein; tetramethyl rhodamine; copy number; ss.

XX Synthetic.  
OS  
XX Key modified\_base Location/Qualifiers  
PH 1  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "5' end attached to 6-carboxy fluorescein"  
FT 21.  
FT /\*tag= b  
FT /mod\_base= OTHER  
FT /note= "3' end attached to TAMRA"  
XX  
XX US6180349-B1.  
XX 30-JAN-2001.  
XX 18-MAY-1999; 99US-00314246.  
XX 18-MAY-1999; 99US-00314246.  
XX (REGC ) UNIV CALIFORNIA.  
XX Ginzinger DG, Godfrey TE, Jensen RH, Gray JW;  
XX WPI; 2001-225787/23.  
XX Measuring copy number of a polynucleotide locus in sample useful as  
PT diagnostic and prognostic tool, comprises quantifying amount of test  
PT locus and reference loci in test and control subject.  
XX  
XX Claim 25; Col 33; 27pp; English.  
XX  
XX The present invention relates to measuring the copy number of a locus by  
CC amplifying and comparing test and reference loci. The invention is useful  
CC as diagnostic and prognostic tools and in correlating abnormal copy  
CC number values for specific loci with disease and effectiveness of  
CC different treatment options. The present sequence is a CA repeat  
CC fluorogenic probe used in the invention  
XX  
XX Sequence 21 BP; 0 A; 0 C; 10 G; 9 T; 0 U; 2 Other;

Query Match 1.8%; Score 19; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 81;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTGTGT 1812  
Db 2 GTGTGTGTGTGTGTGTGTGT 20

RESULT 150  
ABL44374  
ID ABL44374 standard; DNA; 21 BP.  
XX  
XX AC ABL44374;  
XX DT 11-APR-2002 (first entry)  
XX  
XX Human chromosome 1p36-35 PCR primer SEQ ID NO:1418.  
XX Human; chromosome 1p36-35; chromosome 21q22.1; genetic analysis; genome;  
XX PCR primer; ss.  
XX Homo sapiens.  
XX JP2001321190-A.  
XX 20-NOV-2001.  
XX 12-MAR-2001; 2001JP-00068285.  
XX 10-MAR-2000; 2000JP-00066716.  
PR



disorder-related traits.

Example 16; Page 131; 714pp; English.

This invention relates to the sequence of an isolated nucleic acid molecule comprising at least one base variation from that of a known human cytochrome P450 A1 (CYP450A1), cytochrome P450 A2 (CYP450A2), cytochrome P450 2E1 (CYP4502E1), adrenergic receptor beta1 (ADRB1), aryl hydrocarbon (AHR), aryl hydrocarbon receptor nuclear translocator (ARNT), catepsin S (CTSS), cyclooxygenase 2 (COX2), diazepam binding inhibitor (DBI), epoxide hydrolase 2 (EPHX2), 5-lipoxygenase activating protein (FLAP), glutathione-S-transferase 12 (GST12), histamine-N-methyl transferase (HNMT), kallikrein 2 (KLK2), nicotinamide-N-methyl transferase (NNMT), NADPH quinone oxidoreductase 2 (NQO2), sulfoxtransferase thermolabile (STM), UDP-glucuronosyl transferase 2B4 (UGT2B4), UDP-glucuronosyl transferase 2B7 (UGT2B7), UDP-glucuronosyl transferase (UGT2B5), uronidase receptor (UPA), multidrug resistance 1 (MDR1), lactotransferrin (LTF), multidrug resistance associated protein 3 (MRP3), orphan nuclear receptor (NR112), or acetylcholine muscarinic receptor 1, 2, 3, 4, or 5 (CHMR1, CHMR2, CHMR3, CHMR4 or CHMR5) sequence. The polymorphisms in the human genes cited in the invention are useful as genetic linkage markers for locating and characterising the genes that are responsible for specific traits within the genome and eventually are responsible for a variety of disorder-related traits as a result of their e.g., overexpression, constitutive expression, mutation or underexpression, which may be used in diagnosing and/or treating the disorders. The nucleic acid molecules comprising the polymorphic sequences contained in CYP450A1, CYP450A2, CYP4502E1, ARNT, EPHX2, GST12, NNMT, NQO2, NR112, STM, UGT2B4, UGT2B7, UGT2B15, AHR, MDR1 and/or MDR3 are useful for screening individuals for altered drug metabolism. The polymorphic sequences contained in CYP450A1, CYP450A2, AHR, MDR1 and/or MDR3 may also be used to screen individuals for susceptibility to cancer. Polymorphic sequences in ADRB1 or CHMR2 are used to screen for altered cardiovascular function, in COX2 for altered susceptibility to colorectal tumours, in DBI or CHMR1 for altered central nervous system function, in FLAP and HNMT for altered pulmonary, immunological or haematological function, in KLK2 for altered serine protease activity in the prostate, in LTF for altered immunological or haematological function, in CHMR3, CHMR4 or CHMR5 for altered central and peripheral nervous system function. The present sequence represents a polymorphic DNA sequence of the invention.

Sequence 20 BP; 10 A; 9 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 1.8%; Score 18.4; DB 1; Length 20;  
Best Local Similarity 95.0%; Pred. No. 92;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTGTGT 1813  
DB 20 GTATGTGTGTGTGTGTGTGT 1

RESULT 153  
ADB25760/c  
ID ADB25760 standard; DNA; 20 BP.

AC ADB25760;

XX 20-NOV-2003 (first entry)

XX Mouse connective tissue growth factor antisense oligo DNA (seqid 153).

XX antisense; mouse; murine; ss; connective tissue growth factor; CTGF;  
KW chromosome 6q23.1; ctgofact; fibroblast inducible secreted protein;  
KW fisp-12; NOV2;  
KW insulin-like growth factor binding protein-related protein 2; IGFBP-rp2;  
KW IGFBP-8; Hcs24; ecogenin; acute lymphoblastic leukaemia; gene therapy;  
KW hyperproliferative disorder; cancer; pulmonary fibrosis; renal fibrosis;  
KW scleroderma; atherosclerosis; cytostatic; dermatological;  
KW antiarteriosclerotic.

XX Mus sp.

XX FH Key Location/Qualifiers  
XX modified\_base 1..20  
XX FT /\*tag= a  
XX FT /mod\_base= OTHER  
XX FT /note= "OTHER= phosphorothioate backbone, where 1-5 and  
XX FT 16-20 are 2' methoxyethyl nucleotides. All cytidines are  
XX FT 5-methylcytidines"  
XX WO2003053340-A2.  
XX 03-JUL-2003.  
XX 09-DEC-2002; 2002WO-US038618.  
XX 10-DEC-2001; 2001US-00006191.  
XX (ISIS-) ISIS PHARM INC.  
XX Gaarde WA, Watt AT;  
XX WPI; 2003-559091/52.  
XX New antisense oligonucleotides for modulating connective tissue growth  
XX factor expression, particularly useful for treating cancers (e.g. breast  
XX or prostate cancer), pulmonary or renal fibrosis, scleroderma or  
XX atherosclerosis.  
XX Claim 3; Page 89; 139pp; English.  
XX This invention relates to novel methods for modulating the expression of  
XX connective tissue growth factor (CTGF) by antisense oligonucleotides.  
XX CTGF has been mapped to human chromosome region 6q23.1, and is also known  
XX as ctgofact, fibroblast inducible secreted protein, fisp-12, NOV2,  
XX insulin-like growth factor binding protein-related protein 2, IGFBP-rp2,  
XX IGFBP-8, Hcs24 and ecogenin. It is known to stimulate DNA synthesis and  
XX promote chemotaxis of fibroblasts, however, it is also upregulated in  
XX acute lymphoblastic leukaemia and in tumour or endothelial cells  
XX associated with the vasculature. Accordingly, antisense oligonucleotides  
XX that inhibit the expression of CTGF in cells or tissues can be used in  
XX gene therapy to treat various conditions including hyperproliferative  
XX disorders (particularly cancer, e.g. breast, prostate or renal cancer),  
XX pulmonary fibrosis, renal fibrosis, scleroderma and atherosclerosis. As  
XX such, the present invention describes these antisense oligos as having  
XX cytostatic, dermatological and antiarteriosclerotic activities. This  
XX oligonucleotide sequence is a chimeric phosphorothioate antisense oligo  
XX with 2' MOE wings and a deoxy gap, which is used to inhibit expression of  
XX mouse CTGF of the invention.  
XX Sequence 20 BP; 7 A; 3 C; 0 G; 10 T; 0 U; 0 Other;  
XX Query Match 1.8%; Score 18.4; DB 1; Length 20;  
XX Best Local Similarity 95.0%; Pred. No. 92;  
XX Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2247 TAGTTGAATTAAGTGTAT 2266  
DB 20 TAGTTGAATTAAGTGTAT 1  
RESULT 154  
AAQ34125  
ID AAQ34125 standard; DNA; 18 BP.  
XX AC AAQ34125;  
XX AC AAQ34125;  
XX 25-MAR-2003 (revised)  
DT 02-FEB-1993 (first entry)  
XX Sequence of a microsatellite from clone TGLA69.  
XX PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;  
XX Genetic mapping; traits; amplification; ss.

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XX OS Bos taurus.
XX PN WO9213102-A1.
XX PD 06-AUG-1992.
XX PF 15-JAN-1992; 92WO-US000340.
XX PR 15-JAN-1991; 91US-00642342.
XX PA (GENM-) GENMARK.
XX PI Georges M, Massey JM;
XX DR WPI; 1992-284684/34.
XX PT Polymorphic bovine DNA markers - used in genetic identification, gene
XX mapping, and selective breeding.
XX PS Table 7; Page 381; 517pp; English.
XX CC The sequence is that of a bovine microsatellite sequence obt'd. by
XX screening a library of bovine MboI DNA fragments of between 250 and 500
XX bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
XX clones cross-hybridised. Assuming independent distribution of
XX microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites
XX in the bovine genome is estimated at >100,000. The sequence information
XX for ca. 230 such bovine microsatellites is summarised in the
XX specification and indexed herein (see below). The sequences upstream and
XX downstream of the microsatellite sequence were used to generate the
XX required PCR primers for in vitro amplification of the corresp.
XX microsatellite (using the program Optiprim). The microsatellites may be
XX used to identify individuals, for parentage testing, and in the genetic
XX mapping of economic trait loci, or genes involved in the determination of
XX economically important traits esp. in cattle, to allow selective
XX breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
XX field.)
XX SQ Sequence 18 BP; 0 A; 0 C; 9 G; 9 T; 0 U; 0 Other;

Query Match 1.7%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTG 1810
DB 1 TGTGTGTGTGTGTGTGTG 18

RESULT 155
AAQ33722
ID AAQ33722 standard; DNA; 18 BP.
XX AC AAQ33722;
XX OS Bos taurus.
XX PN WO9213102-A1.
XX DT 02-FEB-1993 (first entry)
XX DE Microsatellite sequence from clone TGLA141.
XX KW PCR; selection; primers; Optiprim; breeding; cattle; parentage;
XX genetic mapping; traits; amplification; ss.
XX OS Bos taurus.
XX PN WO9213102-A1.
XX PD 06-AUG-1992.
XX PF 15-JAN-1992; 92WO-US000340.
XX PR 15-JAN-1991; 91US-00642342.
XX PA (GENM-) GENMARK.
XX PI Georges M, Massey JM;
XX DR WPI; 1992-284684/34.
XX PT Polymorphic bovine DNA markers - used in genetic identification, gene
XX mapping, and selective breeding.
XX PR 15-JAN-1991; 91US-00642342.

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XX PA (GENM-) GENMARK.
XX PI Georges M, Massey JM;
XX DR WPI; 1992-284684/34.
XX PT Polymorphic bovine DNA markers - used in genetic identification, gene
XX mapping, and selective breeding.
XX PS Table 7; Page 219; 517pp; English.
XX CC The sequence is that of a bovine microsatellite sequence obt'd. by
XX screening a library of bovine MboI DNA fragments of between 250 and 500
XX bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
XX clones cross-hybridised. Assuming independent distribution of
XX microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites
XX in the bovine genome is estimated at >100,000. The sequence information
XX for ca. 230 such bovine microsatellites is summarised in the
XX specification and indexed herein (see below). The sequences upstream and
XX downstream of the microsatellite sequence were used to generate the
XX required PCR primers for in vitro amplification of the corresp.
XX microsatellite (using the program Optiprim). The microsatellites may be
XX used to identify individuals, for parentage testing, and in the genetic
XX mapping of economic trait loci, or genes involved in the determination of
XX economically important traits esp. in cattle, to allow selective
XX breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
XX field.)
XX SQ Sequence 18 BP; 0 A; 0 C; 9 G; 9 T; 0 U; 0 Other;

Query Match 1.7%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTGT 1811
DB 1 GTGTGTGTGTGTGTGTGT 18

RESULT 156
AAQ33950
ID AAQ33950 standard; DNA; 18 BP.
XX AC AAQ33950;
XX DT 25-MAR-2003 (revised)
XX DT 02-FEB-1993 (first entry)
XX DE Microsatellite sequence from clone TGLA346.
XX KW PCR; selection; primers; Optiprim; breeding; cattle; parentage;
XX genetic mapping; traits; amplification; ss.
XX OS Bos taurus.
XX PN WO9213102-A1.
XX PD 06-AUG-1992.
XX PF 15-JAN-1992; 92WO-US000340.
XX PR 15-JAN-1991; 91US-00642342.
XX PA (GENM-) GENMARK.
XX PI Georges M, Massey JM;
XX DR WPI; 1992-284684/34.
XX PT Polymorphic bovine DNA markers - used in genetic identification, gene
XX mapping, and selective breeding.
XX PR 15-JAN-1991; 91US-00642342.

```

PS Table 7; Page 310; 517pp; English.

XX The sequence is that of a bovine microsatellite sequence obtd. by  
CC screening a library of bovine MboI DNA fragments of between 250 and 500  
CC bp with an (AC)<sub>15</sub> and a (TC)<sub>15</sub> oligonucleotide probe. One out of 50  
CC clones cross-hybridised. Assuming independent distribution of  
CC microsatellites and MboI sites, the frequency of (TC)<sub>n</sub> > 9 microsatellites  
CC in the bovine genome is estimated at >100, 000. The sequence information  
CC for ca. 230 such bovine microsatellites is summarised in the  
CC specification and indexed herein (see below). The sequences upstream and  
CC downstream of the microsatellite sequence were used to generate the  
CC required PCR primers for in vitro amplification of the corresp.  
CC microsatellite (using the program OPTIPRIM). The microsatellites may be  
CC used to identify individuals, for parentage testing, and in the genetic  
CC mapping of economic trait loci, or genes involved in the determination of  
CC economically important traits esp. in cattle, to allow selective  
CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN  
CC field.)

XX SQ Sequence 18 BP; 0 A; 0 C; 9 G; 9 T; 0 U; 0 Other;  
Query Match 1.7%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 94;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTGTGTGTG 1810  
Db 1 TGTGTGTGTGTGTGTG 18

RESULT 157

AAQ33997

ID AAQ33997 standard; DNA; 18 BP.

XX AC AAQ33997;

XX DT 25-MAR-2003 (revised)

XX DT 02-FEB-1993 (first entry)

XX DE Microsatellite sequence from clone TGLA4.

XX PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;  
KW genetic mapping; traits; amplification; ss.  
XX Bos taurus.

XX OS

XX PN WO9211102-A1.

XX PD 06-AUG-1992.

XX PF 15-JAN-1992; 92WO-US000340.

XX PR 15-JAN-1991; 91US-00642342.

XX PA (GENM-) GENMARK.

XX PI Georges M, Massey JM;

XX DR WPI; 1992-284684/34.

XX Polymorphic bovine DNA markers - used in genetic identification, gene  
FT mapping, and selective breeding.  
XX Table 7; Page 329; 517pp; English.

XX The sequence is that of a bovine microsatellite sequence obtd. by  
CC screening a library of bovine MboI DNA fragments of between 250 and 500  
CC bp with an (AC)<sub>15</sub> and a (TC)<sub>15</sub> oligonucleotide probe. One out of 50  
CC clones cross-hybridised. Assuming independent distribution of  
CC microsatellites and MboI sites, the frequency of (TC)<sub>n</sub> > 9 microsatellites  
CC in the bovine genome is estimated at >100, 000. The sequence information  
CC for ca. 230 such bovine microsatellites is summarised in the  
CC specification and indexed herein (see below). The sequences upstream and

CC downstream of the microsatellite sequence were used to generate the  
CC required PCR primers for in vitro amplification of the corresp.  
CC microsatellite (using the program OPTIPRIM). The microsatellites may be  
CC used to identify individuals, for parentage testing, and in the genetic  
CC mapping of economic trait loci, or genes involved in the determination of  
CC economically important traits esp. in cattle, to allow selective  
CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN  
CC field.)

XX SQ Sequence 18 BP; 0 A; 0 C; 9 G; 9 T; 0 U; 0 Other;

Query Match 1.7%; Score 18; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 94;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1794 GTGTGTGTGTGTGTGTGT 1811

Db 1 GTGTGTGTGTGTGTGTGT 18

RESULT 158

AAQ46589

ID AAQ46589 standard; DNA; 18 BP.

XX AC AAQ46589;

XX DT 25-MAR-2003 (revised)

XX DT 10-MAR-2003 (revised)

XX DT 23-DEC-1993 (first entry)

XX DE Simple sequence repeat (GT)<sub>9</sub>.

XX KW Microsatellite; simple sequence repeat; SSR; polymorphism; variation;

XX KW Genetic marker; human genome; mapping; ligation reaction; ss.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT repeat\_region 1..18

FT /tag= a

FT /note= "SSR"

FT repeat\_unit 1..2

FT /tag= b

FT /rpt\_type= TANDEM

XX EP552545-A1.

XX PD 28-JUL-1993.

XX PF 09-DEC-1992; 92EP-00311242.

XX PR 17-JAN-1992; 92US-00826930.

XX PA (PION-) PIONEER HI-BRED INT INC.

XX PI Grant D;

XX DR WPI; 1993-236281/30.

XX Detecting genetic variation between organisms - by detecting  
FT polymorphisms in simple sequence repeats in DNA of organisms.  
XX Disclosure; Page 5; 8pp; English.

XX A (CA)<sub>9</sub> simple sequence repeat is used to illustrate the novel method for  
CC detecting SSR polymorphisms without the need for direct sequencing or gel  
CC electrophoresis. The length of a particular repeat region (i.e. number of  
CC repeats) can be highly polymorphic; the sequences flanking the repeat  
CC region, however, are conserved. Detection of a SSR of a specific length  
CC is achieved by successful ligation of two oligonucleotides, one being  
CC exactly complementary to the repeat region and one of its conserved  
CC flanking sequences (i.e. comprising the sequence (GT)<sub>9</sub>) and the other  
CC being complementary to the other conserved flanking sequence. (Updated on



CC 10-MAR-2003 to add missing OS field.) (Updated on 25-MAR-2003 to correct  
CC FN field.)  
XX Sequence 18 BP; 0 A; 0 C; 9 G; 9 T; 0 U; 0 Other;  
SQ Query Match 1.7%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 94;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1794 GTGTGTGTGTGTGTGTGT 1811  
DB 1 GTGTGTGTGTGTGTGTGT 18  
RESULT 159  
AAQ46588/C  
ID AAQ46588 standard; DNA; 18 BP.  
XX AC AAQ46588;  
XX 25-MAR-2003 (revised)  
DT 10-MAR-2003 (revised)  
DT 23-DEC-1993 (first entry)  
XX 23-DEC-1993 (first entry)  
DE Simple sequence repeat (CA)9.  
XX Microsatellite; simple sequence repeat; SSR; polymorphism; variation;  
KW genetic marker; human genome; mapping; ligation reaction; ss.  
XX Synthetic.  
XX Key Location/Qualifiers  
FT repeat\_region 1..18  
FT /\*tag= a  
FT /\*note= "SSR"  
FT repeat\_unit 1..2  
FT /\*tag= b  
FT /\*rpt\_type= TANDEM  
XX EP552545-A1.  
XX EP552545-A1.  
XX 28-JUL-1993.  
XX 09-DEC-1992; 92EP-00311242.  
XX 17-JAN-1992; 92US-00826930.  
XX (PION-) PIONEER HI-BRED INT INC.  
XX Grant D;  
XX WPI; 1993-236281/30.  
XX Detecting genetic variation between organisms - by detecting  
PT polymorphisms in simple sequence repeats in DNA of organisms.  
PS Disclosure; Page 5; 8pp; English.  
XX This (CA)9 simple sequence repeat is used to illustrate the novel method  
CC for detecting SSR polymorphisms without the need for direct sequencing or  
CC gel electrophoresis. The length of a particular repeat region (i.e.  
CC number of repeats) can be highly polymorphic; the sequences flanking the  
CC repeat region, however, are conserved. Detection of a SSR of a specific  
CC length is achieved by successful ligation of two oligonucleotides, one  
CC being exactly complementary to the repeat region and one of its conserved  
CC flanking sequences and the other being complementary to the other  
CC conserved flanking sequence. (Updated on 10-MAR-2003 to add missing OS  
CC field.) (Updated on 25-MAR-2003 to correct PN field.)  
XX Sequence 18 BP; 9 A; 9 C; 0 G; 0 T; 0 U; 0 Other;  
SQ Query Match 1.7%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 94;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1793 TGTGTGTGTGTGTGTGTGT 1810  
DB 18 TGTGTGTGTGTGTGTGTGT 1  
RESULT 160  
AAV21968/C  
ID AAV21968 standard; DNA; 18 BP.  
XX AC AAV21968;  
XX 14-JUL-1998 (first entry)  
DT Nuclease resistant antisense oligo NBT 141 targeted against (AC)9.  
DE Nuclease resistant; bacterial infection; antibiotic; target;  
XX Nuclease resistant; bacterial infection; antibiotic; target;  
KW veterinary medicine; treatment; human; industrial process;  
KW bacterial control; ss.  
XX Synthetic.  
XX WO9803533-A1.  
XX 29-JAN-1998.  
XX 23-JUL-1997; 97WO-US012961.  
XX 24-JUL-1996; 96US-00685575.  
XX (OLIG-) OLIGOS ETC & OLIGOS THERAPEUTICS INC.  
XX Arrow A, Dale RMK, Thompson TL;  
DR WPI; 1998-120687/11.  
XX Treating bacterial infections in humans or animals with  
PT oligo:nucleotide(s) - resistant to nuclease and targetted to bacterial  
PT nucleic acid or proteins, also conjugates of these oligo:nucleotide(s)  
PT with antibiotics.  
PS Claim 49; Page 87; 163pp; English.  
XX This antisense oligonucleotide is nuclease resistant and can be used in  
CC the treatment of animals, including humans, having a bacterial infection.  
CC The treatment comprises administration of such nuclease resistant  
CC oligonucleotides, targeted to a nucleic acid or protein of the bacterium,  
CC and formulated with a carrier. A compound comprising this nuclease  
CC resistant oligonucleotide can be covalently linked to an antibiotic. The  
CC method is used to treat infections by a wide variety of Gram-positive and  
CC Gram-negative, or acid-fast, bacteria, in human and veterinary medicine.  
CC The methods are particularly used in immuno-compromised individuals (e.g.  
CC patients with acquired immunodeficiency syndrome or those receiving  
CC chemotherapy or radiation therapy), optionally in combination with, or  
CC fused to, antiviral or other antimicrobial oligonucleotides. Apart from  
CC laboratory cultures, foods, beverages and industrial processes. The  
CC oligonucleotides are specific for bacteria, without affecting metabolism  
CC in mammalian cells. They may also activate RNase H and have a general,  
CC non-specific immune-stimulating effect. The oligonucleotides can be  
CC administered orally, intranasally, rectally, topically or by injection,  
CC optionally coupled to an agent (e.g. carbohydrate or polyamine) that  
CC enhances cellular uptake  
XX Sequence 18 BP; 9 A; 9 C; 0 G; 0 T; 0 U; 0 Other;  
SQ Query Match 1.7%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 94;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1794 GTGTGTGTGTGTGTGTGT 1811

DB	18	GTGTGTGTGTGTGTGT	1
AC	XX	05-AUG-1999	(first entry)
DE	XX	US5912147	primer 5.
XX	XX	Primer; quantitation; genetic instability; tumour cell; detection;	
XX	XX	neoplastic transformation; carcinogenesis; DNA/RNA hybrid; ss.	
XX	XX	Synthetic.	
XX	XX	Key	Location/Qualifiers
XX	XX	misc RNA	18
XX	XX	/*tag= a	
XX	XX	/note= "uracil"	
XX	XX	US5912147-A.	
XX	XX	15-JUN-1999.	
XX	XX	22-OCT-1996;	96US-00734973.
XX	XX	22-OCT-1996;	96US-00734973.
XX	XX	(HEAL-) HEALTH RES INC.	
XX	XX	Anderson G, Stoler D, Basik M;	
XX	XX	WPI; 1999-357197/30.	
XX	XX	Quantitating genetic instability.	
XX	XX	Claim 4; Col 17-18; 27pp; English.	
XX	XX	This invention describes a novel method for quantitating genetic	
XX	XX	instability independent of microsatellite alterations by treating a	
XX	XX	comparison pair comprising genomic DNA from tumour cells and genomic DNA	
XX	XX	from normal cells. The method involves the cells from the same individual	
XX	XX	with oligonucleotide primers selected from (i) a nucleotide sequence	
XX	XX	(CG)XRG, where R is a purine selected from adenine and guanine and x = 3-	
XX	XX	7, (ii) a nucleotide sequence (CG)XRY, where R is as in (i) and Y is a	
XX	XX	pyrimidine selected from cytosine, thymine, and uracil and x = 3-7, (iii)	
XX	XX	a nucleotide sequence (CG)XRR, where R is as in (i) and x = 3-7, (iv) a	
XX	XX	nucleotide sequence (CG)XYY, where Y is a pyrimidine selected from	
XX	XX	cytosine, thymine, and uracil and x = 3-7, (v) a nucleotide sequence	
XX	XX	(CA)XRG, where R is a purine selected from adenine and guanine and x = 6-	
XX	XX	16, (vi) a nucleotide sequence (CA)XRY, where R is a purine selected from	
XX	XX	adenine and guanine and Y is a pyrimidine selected from cytosine,	
XX	XX	thymine, and uracil, and x = 6-16, (vii) a nucleotide sequence (CA)XRR,	
XX	XX	where R is a purine selected from adenine and guanine and x = 6-16,	
XX	XX	(viii) a nucleotide sequence (CA)XYY, where Y is a pyrimidine selected	
XX	XX	from cytosine, thymine, and uracil and x = 6-16, and (ix) a combination	
XX	XX	of the primers. The method is useful for detecting genomic instability	
XX	XX	of the primers. The method is useful for detecting genomic instability	
XX	XX	which are commonly associated with the various stages of neoplastic	
XX	XX	transformation and carcinogenesis. The method is rapid and simple	
XX	XX	Sequence 18 BP; 9 A; 8 C; 0 G; 1 T; 0 U; 0 Other;	
XX	XX	Query Match	1.7%; Score 18; DB 1; Length 18;
XX	XX	Best Local Similarity	100.0%; Pred. NO. 94;
XX	XX	Matches 18; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
XX	XX	1791 ATTGTGTGTGTGTGTGTG 1808	
XX	XX	18 ATTGTGTGTGTGTGTGTG 1	
XX	XX	RESULT 163	
XX	XX	AAAX77461/c	
XX	XX	ID	AAAX77461 standard; DNA; 18 BP.
XX	XX	AC	AAAX77461/c
XX	XX	XX	AAAX77461/c

DT 05-AUG-1999 (first entry)  
 DE Sequencing reagent array oligonucleotide primer #28.  
 XX  
 KW Sequencing reagent array; primer; capture moiety; hybridisation;  
 KW detection; mutation; diagnosis; infectious disease; genetic disease; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9927137-A1.  
 XX  
 PD 03-JUN-1999.  
 XX  
 XX 20-NOV-1998; 98WO-US024966.  
 PF  
 XX 21-NOV-1997; 97US-00976427.  
 PR  
 XX (ORCH-) ORCHID BIOCOMPUTER INC.  
 PA  
 XX Head SR, Golet P, Karn J, Boyce-Jacino M;  
 PI WPI; 1999-357855/30.  
 XX  
 DR Reagent for nucleic acid sequencing by primer extension, used to detect  
 PT mutations and to diagnose infectious or genetic diseases.  
 PT  
 XX Example 7; Page 27; 47pp; English.  
 PS  
 CC The present invention describes a sequencing reagent (I) comprising: (a)  
 CC a capture group (CG) that can form a stable complex with a region of a  
 CC template nucleic acid (II); (b) spacer region (SR); and (c) sequence-  
 CC specific hybridisation region (SSHR) of 4-8 bases able to hybridise to a  
 CC complementary sequence on (II). Also described are: (I) array comprising  
 CC an orderly arrangement of many (I), immobilized on a solid support; and  
 CC (2) method of sequencing (II) using a combinatorial array of (I). Arrays  
 CC of (I) are used for sequencing nucleic acids by a primer extension  
 CC method, e.g. to scan for mutations (particularly a single-nucleotide  
 CC polymorphisms) and for diagnosis of infectious and genetic diseases.  
 CC Arrays of (I) allow sequencing of templates without any prior knowledge  
 CC of the wild-type or expected sequence. By separating the capture and  
 CC specific hybridisation functions, it becomes possible to use smaller  
 CC primers, simplifying array analysis, reducing costs and allowing  
 CC thousands of hybridisation reactions to be done simultaneously.  
 CC Particularly, 4 times fewer primers are required, compared with standard  
 CC methods, i.e. since primer extension increases the effective length of  
 CC the primer by 1 base, an array of n-mers will be as effective as an array  
 CC of n+1-mers in usual methods. The method will be applied to single- or  
 CC double-stranded DNA. AAX76410 to AAX76440 represent sequencing reagent  
 CC array oligonucleotide primers used in an example from the present  
 CC invention  
 XX  
 SQ Sequence 18 BP; 0 A; 0 C; 9 G; 9 T; 0 U; 0 Other;  
 Query Match 1.7%; Score 18; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 94;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1793 TGTGTGTGTGTGTGTGTG 1810  
 DB 1 TGTGTGTGTGTGTGTGTG 18  
 RESULT 164  
 AAS13765  
 ID AAS13765 standard; DNA; 18 BP.  
 XX  
 AC AAS13765;  
 XX  
 XX 08-MAY-2002 (first entry)  
 DT  
 XX Simple sequence repeat, SSR, #37.  
 DE  
 XX Simple sequence repeat; plant; ds; SSR; ryegrass; fescue; tandem repeat;  
 KW Simple sequence repeat; plant; ds; SSR; ryegrass; fescue; tandem repeat;  
 KW cereal profiling; grass profiling; seed batch purity testing.

KW cereal profiling; grass profiling; seed batch purity testing.  
 XX Lolium multiflorum.  
 OS  
 XX NZ509193-A.  
 PN  
 XX 25-MAY-2001.  
 PD  
 XX 03-JAN-2001; 2001NZ-00509193.  
 PF  
 XX 24-DEC-1999; 99AU-00004906.  
 PR  
 XX 04-MAY-2000; 2000AU-00007310.  
 PR  
 XX (SAUS-) STATE SOUTH AUSTRALIA SOUTH AUSTRALIAN R.  
 PA (UYSC-) UNIV SOUTHERN CROSS.  
 PA (VICT-) STATE VICTORIA DEPT NATURAL RES & ENVIRO.  
 PA (UYAD-) UNIV ADELAIDE.  
 PA (ITMA-) INT MAIZE & WHEAT IMPROVEMENT CENT.  
 XX  
 XX Forster JW, Jones ES;  
 PI WPI; 2001-512563/56.  
 XX  
 DR New simple sequence repeats having 2 or more tandemly repeated nucleotide  
 PT core elements isolated from ryegrass and fescue, useful for selecting of  
 PT genes in grass or cereal breeding or profiling grass or cereal species  
 PT varieties.  
 XX  
 PS Example 1; Fig 6; 72pp; English.  
 CC The invention relates to a substantially purified or isolated nucleic  
 CC acid (I) from ryegrass or fescue species including a simple sequence  
 CC repeat (SSR), having 2 or more tandemly repeated nucleotide core elements  
 CC 2-6 nucleotides in length. Also included are a nucleic acid primer  
 CC suitable for amplifying an SSR, identifying (M1) an SSR by preparing a  
 CC library of ryegrass or fescue genomic DNA enriched for SSRs and  
 CC identifying clones in the library containing SSRs, a library of ryegrass  
 CC or fescue genomic DNA enriched for SSRs prepared by the M1, selecting for  
 CC a gene in grass or cereal breeding by identifying an SSR that is closely  
 CC associated with the gene such that the SSR and the gene are  
 CC preferentially co-inherited, and selecting for the SSR in the breeding, a  
 CC method for DNA profiling grass or cereal species varieties by assessing  
 CC variation between SSR varieties and testing the purity of grass or cereal  
 CC seed batches by assessing variation within seed batch of an SSR. The SSRs  
 CC may be used in the selection of genes in grass or cereal breeding, for  
 CC profiling grass or cereal species varieties, for testing the purity of  
 CC grass or cereal seed batches, and for DNA profiling to establish the  
 CC distinct identity, uniformity and/or stability of a cultivar. The present  
 CC sequence is a ryegrass or fescue SSR  
 XX  
 SQ Sequence 18 BP; 0 A; 0 C; 9 G; 9 T; 0 U; 0 Other;  
 Query Match 1.7%; Score 18; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 94;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1794 GTGTGTGTGTGTGTGTGT 1811  
 DB 1 GTGTGTGTGTGTGTGTGT 18  
 RESULT 165  
 AAS13732/c  
 ID AAS13732 standard; DNA; 18 BP.  
 XX  
 AC AAS13732;  
 XX  
 XX 08-MAY-2002 (first entry)  
 DT  
 XX Simple sequence repeat, SSR, #29.  
 DE  
 XX Simple sequence repeat; plant; ds; SSR; ryegrass; fescue; tandem repeat;  
 KW Simple sequence repeat; plant; ds; SSR; ryegrass; fescue; tandem repeat;  
 KW cereal profiling; grass profiling; seed batch purity testing.

OS	Poeae.
XX	
PN	NZ509193-A..
XX	
PD	25-MAY-2001.
XX	
XX	03-JAN-2001; 2001NZ-00509193.
PF	
XX	
XX	24-DEC-1999; 99AU-00004906.
PR	
XX	04-MAY-2000; 2000AU-00007310.
XX	
PA	(SAUS-) STATE SOUTH AUSTRALIA SOUTH AUSTRALIAN R.
XX	
PA	(OISC-) UNIV SOUTHERN CROSS.
XX	
PA	(VIC-) STATE VICTORIA DEPT NATURAL RES & ENVIRO.
XX	
PA	(UYAD-) UNIV ADELAIDE.
XX	
PA	(ITWA-) INT MAIZE & WHEAT IMPROVEMENT CENT.
XX	
PI	Forster JW, Jones BS;
XX	
DR	WPI; 2001-512563/56.
XX	
XX	New simple sequence repeats having 2 or more tandemly repeated nucleotide
PT	core elements isolated from ryegrass and fescue, useful for selecting of
PT	genes in grass or cereal breeding or profiling grass or cereal species
PT	varieties.
PS	
XX	Claim 6; Page 51; 72pp; English.
CC	The invention relates to a substantially purified or isolated nucleic
CC	acid (I) from ryegrass or fescue species including a simple sequence
CC	repeat (SSR), having 2 or more tandemly repeated nucleotide core elements
CC	2-6 nucleotides in length. Also included are a nucleic acid primer
CC	suitable for amplifying an SSR, identifying (M1) an SSR by preparing a
CC	library of ryegrass or fescue genomic DNA enriched for SSRs and
CC	identifying clones in the library containing SSRs, a library of ryegrass
CC	or fescue genomic DNA enriched for SSRs prepared by the M1, selecting for
CC	a gene in grass or cereal breeding by identifying an SSR that is closely
CC	associated with the gene such that the SSR and the gene are
CC	preferentially co-inherited, and selecting for the SSR in the breeding, a
CC	method for DNA profiling grass or cereal species varieties by assessing a
CC	variation between SSR varieties and testing the purity of grass or cereal
CC	'seed batches' by assessing variation within seed batch of an SSR. The SSRs
CC	may be used in the selection of genes in grass or cereal breeding, for
CC	cereal profiling grass or cereal species varieties, for testing the purity of
CC	grass or cereal seed batches, and for DNA profiling to establish the
CC	distinct identity, uniformity and/or stability of a cultivar. The present
CC	sequence is a ryegrass or fescue SSR
XX	
SQ	Sequence 18 BP; 9 A; 9 C; 0 G; 0 T; 0 U; 0 Other;
	Query Match 1.7%; Score 18; DB 1; Length 18;
	Best Local Similarity 100.0%; Pred.No. 94;
	Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY	1794 GCTGTGTCGTGTGTGT 1811
DB	18 GTGTGTGTGTGTGTGT 1
RESULT 167	
AAS13729	
ID	AAS13729 standard; DNA; 18 BP.
XX	
AC	AAS13729;
XX	
DT	08-MAY-2002 (first entry)
XX	
DE	Simple sequence repeat, SSR, #26.
XX	
XX	Simple sequence repeat; plant; ds; SSR; ryegrass; fescue; tandem repeat;
KW	cereal profiling; grass profiling; seed batch purity testing.
OS	Poeae.

XX NZ509193-A.  
 XX 25-MAY-2001.  
 XX 03-JAN-2001; 2001NZ-00509193.  
 XX 24-DEC-1999; 99AU-00004906.  
 XX 04-MAY-2000; 2000AU-00007310.  
 XX (SAUS-) STATE SOUTH AUSTRALIA SOUTH AUSTRALIAN R.  
 XX (UYSC-) UNIV SOUTHERN CROSS.  
 XX (VICT-) STATE VICTORIA DEPT NATURAL RES & ENVIRO.  
 XX (UYAD-) UNIV ADELAIDE.  
 XX (ITWA-) INT MAIZE & WHEAT IMPROVEMENT CENT.  
 XX Forster JW, Jones ES;  
 XX WPI; 2001-512563/56.  
 XX New simple sequence repeats having 2 or more tandemly repeated nucleotide  
 XX core elements isolated from ryegrass and fescue, useful for selecting of  
 XX genes in grass or cereal breeding or profiling grass or cereal species  
 XX varieties.  
 XX Claim 6; Page 51; 72pp; English.  
 XX The invention relates to a substantially purified or isolated nucleic  
 XX acid (1) from ryegrass or fescue species including a simple sequence  
 XX repeat (SSR), having 2 or more tandemly repeated nucleotide core elements  
 XX 2-6 nucleotides in length. Also included are a nucleic acid primer  
 XX suitable for amplifying an SSR, identifying (M1) an SSR by preparing a  
 XX library of ryegrass or fescue genomic DNA enriched for SSRs and  
 XX identifying clones in the library containing SSRs, a library of ryegrass  
 XX or fescue genomic DNA enriched for SSRs prepared by the M1, selecting for  
 XX a gene in grass or cereal breeding by identifying an SSR that is closely  
 XX associated with the gene such that the SSR and the gene are  
 XX preferentially co-inherited, and selecting for the SSR in the breeding, a  
 XX method for DNA profiling grass or cereal species varieties by assessing  
 XX variation between SSR varieties and testing the purity of grass or cereal  
 XX seed batches by assessing variation within seed batch of an SSR. The SSRs  
 XX may be used in the selection of genes in grass or cereal breeding, for  
 XX profiling grass or cereal species varieties, for testing the purity of  
 XX grass or cereal seed batches, and for DNA profiling to establish the  
 XX distinct identity, uniformity and/or stability of a cultivar. The present  
 XX sequence is a ryegrass or fescue SSR  
 XX SQ Sequence 18 BP; 0 A; 0 C; 9 G; 9 T; 0 U; 0 Other;  
 Query Match 1.7%; Score 18; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 94;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1794 GTGTGTGTGTGTGTGTGT 1811  
 Db 1 GTGTGTGTGTGTGTGTGT 18  
 RESULT 168  
 AAH46012  
 ID AAH46012 standard; DNA; 18 BP.  
 XX AAH46012;  
 XX 12-SEP-2001 (first entry)  
 XX Synthetic oligonucleotide 12.  
 XX Synthetic oligonucleotide; dinucleotide repeat; cytostatic; apoptosis;  
 XX cell cycle arrest; cell proliferation; caspase; cytokine; interleukin;  
 XX tumour necrosis factor; TNF; cancer; carcinoma; sarcoma; leukemia;  
 XX lymphoma; ss.  
 XX

OS Synthetic.  
 XX WO200144465-A2.  
 XX 21-JUN-2001.  
 XX 12-DEC-2000; 2000WO-CA001467.  
 XX 13-DEC-1999; 99US-0170325P.  
 XX 29-AUG-2000; 2000US-022825P.  
 XX (BION-) BIONICHE LIFE SCI INC.  
 XX Phillips NC, Fillion MC;  
 XX WPI; 2001-398150/42.  
 XX Composition comprising synthetic oligonucleotides which comprise multiple  
 XX repeats of dinucleotides such as GT, TG useful for treating cancer by  
 XX inducing cell cycle arrest, inhibiting proliferation, activating  
 XX caspases.  
 XX Claim 5; Page 17; 77pp; English.  
 XX The present sequence is that of a synthetic oligonucleotide useful to the  
 XX invention. The invention relates to a composition, comprises multiple  
 XX base 3'-OH, 5'-OH synthetic oligonucleotide which comprises multiple  
 XX repeats of dinucleotides such as GT, TG, etc., according to specific  
 XX formula and having cytostatic activity. The oligonucleotide compositions  
 XX are useful for inducing cell cycle arrest, inhibition of proliferation,  
 XX activation of caspases and induction of apoptosis or production of  
 XX cytokines such as interleukin (IL)-1-beta, IL-6, IL-10, IL-12 and tumour  
 XX necrosis factor (TNF)-alpha by immune system cells, in an animal having  
 XX cancer such as primary carcinoma, secondary carcinoma, primary sarcoma  
 XX and secondary sarcoma such as, leukemia, lymphoma, breast, prostate,  
 XX colorectal, ovarian or bone cancer. The compositions induce apoptosis  
 XX independent of Fas, p53/p21, p21/waf-1/CIP, p15(ink4B), p16(ink4), drug  
 XX resistance, caspase 3, transforming growth factor (TGF)-beta 1 receptor  
 XX and hormone dependence  
 XX SQ Sequence 18 BP; 0 A; 0 C; 9 G; 9 T; 0 U; 0 Other;  
 Query Match 1.7%; Score 18; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 94;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1794 GTGTGTGTGTGTGTGTGT 1811  
 Db 1 GTGTGTGTGTGTGTGTGT 18  
 RESULT 169  
 AAH46011  
 ID AAH46011 standard; DNA; 18 BP.  
 XX AAH46011;  
 XX 12-SEP-2001 (first entry)  
 XX Synthetic oligonucleotide 11.  
 XX Synthetic oligonucleotide; dinucleotide repeat; cytostatic; apoptosis;  
 XX cell cycle arrest; cell proliferation; caspase; cytokine; interleukin;  
 XX tumour necrosis factor; TNF; cancer; carcinoma; sarcoma; leukemia;  
 XX lymphoma; ss.  
 XX Synthetic.  
 XX WO200144465-A2.  
 XX 21-JUN-2001.  
 XX 12-DEC-2000; 2000WO-CA001467.

XX 13-DEC-1999; 99US-017032SP.  
PR 29-AUG-2000; 2000US-022892SP.  
XX (BION-) BIONICHE LIFE SCI INC.  
XX Phillips NC, Filion MC;  
XX WPI; 2001-398150/42.  
DR WPI; 2001-398150/42.  
XX Composition comprising synthetic oligonucleotides which comprise multiple  
PT repeats of dinucleotides such as GT, TG useful for treating cancer by  
PT inducing cell cycle arrest, inhibiting proliferation, activating  
PT caspases.  
XX Claim 5; Page 17; 77pp; English.  
XX The present sequence is that of a synthetic oligonucleotide useful to the  
CC invention. The invention relates to a composition, comprising a 2 to 20  
CC base 3'-OH, 5'-OH synthetic oligonucleotide which comprises multiple  
CC repeats of dinucleotides such as GT, TG, etc., according to specific  
CC formula and having cytostatic activity. The oligonucleotide compositions  
CC are useful for inducing cell cycle arrest, inhibition of proliferation,  
CC activation of caspases and induction of apoptosis or production of  
CC cytokines such as interleukin (IL)-1-beta, IL-6, IL-10, IL-12 and tumour  
CC necrosis factor (TNF)-alpha by immune system cells, in an animal having  
CC cancer such as primary carcinoma, secondary carcinoma, primary sarcoma  
CC and secondary sarcoma such as, leukemia, lymphoma, breast, prostate,  
CC colorectal, ovarian or bone cancer. The compositions induce apoptosis  
CC independent of Fas, p53/p21, p21/waf-1/CIP, p15(ink4B), p16(ink4), drug  
CC resistance, caspase 3, transforming growth factor (TGF)-beta 1 receptor  
CC and hormone dependence  
XX Sequence 18 BP; 0 A; 0 C; 9 G; 9 T; 0 U; 0 Other;  
SQ Query Match 1.7%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 94;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1793 TGTGTGTGTGTGTGTGTG 1810  
Db 1 TGTGTGTGTGTGTGTGTG 18  
RESULT 170  
AA164454/c  
ID AA164454 standard; DNA; 18 BP.  
XX AC AA164454;  
XX 23-NOV-2001 (first entry)  
XX SSR motif #14.  
XX Simple Sequence Repeat; SSR; clover; microsatellite; genome mapping;  
KW trait mapping; marker-assisted selection; gene selection; legume;  
KW DNA profiling; breeding; ds.  
XX Unidentified.  
OS NZ509194-A.  
XX NZ509194-A.  
XX 25-MAY-2001.  
XX 03-JAN-2001; 2001NZ-00509194.  
XX 24-DEC-1999; 99AU-00004907.  
PR 28-MAR-2000; 2000AU-00006520.  
XX (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
XX Koelliker R, Forster JW;  
XX

DR WPI; 2001-431058/46.  
XX Novel simple sequence repeats in clover species useful for selection of  
PT genes in legume breeding, for profiling legume species varieties and for  
PT testing the purity of legume seed batches.  
XX Claim 6; Page 35; 52pp; English.  
XX The present invention relates to Simple Sequence Repeats (SSRs) from  
CC clover species. SSRs, also called microsatellites, are based on a 1-7  
CC nucleotide core element which is tandemly repeated. The SSR array is  
CC embedded in complex flanking DNA. SSRs are ideal markers for genome  
CC mapping, trait mapping and marker-assisted selection. The SSRs may be  
CC used in methods for selecting genes in clover/ legume breeding. The SSRs  
CC are also useful for DNA profiling of clover varieties and for testing the  
CC purity of legume seed batches. The present sequence is a SSR motif, which  
CC was used in the present invention  
XX Sequence 18 BP; 9 A; 9 C; 0 G; 0 T; 0 U; 0 Other;  
SQ Query Match 1.7%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 94;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1793 TGTGTGTGTGTGTGTGTG 1810  
Db 18 TGTGTGTGTGTGTGTGTG 1  
RESULT 171  
AAQ49455  
ID AAQ49455 standard; DNA; 20 BP.  
XX AC AAQ49455;  
XX 06-MAY-1994 (first entry)  
XX Primer for detecting polymorphisms among highly related plant species.  
XX Detection; polymorphism; genetic fingerprinting; primer; ss.  
XX Synthetic.  
XX JP05244995-A.  
XX 24-SEP-1993.  
XX 24-SEP-1991; 91JP-00243122.  
XX 24-SEP-1991; 91JP-00243122.  
XX (KYOW ) KYOWA HAKKO KOGYO KK.  
XX WPI; 1993-338949/43.  
XX Primer - for detecting polymorphism in DNA among highly interrelated rice  
PT plants or plants of family Brassicaceae.  
XX Disclosure; Page 5; 6pp; Japanese.  
XX The PCR primers (See also AAQ49449-54, AAQ49456) are used to detect  
CC polymorphisms among highly interrelated rice plants or among plants of  
CC family Brassicaceae. They can also be used for genetic fingerprinting of  
CC plants, allowing detection of polymorphism within one or the same species  
CC of plant  
XX Sequence 20 BP; 0 A; 2 C; 9 G; 9 T; 0 U; 0 Other;  
SQ Query Match 1.7%; Score 18; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1e-02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1793 TGTGTGTGTGTGTGTGTG 1810

Ds 1 TGTGTGTGTGTGTGTG 18

RESULT 172  
ADD69468  
ID ADD69468 standard; DNA; 20 BP.

XX AC ADD69468;  
XX DT 15-JAN-2004 (first entry)

XX DE 3' anchored (ISSR)-PCR primer - SEQ ID 26.

XX KW inter-simple sequence repeat; ISSR; SSR; PCR; primer; genotyping; plant;  
KW animal; Basmati rice; ss.

XX OS Synthetic.

XX FN WO2003085133-A2.

XX PD 16-OCT-2003.

XX PF 09-JAN-2003; 2003WO-IB000041.

XX PR 08-APR-2002; 2002IN-CH0000260.

XX PA (DNAF-) CENT DNA FINGERPRINTING & DIAGNOSTICS.

XX PI Nagaraju JG;

XX DR WPI; 2003-804317/75.

XX PT New set of inter-simple sequence repeats (ISSR)-PCR primers for  
PT genotyping eukaryotes, useful for genotyping diverse genomes of plant and  
PT animal systems.

XX PS Claim 1; SEQ ID NO 26; 60bp; English.

XX CC The invention relates to a novel set of inter-simple sequence repeats  
CC (ISSR)-PCR primers for genotyping eukaryotes. The primers of the  
CC invention may be useful for genotyping diverse genomes of plant and  
CC animal systems, in particular for distinguishing Basmati rice varieties  
CC from non-Basmati rice varieties and traditional Basmati rice varieties  
CC from evolved Basmati rice varieties. The current sequence is that of the  
CC 3' anchored (ISSR)-PCR primer of the invention.

XX SQ Sequence 20 BP; 1 A; 2 C; 8 G; 9 T; 0 U; 0 Other;

Query Match 1.7%; Score 18; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1798 GTGTGTGTGTGTGTAT 1815

Ds 1 GTGTGTGTGTGTGTAT 18

RESULT 173

AAQ75727  
ID AAQ75727 standard; DNA; 21 BP.

XX AC AAQ75727;

XX DT 04-AUG-1995 (first entry)

XX DE Reverse transcription primer used in cDNA analysis technique.

XX KW Analysis; gene expression; reverse transcription; primer; cDNA;

XX KW aggregate; restriction enzyme; ss.

XX OS Synthetic.

PN JP06303997-A.

XX PD 01-NOV-1994.

XX PF 16-APR-1993; 93JP-00112515.

XX PR 16-APR-1993; 93JP-00112515.

XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.

XX DR WPI; 1995-018287/03.

XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.

XX PS Disclosure; Page 8; 11pp; Japanese.

XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c) the  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily

XX SQ Sequence 21 BP; 2 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 1.7%; Score 17.8; DB 1; Length 21;  
Best Local Similarity 90.5%; Pred. No. 1.1e-02;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTGTTTGTATG 1885

Ds 1 TTTTATTGTTTGTATG 21

RESULT 174

ABS97830/c  
ID ABS97830 standard; DNA; 21 BP.

XX AC ABS97830;

XX DT 23-DEC-2002 (first entry)

XX DE Human NADPH quinone oxidoreductase 2 (NQO2) polymorphic sequence #38.

XX KW Human; ds; cytochrome P450 A1; CYP450A1; UGT2B4; MDRI;  
KW Cytochrome P450 A2; CYP450A2; cytochrome P450 02E; CYP45002E1; LTF;  
KW adrenergic receptor beta1; ADRB1; aryl hydrocarbon; AHR; MRP3; NR1I2;  
KW cyclooxygenase 2; COX2; diazepam binding inhibitor; DBI; haematological;  
KW epoxide hydrolase 2; EPHX2; 5-lipoxygenase activating protein; FLAP;  
KW glutathione-S-transferase 12; GSTI2; histamine-N-methyl transferase;  
KW HMT; kallikrein 2; KLK2; nicotinamide-N-methyl transferase; NNMT;  
KW NADPH quinone oxidoreductase 2; NQO2; sulfoxyltransferase; thermolabile; STM;  
KW UDP-glucuronosyl transferase 2B4; UDP-glucuronosyl transferase 2B7;  
KW UGT2B7; UDP-glucuronosyl transferase; UGT2B1; uronidase; uPA;  
KW multidrug resistance 1; lactotransferrin; orphan nuclear receptor;  
KW acetylcholine muscarinic receptor; CHMR1; CHMR2; CHMR3; CHMR4; CHMR5;  
KW altered drug metabolism; cardiovascular function; colorectal tumour;  
KW central nervous system; pulmonary; immunological; SNP;  
KW single nucleotide polymorphism.

XX OS Homo sapiens.

XX PN WO200257410-A2.

XX PD 25-JUL-2002.

XX PF 28-NOV-2001; 2001WO-US044838.

```

PR 28-NOV-2000; 2000US-00724389.
XX (DNAS-) DNA SCI LAB INC.
PA
XX Guida M, Hall J;
PI WPI; 2002-698522/75.
XX
XX Isolated nucleic acid molecules having polymorphisms in known human genes
PT e.g. cytochrome p450 and cathepsin S useful as genetic linkage markers
PT for locating, identifying and characterizing the genes responsible for
PT disorder-related traits.
XX
XX Example 16; Page 130; 714pp; English.
XX
XX This invention relates to the sequence of an isolated nucleic acid
CC molecule comprising at least one base variation from that of a known
CC human cytochrome P450 A1 (CYP450A1), cytochrome P450 A2 (CYP450A2),
CC cytochrome P450 02E1 (CYP45002E1), adrenergic receptor beta1 (ADRB1),
CC aryl hydrocarbon (AHR), aryl hydrocarbon receptor nuclear translocator
CC (ARNT), cathepsin S (CTSS), cyclooxygenase 2 (COX2), diazepam binding
CC inhibitor (DBI), epoxide hydroxylase 2 (EPHX2), 5-lipoxygenase activating
CC protein (FLAP), glutathione-S-transferase 12 (GST12), histamine-N-methyl
CC transferase (HNMT), NADPH quinone oxidoreductase 2 (NQO2),
CC sulfoltransferase thermolabile (STM), UDP-glucuronosyl transferase 2B4
CC (UGT2B4), UDP-glucuronosyl transferase 2B7 (UGT2B7), UDP-glucuronosyl
CC transferase (UGT2B15), urokinase receptor (UPA), multidrug resistance 1
CC (MDR1), lactotransferrin (LTF), multidrug resistance associated protein 3
CC (MRP3), orphan nuclear receptor (NR112), or acetylcholine muscarinic
CC receptor 1, 2, 3, 4, or 5 (CHMR1, CHMR2, CHMR3, CHMR4 or CHMR5) sequence.
CC The polymorphisms in the human genes cited in the invention are useful as
CC genetic linkage markers for locating and characterizing the genes that
CC are responsible for specific traits within the genome and eventually
CC identifying the genes responsible for a variety of disorder-related
CC traits as a result of their e.g., overexpression, constitutive
CC expression, mutation or underexpression, which may be used in diagnosing
CC and/or treating the disorders. The nucleic acid molecules comprising the
CC polymorphic sequences contained in CYP450A1, CYP450A2, CYP4502E1,
CC ARNT, EPHX2, GST12, NNMT, NQO2, NR112, STM, UGT2B4, UGT2B7, UGT2B15, AHR,
CC MDR1 and/or MDR3 are useful for screening individuals for altered drug
CC metabolism. The polymorphic sequences contained in CYP450A1, CYP450A2,
CC AHR, MDR1 and/or MDR3 may also be used to screen individuals for
CC susceptibility to cancer. Polymorphic sequences in ADRB1 or CHMR2 are
CC used to screen for altered cardiovascular function, in COX2 for altered
CC nervous system function, in FLAP and HNMT for altered serine
CC immunological or haematological function, in KLK2 for altered serine
CC protease activity in the prostate, in LTF for altered immunological or
CC haematological function, in CHMR3, CHMR4 or CHMR5 for altered central and
CC peripheral nervous system function. The present sequence represents a
CC polymorphic DNA sequence of the invention
XX
XX Sequence 21 BP; 10 A; 9 C; 1 G; 1 T; 0 U; 0 Other;
SQ
Query Match 1.7%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 1.1e-02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1793 TGTGTCGTGTCGTGTCGTGTCGT 1813
DB 21 TATGTCGTGTCGTGTCGTGTCGT 1
RESULT 175
ID ABS97832/c
AC ABS97832 standard; DNA; 21 BP.
XX ABS97832;
XX
XX 23-DEC-2002 (first entry)
XX
XX Human NADPH quinone oxidoreductase 2 (NQO2) polymorphic sequence #40.
DE

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XX Human; ds; cytochrome P450 A1; CYP450A1A1; UGT2B4; MDR1;
XX cytochrome P450 A2; CYP450A2; cytochrome P450 02E; CYP45002E1; LTF;
XX adrenergic receptor beta1; ADRB1; aryl hydrocarbon; AHR; MRP3; NR112;
XX aryl hydrocarbon receptor nuclear translocator; ARNT; cathepsin S; CTSS;
XX cyclooxygenase 2; COX2; diazepam binding inhibitor; DBI; haematological;
XX epoxide hydroxylase 2; EPHX2; 5-lipoxygenase activating protein; FLAP;
XX glutathione-S-transferase 12; GST12; histamine-N-methyl transferase;
XX HNMT; kallikrein 2; KLK2; nicotinamide-N-methyl transferase; NNMT;
XX NADPH quinone oxidoreductase 2; NQO2; sulfoltransferase thermolabile; STM;
XX UDP-glucuronosyl transferase 2B4; UDP-glucuronosyl transferase 2B7; UGA;
XX UGT2B7; UDP-glucuronosyl transferase; UGT2B15; urokinase receptor; UPA;
XX multidrug resistance 1; lactotransferrin; orphan nuclear receptor;
XX acetylcholine muscarinic receptor; CHMR1; CHMR2; CHMR3; CHMR4; CHMR5;
XX aryl hydrocarbon receptor; CHMR1; CHMR2; CHMR3; CHMR4; CHMR5;
XX altered drug metabolism; cardiovascular function; colorectal tumour;
XX central nervous system; pulmonary; immunological; SNP;
XX single nucleotide polymorphism.
XX Homo sapiens.
XX WO200257410-A2.
XX 25-JUL-2002.
XX 28-NOV-2001; 2001WO-US044838.
XX 28-NOV-2000; 2000US-00724389.
XX (DNAS-) DNA SCI LAB INC.
XX Guida M, Hall J;
XX WPI; 2002-698522/75.
XX Isolated nucleic acid molecules having polymorphisms in known human genes
XX e.g. cytochrome p450 and cathepsin S useful as genetic linkage markers
XX for locating, identifying and characterizing the genes responsible for
XX disorder-related traits.
XX Example 16; Page 131; 714pp; English.
XX
XX This invention relates to the sequence of an isolated nucleic acid
XX molecule comprising at least one base variation from that of a known
XX human cytochrome P450 A1 (CYP450A1), cytochrome P450 A2 (CYP450A2),
XX cytochrome P450 02E1 (CYP45002E1), adrenergic receptor beta1 (ADRB1),
XX aryl hydrocarbon (AHR), aryl hydrocarbon receptor nuclear translocator
XX (ARNT), cathepsin S (CTSS), cyclooxygenase 2 (COX2), diazepam binding
XX inhibitor (DBI), epoxide hydroxylase 2 (EPHX2), 5-lipoxygenase activating
XX protein (FLAP), glutathione-S-transferase 12 (GST12), histamine-N-methyl
XX transferase (HNMT), (kallikrein 2) KLK2, nicotinamide-N-methyl
XX transferase (NNMT), NADPH quinone oxidoreductase 2 (NQO2),
XX sulfoltransferase thermolabile (STM), UDP-glucuronosyl transferase 2B4
XX (UGT2B4), UDP-glucuronosyl transferase 2B7 (UGT2B7), UDP-glucuronosyl
XX transferase (UGT2B15), urokinase receptor (UPA), multidrug resistance 1
XX (MDR1), lactotransferrin (LTF), multidrug resistance associated protein 3
XX (MRP3), orphan nuclear receptor (NR112), or acetylcholine muscarinic
XX receptor 1, 2, 3, 4, or 5 (CHMR1, CHMR2, CHMR3, CHMR4 or CHMR5) sequence.
XX The polymorphisms in the human genes cited in the invention are useful as
XX genetic linkage markers for locating and characterizing the genes that
XX are responsible for specific traits within the genome and eventually
XX identifying the genes responsible for a variety of disorder-related
XX traits as a result of their e.g., overexpression, constitutive
XX expression, mutation or underexpression, which may be used in diagnosing
XX and/or treating the disorders. The nucleic acid molecules comprising the
XX polymorphic sequences contained in CYP450A1, CYP450A2, CYP4502E1,
XX ARNT, EPHX2, GST12, NNMT, NQO2, NR112, STM, UGT2B4, UGT2B7, UGT2B15, AHR,
XX MDR1 and/or MDR3 are useful for screening individuals for altered drug
XX metabolism. The polymorphic sequences contained in CYP450A1, CYP450A2,
XX AHR, MDR1 and/or MDR3 may also be used to screen individuals for
XX susceptibility to cancer. Polymorphic sequences in ADRB1 or CHMR2 are
XX used to screen for altered cardiovascular function, in COX2 for altered
XX nervous system function, in FLAP and HNMT for altered serine
XX immunological or haematological function, in KLK2 for altered serine
XX protease activity in the prostate, in LTF for altered immunological or
XX haematological function, in CHMR3, CHMR4 or CHMR5 for altered central and
XX peripheral nervous system function. The present sequence represents a
XX polymorphic DNA sequence of the invention
XX
XX Sequence 21 BP; 10 A; 9 C; 1 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 1.7%; Score 17.8; DB 1; Length 21;
XX Best Local Similarity 90.5%; Pred. No. 1.1e-02;
XX Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1793 TGTGTCGTGTCGTGTCGTGTCGT 1813
XX DB 21 TATGTCGTGTCGTGTCGTGTCGT 1
XX
XX RESULT 175
XX ID ABS97832/c
XX AC ABS97832 standard; DNA; 21 BP.
XX
XX ABS97832;
XX
XX 23-DEC-2002 (first entry)
XX
XX Human NADPH quinone oxidoreductase 2 (NQO2) polymorphic sequence #40.
XX

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CC nervous system function, in FLAP and HNMT for altered pulmonary,  
CC immunological or haematological function, in KLR2 for altered serine  
CC protease activity in the prostate, in LTF for altered immunological or  
CC haematological function, in CHMR3, CHMR4 or CHMR5 for altered central and  
CC peripheral nervous system function. The present sequence represents a  
CC polymorphic DNA sequence of the invention  
XX  
SQ Sequence 21 BP; 10 A; 9 C; 1 G; 1 T; 0 U; 0 Other;  
Query Match 1.7%; Score 17.8; DB 1; Length 21;  
Best Local Similarity 90.5%; Pred. No. 1.1e+02;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1793 TGTGTGTGTGTGTGTGTGTGT 1813  
DB 21 TGTATGTGTGTGTGTGTGTGTGT 1  
RESULT 176  
AAQ33888  
ID AAQ33888 standard; DNA; 22 BP.  
XX  
AC AAQ33888;  
XX  
25-MAR-2003 (revised)  
DT 02-FEB-1993 (first entry)  
XX  
DE Microsatellite sequence from clone TGLA306.  
XX  
PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;  
KW genetic mapping; traits; amplification; ss.  
XX  
XX Bos taurus.  
XX  
XX WO9213102-A1.  
XX  
06-AUG-1992.  
XX  
15-JAN-1992; 92WO-US000340.  
XX  
15-JAN-1991; 91US-00642342.  
XX  
XX (GENM-) GENMARK.  
XX  
XX Georges M, Massey JM;  
XX  
XX WPI; 1992-284684/34.  
XX  
XX Polymorphic bovine DNA markers - used in genetic identification, gene  
XX mapping, and selective breeding.  
XX  
XX Table 7; Page 285; 517pp; English.  
XX  
XX The sequence is that of a bovine microsatellite sequence obtd. by  
XX screening a library of bovine Mbol DNA fragments of between 250 and 500  
XX bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50  
XX clones cross-hybridised. Assuming independent distribution of  
XX microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites  
XX in the bovine genome is estimated at >100, 000. The sequence information  
XX for ca. 230 such bovine microsatellites is summarised in the  
XX specification and indexed herein (see below). The sequences upstream and  
XX downstream of the microsatellite sequence were used to generate the  
XX required PCR primers for in vitro amplification of the corresp.  
XX microsatellite (using the program OPTIPRIM). The microsatellites may be  
XX used to identify individuals, for parentage testing, and in the genetic  
XX mapping of economic trait loci, or genes involved the determination of  
XX economically important traits esp. in cattle, to allow selective  
XX breeding. See also AAQ3501-34437. (Updated on 25-MAR-2003 to correct PN  
XX field.)  
XX  
XX Sequence 22 BP; 1 A; 0 C; 11 G; 10 T; 0 U; 0 Other;  
SQ  
Query Match 1.7%; Score 17.8; DB 1; Length 22;

Best Local Similarity 90.5%; Pred. No. 1.2e+02;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1793 TGTGTGTGTGTGTGTGTGTGT 1813  
DB 1 TGTGATGTGTGTGTGTGTGTGT 21  
RESULT 177  
AAI64468/C  
ID AAI64468 standard; DNA; 22 BP.  
XX  
AC AAI64468;  
XX  
23-NOV-2001 (first entry)  
DT  
XX  
DE SSR motif #18.  
XX  
Simple Sequence Repeat; SSR; clover; microsatellite; genome mapping;  
KW trait mapping; marker-assisted selection; gene selection; legume;  
KW DNA profiling; breeding; ds.  
XX  
XX Unidentified.  
XX  
XX NZ509194-A.  
XX  
25-MAY-2001.  
XX  
03-JAN-2001; 2001NZ-00509194.  
XX  
24-DEC-1999; 99AU-00004907.  
XX  
28-MAR-2000; 2000AU-00006520.  
XX  
XX (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
XX  
XX Koelliker R, Forster JW;  
XX  
XX WPI; 2001-431058/46.  
XX  
XX Novel simple sequence repeats in clover species useful for selection of  
XX genes in legume breeding, for profiling legume species varieties and for  
XX testing the purity of legume seed batches.  
XX  
XX Example 1; Page 19; 52pp; English.  
XX  
XX The present invention relates to Simple Sequence Repeats (SSRs) from  
XX clover species. SSRs, also called microsatellites, are based on a 1-7  
XX nucleotide core element which is tandemly repeated. The SSR array is  
XX embedded in complex flanking DNA. SSRs are ideal markers for genome  
XX mapping, trait mapping and marker-assisted selection. The SSRs may be  
XX used in methods for selecting genes in clover/ legume breeding. The SSRs  
XX are also useful for DNA profiling of clover varieties and for testing the  
XX purity of legume seed batches. The present sequence is a SSR motif, which  
XX was used in the present invention  
XX  
XX Sequence 22 BP; 10 A; 10 C; 2 G; 0 T; 0 U; 0 Other;  
SQ  
Query Match 1.7%; Score 17.8; DB 1; Length 22;  
Best Local Similarity 90.5%; Pred. No. 1.2e+02;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1793 TGTGTGTGTGTGTGTGTGTGT 1813  
DB 21 TGTGTGTGTGTGTGTGTGTGT 1  
RESULT 178  
ABS97834/c  
ID ABS97834 standard; DNA; 22 BP.  
XX  
XX ABS97834;  
XX  
XX 23-DEC-2002 (first entry)  
DT

XX Human NADPH quinone oxidoreductase 2 (NQO2) polymorphic sequence #42.  
 DE Human; ds; cytochrome P450 A1; CYP450A1; UGT2B4; MDR1;  
 KW cytochrome P450 A2; CYP450A2; cytochrome P450 02E; CYP45002E1; LTF;  
 KW adrenergic receptor beta1; ADRB1; aryl hydrocarbon; AHR; MRP3; NR112;  
 KW aryl hydrocarbon receptor nuclear translocator; ARNT; cathepsin S; CTSS;  
 KW cyclooxigenase 2; COX2; diazepam binding inhibitor; DBI; haematological;  
 KW epoxide hydroxylase 2; EPHX2; 5-lipoxygenase activating protein; FLAP;  
 KW glutathione-S-transferase 12; GST12; histamine-N-methyl transferase;  
 KW HMT; kallikrein 2; KLK2; nicotinamide-N-methyl transferase; NNMT;  
 KW NADPH quinone oxidoreductase 2; NQO2; sulfoxidoreductase thermolabile; STM;  
 KW UDP-glucuronosyl transferase 2B4; UDP-glucuronosyl transferase 2B7;  
 KW UGT2B7; UDP-glucuronosyl transferase; UGT2B15; urokinase receptor; UPA;  
 KW multidrug resistance 1; lactotransferrin; orphan nuclear receptor;  
 KW multidrug resistance associated protein 3; cancer; prostate;  
 KW acetylcholine muscarinic receptor; CHMR1; CHMR2; CHMR3; CHMR4; CHMR5;  
 KW altered drug metabolism; cardiovascular function; colorectal tumour;  
 KW central nervous system; pulmonary; immunological; SNP;  
 KW single nucleotide polymorphism.  
 XX Homo sapiens.  
 XX WO200257410-A2.  
 XX 25-JUL-2002.  
 XX 28-NOV-2001; 2001WO-US044838.  
 XX 28-NOV-2000; 2000US-00724389.  
 XX (DNAS-) DNA SCI LAB INC.  
 XX Guida M, Hall J;  
 XX WPI; 2002-698522/75.  
 XX Isolated nucleic acid molecules having polymorphisms in known human genes  
 PT e.g. cytochrome P450 and cathepsin S useful as genetic linkage markers  
 PT for locating, identifying and characterizing the genes responsible for  
 PT disorder-related traits.  
 XX Example 16; Page 131; 714pp; English.

CC used to screen for altered cardiovascular function, in COX2 for altered  
 CC susceptibility to colorectal tumours, in DBI or CHMR1 for altered central  
 CC nervous system function, in FLAP and NNMT for altered pulmonary,  
 CC immunological or haematological function, in KLK2 for altered serine  
 CC protease activity in the prostate, in LTF for altered immunological or  
 CC haematological function, in CHMR3, CHMR4 or CHMR5 for altered central and  
 CC peripheral nervous system function. The present sequence represents a  
 CC polymorphic DNA sequence of the invention  
 XX SQ Sequence 22 BP; 10 A; 10 C; 1 G; 1 T; 0 U; 0 Other;  
 Query Match 1.7%; Score 17.8; DB 1; Length 22;  
 Best Local Similarity 90.5%; Pred. No. 1.2e+02;  
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1793 TGTGTGTGTGTGTGTGTGTGTGTGTGT 1813  
 DB 21 TATGTGTGTGTGTGTGTGTGTGTGTGT 1  
 RESULT 179  
 AAF62964  
 ID AAF62964 standard; DNA; 20 BP.  
 XX AC AAF62964;  
 XX DT 08-MAY-2001 (first entry)  
 XX DE Mouse PEPCCK-cytosolic antisense oligonucleotide ISIS 113342.  
 KW Mouse; antiinflammatory; cytostatic; antisense gene therapy;  
 KW phosphoenol pyruvate carboxykinase-cytosolic; PEPCCK-cytosolic; infection;  
 KW inflammation; tumour formation; phosphorothioate; ss.  
 XX OS Mus musculus.  
 XX PN US6187545-B1.  
 XX PD 13-FEB-2001.  
 XX PF 21-JAN-2000; 2000US-00488671.  
 XX PR 21-JAN-2000; 2000US-00488671.  
 XX (ISIS-) ISIS PHARM INC.  
 XX Mckay R, Butler MM, Wyatt J, Cowse LM;  
 WPI; 2001-190979/19.  
 XX Antisense compound capable of modulating the expression of phosphoenol  
 PT pyruvate carboxykinase-cytosolic, useful for preventing or delaying  
 PT infection, inflammation or tumor formation.  
 PS Example 17; Col 44; 64pp; English.  
 XX The present sequence is one of a number of antisense compounds of up to  
 CC 30 nucleobases in length that are capable of inhibiting the expression of  
 CC phosphoenol pyruvate carboxykinase-cytosolic (PEPCCK-cytosolic). The  
 CC antisense compounds are useful for inhibiting the expression of PEPCCK-  
 CC cytosolic in cells or tissues. They are commonly used as research  
 CC reagents and in diagnostics, e.g. to elucidate the function of particular  
 CC genes. They are also useful for distinguishing between functions of  
 CC various members of a biological pathway and for research use. The  
 CC antisense compounds are also useful prophylactically, e.g. to prevent or  
 CC delay infection, inflammation or tumour formation. The present sequence  
 CC is a chimeric phosphorothioate oligonucleotide with 2'-MOE wings and a  
 CC deoxy gap  
 XX SQ Sequence 20 BP; 2 A; 0 C; 10 G; 8 T; 0 U; 0 Other;  
 Query Match 1.7%; Score 17.4; DB 1; Length 20;  
 Best Local Similarity 94.7%; Pred. No. 1.2e+02;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
Qy 1794	GTGTGTGTGTGTGTGTGTG 1812
Db 1	GTGTGTGTGTGTGTGTGTG 19
RESULT 180	
AAS21755/c	
ID	AAS21755 standard; DNA; 20 BP.
XX	
AC	AAS21755;
XX	
DT	21-NOV-2001 (first entry)
XX	
DE	Mouse Survivin antisense oligonucleotide #57.
XX	
KW	Survivin; human; mouse; cytostatic; antisense oligonucleotide;
KW	hyperproliferative condition; cancer; apoptosis; cytokinesis; ss.
XX	
OS	Mus musculus.
OS	Synthetic.
XX	
PN	WO200157059-A1.
XX	
PD	09-AUG-2001.
XX	
PF	30-JAN-2001; 2001WO-US002939.
XX	
PR	02-FEB-2000; 2000US-00496694.
XX	
PA	(ISIS-) ISIS PHARM INC.
XX	
PI	Bennett CF, Ackermann EJ, Swayze EE, Cowsett LM;
XX	
DR	WPI; 2001-488863/53.
XX	
PT	Novel antisense compounds for modulating the expression of Survivin and treatment of cancer.
PS	Example 18; Page 62; 120pp; English.
XX	
CC	The invention relates to antisense oligonucleotides targeted to a nucleic acid molecule encoding human Survivin, where the antisense oligonucleotide inhibits the expression of human Survivin. These antisense oligonucleotides are used in the treatment of an animal suffering from a disease or condition associated with Survivin, e.g. a hyperproliferative condition such as cancer, and comprises administering a therapeutically or prophylactically effective amount of the antisense oligonucleotide so that expression of Survivin is inhibited. The oligonucleotides can also be used to treat a human suffering from a disease or condition characterised by a reduction in apoptosis comprising administering the antisense oligonucleotide to a human. In addition, the antisense oligonucleotide and a cytotoxic chemotherapeutic agent e.g. taxol or cisplatin, can be used to modulate apoptosis, cytokinesis or the cell cycle, or inhibit the proliferation in a cancer cell by contacting the cell with the antisense oligonucleotide. AAS21521-AAS21768 represent Survivin nucleic acids, and antisense oligonucleotides targeted to Survivin, used in the method of the invention
SQ	Sequence 20 BP; 11 A; 2 C; 0 G; 7 T; 0 U; 0 Other;
Query Match 1.7%; Score 17.4; DB 1; Length 20;	
Best Local Similarity 94.7%; Pred. No. 1.2e+02;	
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
Qy 1811	TGTATATATATATATATGT 1829
Db 19	TGTTATATATATATATGT 1
RESULT 181	
ABS97835/c	

ID	ABS97835 standard; DNA; 20 BP.
XX	
AC	ABS97835;
XX	
DT	23-DEC-2002 (first entry)
XX	
DE	Human NADPH quinone oxidoreductase 2 (NQO2) polymorphic sequence #43.
XX	
KW	Human; ds; cytochrome P450 A1; CYP4501A1; UGT2B4; MDR1;
KW	cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002E1; LTF;
KW	adrenergic receptor beta1; ADRB1; aryl hydrocarbon; AHR; MRP3; NR1I2;
KW	aryl hydrocarbon receptor nuclear translocator; ARNT; cathepsin S; CTSS;
KW	cytochrome P450 02E1 (CYP45002E1), adrenergic receptor beta1 (ADRB1),
KW	aryl hydrocarbon (AHR), aryl hydrocarbon receptor nuclear translocator
KW	(ARNT), cathepsin S (CTSS), cyclooxygenase 2 (COX2), diazepam binding
KW	inhibitor (DBI), epoxide hydroxylase 2 (EPHX2), 5-lipoxygenase activating
KW	protein (FLAP), glutathione-S-transferase 12 (GST12), histamine-N-methyl
KW	transferase (HNMT), (kallikrein 2) KLK2, nicotinamide -N-methyl
KW	transferase (NNMT), NADPH quinone oxidoreductase 2 (NQO2),
KW	sulfotransferase thermolabile (STM), UDP-glucuronosyl transferase 2B4
KW	(UGT2B4), UDP-glucuronosyl transferase 2B7 (UGT2B7), UDP-glucuronosyl
KW	transferase (UGT2B15), uronidine transferase (UPT), multidrug resistance protein 1
KW	(MDR1), lactotransferrin (LTF), multidrug resistance associated protein 3
KW	(MRP3), orphan nuclear receptor (NR1I2), or acetylcholine muscarinic
KW	receptor 1, 2, 3, 4, or 5 (CHMR1, CHMR2, CHMR3, CHMR4 or CHMR5) sequence.
KW	The polymorphisms in the human genes cited in the invention are useful as
KW	genetic linkage markers for locating and characterizing the genes that
KW	are responsible for specific traits within the genome and eventually
KW	identifying the genes responsible for a variety of disorder-related
KW	traits as a result of their e.g., overexpression, constitutive
KW	expression, mutation or underexpression, which may be used in diagnosing
KW	and/or treating the disorders. The nucleic acid molecules comprising the
KW	polymorphic sequences contained in CYP4501A1, CYP4501A2, CYP4502E1,
OS	Homo sapiens.
XX	
WO	WO200257410-A2.
PD	25-JUL-2002.
XX	
PF	28-NOV-2001; 2001WO-US044838.
XX	
PR	28-NOV-2000; 2000US-00724389.
XX	
PA	(DNAS-) DNA SCI LAB INC.
XX	
PI	Guida M, Hall J;
XX	
DR	WPI; 2002-698522/75.
XX	
PT	Isolated nucleic acid molecules having polymorphisms in known human genes e.g. cytochrome p450 and cathepsin S useful as genetic linkage markers for locating, identifying and characterizing the genes responsible for disorder-related traits.
PS	Example 16; Page 131; 714pp; English.
XX	
CC	This invention relates to the sequence of an isolated nucleic acid molecule comprising at least one base variation from that of a known human cytochrome P450 A1 (CYP4501A1), cytochrome P450 A2 (CYP4501A2), cytochrome P450 02E1 (CYP45002E1), adrenergic receptor beta1 (ADRB1), aryl hydrocarbon (AHR), aryl hydrocarbon receptor nuclear translocator (ARNT), cathepsin S (CTSS), cyclooxygenase 2 (COX2), diazepam binding inhibitor (DBI), epoxide hydroxylase 2 (EPHX2), 5-lipoxygenase activating protein (FLAP), glutathione-S-transferase 12 (GST12), histamine-N-methyl transferase (HNMT), (kallikrein 2) KLK2, nicotinamide -N-methyl transferase (NNMT), NADPH quinone oxidoreductase 2 (NQO2), sulfotransferase thermolabile (STM), UDP-glucuronosyl transferase 2B4 (UGT2B4), UDP-glucuronosyl transferase 2B7 (UGT2B7), UDP-glucuronosyl transferase (UGT2B15), uronidine transferase (UPT), multidrug resistance protein 1 (MDR1), lactotransferrin (LTF), multidrug resistance associated protein 3 (MRP3), orphan nuclear receptor (NR1I2), or acetylcholine muscarinic receptor 1, 2, 3, 4, or 5 (CHMR1, CHMR2, CHMR3, CHMR4 or CHMR5) sequence. The polymorphisms in the human genes cited in the invention are useful as genetic linkage markers for locating and characterizing the genes that are responsible for specific traits within the genome and eventually identifying the genes responsible for a variety of disorder-related traits as a result of their e.g., overexpression, constitutive expression, mutation or underexpression, which may be used in diagnosing and/or treating the disorders. The nucleic acid molecules comprising the polymorphic sequences contained in CYP4501A1, CYP4501A2, CYP4502E1,

CC ARNT, EPHX2, GST12, NNMT, NQO2, NR112, STM, UGT2B4, UGT2B7, UGT2B15, AHR,  
 CC MDR1 and/or MDR3 are useful for screening individuals for altered drug  
 CC metabolism. The polymorphic sequences contained in CYP450A1, CYP450A2,  
 CC AHR, MDR1 and/or MDR3 may also be used to screen individuals for  
 CC susceptibility to cancer. Polymorphic sequences in ADRB1 or CHMR2 are  
 CC used to screen for altered cardiovascular function, in COX2 for altered  
 CC susceptibility to colorectal tumours, in DBI or CHMR1 for altered central  
 CC nervous system function, in FLAP and HMMT for altered pulmonary  
 CC immunological or haematological function, in KLX2 for altered serine  
 CC protease activity in the prostate, in LTF for altered immunological or  
 CC haematological function, in CHMR3, CHMR4 or CHMR5 for altered central and  
 CC peripheral nervous system function. The present sequence represents a  
 CC polymorphic DNA sequence of the invention  
 XX  
 SQ Sequence 20 BP; 10 A; 8 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 1.7%; Score 17.4; DB 1; Length 20;  
 Best Local Similarity 94.7%; Pred. No. 1.2e+02;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGT 1811  
 |||||  
 Db 19 TGTGTGTGTGTGTGTGT 1

RESULT 182  
 AAQ34164  
 ID AAQ34164 standard; DNA; 17 BP.  
 XX  
 AC AAQ34164;  
 XX  
 XX 25-MAR-2003 (revised)  
 DT 02-FEB-1993 (first entry)  
 XX  
 XX Sequence of a microsatellite from clone TGLA84.  
 DE  
 XX PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;  
 XX genetic mapping; traits; amplification; ss.  
 XX  
 XX Bos taurus.  
 OS  
 XX WO9213102-A1.  
 FN  
 XX 06-AUG-1992.  
 PD  
 XX 15-JAN-1992; 92WO-US000340.  
 XX  
 PF 15-JAN-1991; 91US-00642342.  
 XX  
 PR (GENM-) GENMARK.  
 XX  
 PA Georges M, Massey JM;  
 FI  
 XX WPI; 1992-284684/34.  
 DR  
 XX Polymorphic bovine DNA markers - used in genetic identification, gene  
 PT mapping, and selective breeding.  
 PT  
 XX Table 7; Page 396; 517pp; English.

XX The sequence is that of a bovine microsatellite sequence obtd. by  
 XX screening a library of bovine MboI DNA fragments of between 250 and 500  
 CC bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50  
 CC clones cross-hybridised. Assuming independent distribution of  
 CC microsatellites and MboI sites, the frequency of (T6)n > 9 microsatellites  
 CC in the bovine genome is estimated at >100, 000. The sequence information  
 CC for ca. 230 such bovine microsatellites is summarised in the  
 CC specification and indexed herein (see below). The sequences upstream and  
 CC downstream of the microsatellite sequence were used to generate the  
 CC required PCR primers for in vitro amplification of the corresp.  
 CC microsatellite (using the program OPTIPRIM). The microsatellites may be  
 CC used to identify individuals, for parentage testing, and in the genetic  
 CC mapping of economic trait loci, or genes involved in the determination of

CC economically important traits esp. in cattle, to allow selective  
 CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN  
 CC field.)  
 XX  
 SQ Sequence 17 BP; 0 A; 0 C; 8 G; 9 T; 0 U; 0 Other;

Query Match 1.6%; Score 17; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGT 1809  
 |||||  
 Db 1 TGTGTGTGTGTGTGTGT 17

RESULT 183  
 AAQ33783  
 ID AAQ33783 standard; DNA; 17 BP.  
 XX  
 AC AAQ33783;  
 XX  
 XX 25-MAR-2003 (revised)  
 DT 02-FEB-1993 (first entry)  
 XX  
 XX Microsatellite sequence from clone TGLA188.  
 DE  
 XX PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;  
 XX genetic mapping; traits; amplification; ss.  
 XX  
 XX Bos taurus.  
 OS  
 XX WO9213102-A1.  
 FN  
 XX 06-AUG-1992.  
 PD  
 XX 15-JAN-1992; 92WO-US000340.  
 XX  
 PF 15-JAN-1991; 91US-00642342.  
 XX  
 PR (GENM-) GENMARK.  
 XX  
 PA Georges M, Massey JM;  
 FI  
 XX WPI; 1992-284684/34.  
 DR  
 XX Polymorphic bovine DNA markers - used in genetic identification, gene  
 PT mapping, and selective breeding.  
 PT  
 XX Table 7; Page 242; 517pp; English.

XX The sequence is that of a bovine microsatellite sequence obtd. by  
 XX screening a library of bovine MboI DNA fragments of between 250 and 500  
 CC bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50  
 CC clones cross-hybridised. Assuming independent distribution of  
 CC microsatellites and MboI sites, the frequency of (T6)n > 9 microsatellites  
 CC in the bovine genome is estimated at >100, 000. The sequence information  
 CC for ca. 230 such bovine microsatellites is summarised in the  
 CC specification and indexed herein (see below). The sequences upstream and  
 CC downstream of the microsatellite sequence were used to generate the  
 CC required PCR primers for in vitro amplification of the corresp.  
 CC microsatellite (using the program OPTIPRIM). The microsatellites may be  
 CC used to identify individuals, for parentage testing, and in the genetic  
 CC mapping of economic trait loci, or genes involved in the determination of  
 CC economically important traits esp. in cattle, to allow selective  
 CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN  
 CC field.)  
 XX  
 SQ Sequence 17 BP; 0 A; 0 C; 8 G; 9 T; 0 U; 0 Other;

Query Match 1.6%; Score 17; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGT 1809  
DB 1 TGTGTGTGTGTGTGTGT 17

RESULT 184  
AAX56865  
ID AAX56865 standard; DNA; 17 BP.  
XX AC AAX56865;  
XX DT 16-JUL-1999 (first entry)  
XX DE W09513834 oligonucleoside 10.  
XX KW Oligonucleoside, RNaseH-mediated cleavage; target; RNaseH; inhibitor;  
XX KW internucleoside linkage; antisense; diagnosis; treatment; disease;  
XX KW binding affinity; Ka; nuclease resistance; ss.  
XX OS Synthetic.  
XX PN W09513834-A1.  
XX PD 26-MAY-1995.  
XX PF 16-NOV-1994; 94WO-US013387.  
XX PR 16-NOV-1993; 93US-00154013.  
XX PR 16-NOV-1993; 93US-00154014.  
XX PR 26-APR-1994; 94US-00233778.  
XX PR 04-MAY-1994; 94US-00238177.  
XX PA (GENT-) GENTA INC.  
XX PI Arnold LJ, Reynolds MA, Giachetti C;  
XX DR WPI; 1995-254769/33.  
XX PT New oligo: nucleotide(s) causing cleavage of target RNA - with RNaseH  
XX PT activated segment having charged inter-nucleoside links and second  
XX PT segment with chirally selected links.  
XX PS Disclosure; Page 137; 165pp; English.  
XX CC This invention describes novel oligonucleosides that causes RNaseH-  
XX CC mediated cleavage of target RNA comprising (a) an RNaseH-activating  
XX CC region (R1) of at least 3 consecutive 2'-unsubstituted nucleosides  
XX CC connected by charged internucleoside links and (b) a non-RNase activating  
XX CC region (R2) of at least 2 nucleosides, with at least one chirally  
XX CC selected internucleoside link. The oligonucleosides of the invention have  
XX CC base sequences complementary to that of target RNA. The products of the  
XX CC invention are used to inhibit transcription of target RNA in a cell or  
XX CC organism, they are antisense molecules that also activate RNaseH.  
XX CC Particularly the oligonucleosides are used in diagnosis and treatment of  
XX CC disease associated with endogenous or foreign gene expression. Use  
XX CC against human papilloma virus is exemplified. The modified  
XX CC internucleoside links improve target specificity, potency and binding  
XX CC affinity (Ka) compared with racemic analogues. They are also more  
XX CC resistant to nuclease and so have better in-vivo lifetimes. The chirally  
XX CC selected linkages in R2 allow control of binding affinity. AAX56855-  
XX CC X56881 represent oligonucleosides used in the method of the invention  
XX SQ Sequence 17 BP; 1 A; 0 C; 8 G; 8 T; 0 U; 0 Other;

Query Match 1.6%; Score 17; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1798 GTGTGTGTGTGTGTGTGT 1814  
DB 1 GTGTGTGTGTGTGTGT 17

RESULT 185  
AAT6099/C  
ID AAT6099 standard; DNA; 17 BP.  
XX AC AAT6099;  
XX DT 25-MAR-2003 (revised)  
XX DT 18-JUN-1997 (first entry)  
XX DE Repeat sequence found in the angiogenin gene.  
XX KW Polymorphism; repeat sequence; genetic marker; primer; amplification;  
XX KW PCR; polymerase chain reaction; paternity; maternity; human; pedigree;  
XX KW linkage analysis; genetic disease; animal; plant; breeding; locus;  
XX KW hybridisation; chromosome; ds.  
XX OS Homo sapiens.  
XX PN US5582979-A.  
XX PD 10-DEC-1996.  
XX PF 04-APR-1994; 94US-00222177.  
XX PR 21-APR-1989; 89US-00341562.  
XX PR 05-SEP-1991; 91US-00754351.  
XX PA (MARS-) MARSHFIELD CLINIC.  
XX PI Weber JL;  
XX DR WPI; 1997-042299/04.  
XX PT Detection of polymorphic genetic markers of the form (dC-da)n(dG-dT)n -  
XX PT using novel nucleic acid mols. as primers.  
XX PS Example 9; Col 61-62; 186pp; English.  
XX CC The invention relates to the isolation of polymorphic repeat sequences  
XX CC having the sequence (dC-da)n.(dG-dT)n which can be used as genetic  
XX CC markers. Primers based on these sequences can be used to detect these  
XX CC repeats, especially for use in e.g paternity or maternity testing, human  
XX CC genetic analysis such as linkage analysis of genetic disease, commercial  
XX CC animal or plant breeding or pedigree analysis. The sequences AAT6084-  
XX CC T66107 represent repeat sequences of low informativeness found in  
XX CC specific human genes. This repeat sequence is found in the angiogenin  
XX CC gene located at chromosomal position 14q11-q13. The sequence is amplified  
XX CC by primers AAT66100-1. (Updated on 25-MAR-2003 to correct PF field.)  
XX SQ Sequence 17 BP; 9 A; 8 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.6%; Score 17; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGT 1809  
DB 17 TGTGTGTGTGTGTGTGT 1

RESULT 186  
AAX91062  
ID AAX91062 standard; DNA; 17 BP.  
XX AC AAX91062;  
XX DT 15-NOV-1999 (first entry)

XX DE Methylphosphonate oligomer 2517-1.  
XX KW Phosphonate internucleosidyl linkage; chirality; hybridization; racemic;  
XX KW binding affinity; ss.

OS Synthetic.

PN US5955597-A.

XX

PD 21-SEP-1999.

XX

XX 30-JUN-1997; 97US-00885126.

XX

XX 16-NOV-1993; 93US-00154013.

PR 21-NOV-1994; 94US-00343018.

XX

XX (GENT-) GENTA INC.

XX

XX Schwartz DA, Vaghefi MM, Riley TA, Arnold LJ, Reynolds MA;

XX WPI; 1999-539600/45.

XX

XX Oligomers made using chirally pure nucleoside dimers, trimers, or

XX tetramers with enhanced binding affinities.

XX

XX Example 19; Col 39-40; 30pp; English.

XX

XX The invention provides methods for preparing oligomers having phosphonate

XX internucleosidyl linkages of a preselected chirality which hybridize to a

XX target RNA sequence. The method of making comprises: (a) synthesizing a

XX nucleoside dimer, trimer, or tetramer with racemic internucleosidyl

XX phosphonate linkages; (b) purifying the racemic nucleoside to a chirally

XX pure nucleoside; and (c) sequentially linking at least 2 of the chirally

XX pure nucleosides to form a synthetic oligomer that is enriched for

XX phosphonate internucleosidyl linkages of a preselected chirality and is

XX complementary to an RNA target sequence. The methods are useful for

XX providing chirally enriched synthetic oligomers. Rp chirally enriched

XX synthetic oligomers have enhanced binding affinities for RNA compared to

XX oligomers with racemic all methylphosphonate internucleosidyl linkages.

XX Sequences MAX91054-75 represent oligomers chemically synthesised using

XX the method of the invention

XX

XX Sequence 17 BP; 1 A; 0 C; 8 G; 8 T; 0 U; 0 Other;

XX

Query Match 1.6%; Score 17; DB 1; Length 17;

Best Local Similarity 100.0%; Pred.No. 1.2e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1798 GTGTGTGTGTGTGTGTGA 1814

DB 1 GTGTGTGTGTGTGTGTGA 17

RESULT 187

AAAD17594

ID ADAD17594 standard; DNA; 17 BP.

XX

AC ADAD17594;

XX

XX 10-DEC-2001 (first entry)

XX

XX 5' variation generator oligonucleotide PCR primer #9.

XX

XX Genomic DNA analysis; 5' variation generator; 3' fragment generator;

XX endangered animal identification; PCR primer; ss.

XX Unidentified.

XX

XX EF1130114-Al.

XX

XX 05-SEP-2001.

XX

XX 03-MAR-2000; 2000EP-00200757.

XX

XX 03-MAR-2000; 2000EP-00200757.

XX

XX (VHAE-) VAN HAERINGEN LAB BV.

XX

XX The invention relates to the isolation of 6327 nucleotide sequences, CC  
CC fragments of at least 15 consecutive nucleotides of these nucleotides, a CC  
CC sequence having at least 80% identity, after optimal alignment, with the CC  
CC nucleotides, a sequence that hybridizes under stringent conditions with CC  
CC the nucleotides, or the complement, or corresponding RNA, of the CC  
CC nucleotides. The nucleotides are used as probes or primers for detecting, CC  
CC identifying, quantifying and/or amplifying nucleic acids, as in vitro CC  
CC sense and antisense sequences, of nucleotides involved in tumour CC  
CC suppression or reversion, apoptosis and or viral resistance, to produce CC  
CC recombinant polypeptides, and to prepare transgenic animals, as CC  
CC experimental models. The nucleotides (also vectors containing them and CC  
CC cells containing the vectors), the encoded polypeptides and antibodies CC  
CC (Ab) against the polypeptide are useful for prevention and/or treatment CC  
CC of viral infections or diseases characterized by development of tumours CC  
CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia). CC  
CC Analysis of the expression of the nucleotides can be used for diagnosis CC  
CC and/or prognosis of these diseases. The nucleotides and polypeptides can CC  
CC also be used to screen for their specific interactive molecules, CC  
CC potentially useful for treating diseases associated with abnormal CC  
CC expression of the nucleotides. CC  
SQ Sequence 17 BP; 3 A; 4 C; 2 G; 8 T; 0 U; 0 Other;

Query Match 1.6%; Score 17; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2141 GATCAGTTTTTCACT 2157  
DB 1 GATCAGTTTTTCACT 17

RESULT 189  
AAAX77487/C  
ID AAAX77487 standard; DNA; 18 BP.  
AC AAAX77487;  
XX  
XX 05-AUG-1999 (first entry)  
XX US912147 primer 31.  
XX  
XX Primer; quantitation; genetic instability; tumour cell; detection;  
XX neoplastic transformation; carcinogenesis; ss.  
XX Synthetic.  
XX US912147-A.  
XX  
XX 15-JUN-1999.  
XX  
XX 22-OCT-1996; 96US-00734973.  
XX  
XX 22-OCT-1996; 96US-00734973.  
XX (HEAL-) HEALTH RES INC.  
XX  
XX Anderson G, Stoler D, Basik M;  
XX WPI; 1999-357197/30.  
XX  
XX Quantitating genetic instability.  
XX  
XX Claim 4; Col 29-30; 27pp; English.  
XX  
XX This invention describes a novel method for quantitating genetic CC  
XX instability independent of microsatellite alterations by treating a CC  
XX comparison pair comprising genomic DNA from tumour cells and genomic DNA CC  
XX from normal cells. The method involves the cells from the same individual CC  
XX with oligonucleotide primers selected from (i) a nucleotide sequence CC  
XX (CG)XRG, where R is a purine selected from adenine and guanine and x = 3- CC  
XX 7, (ii) a nucleotide sequence (CG)XRY, where R is as in (i) and Y is a CC

CC pyrimidine selected from cytosine, thymine, and uracil and x = 3-7, (iii) CC  
CC a nucleotide sequence (CG)XRR, where R is as in (i) and x = 3-7, (iv) a CC  
CC nucleotide sequence (CG)XY, where Y is a pyrimidine selected from CC  
CC cytosine, thymine, and uracil and x = 3-7, (v) a nucleotide sequence CC  
CC (CA)XRG, where R is a purine selected from adenine and guanine and x = 6- CC  
CC 16, (vi) a nucleotide sequence (CA)XRY, where R is a purine selected from CC  
CC adenine and guanine and Y is a pyrimidine selected from cytosine, CC  
CC thymine, and uracil, and x = 6-16, (vii) a nucleotide sequence (CA)XRR, CC  
CC where R is a purine selected from adenine and guanine and x = 6-16, CC  
CC (viii) a nucleotide sequence (CA)XY, where Y is a pyrimidine selected CC  
CC from cytosine, thymine, and uracil and x = 6-16, and (ix) a combination CC  
CC of the primers. The method is useful for detecting genomic instability CC  
CC which are commonly associated with the various stages of neoplastic CC  
CC transformation and carcinogenesis. The method is rapid and simple CC  
SQ Sequence 18 BP; 8 A; 9 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 1.6%; Score 17; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1794 GTGTGTGTGTGTGTGTG 1810  
DB 17 GTGTGTGTGTGTGTGTG 1

RESULT 190  
AAAX77486/C  
ID AAAX77486 standard; DNA; 18 BP.  
AC AAAX77486;  
XX  
XX 05-AUG-1999 (first entry)  
XX US912147 primer 30.  
XX  
XX Primer; quantitation; genetic instability; tumour cell; detection;  
XX neoplastic transformation; carcinogenesis; ss.  
XX Synthetic.  
XX US912147-A.  
XX  
XX 15-JUN-1999.  
XX  
XX 22-OCT-1996; 96US-00734973.  
XX  
XX 22-OCT-1996; 96US-00734973.  
XX (HEAL-) HEALTH RES INC.  
XX  
XX Anderson G, Stoler D, Basik M;  
XX WPI; 1999-357197/30.  
XX  
XX Quantitating genetic instability.  
XX  
XX Claim 4; Col 29-30; 27pp; English.  
XX  
XX This invention describes a novel method for quantitating genetic CC  
XX instability independent of microsatellite alterations by treating a CC  
XX comparison pair comprising genomic DNA from tumour cells and genomic DNA CC  
XX from normal cells. The method involves the cells from the same individual CC  
XX with oligonucleotide primers selected from (i) a nucleotide sequence CC  
XX (CG)XRG, where R is a purine selected from adenine and guanine and x = 3- CC  
XX 7, (ii) a nucleotide sequence (CG)XRY, where R is as in (i) and Y is a CC  
XX pyrimidine selected from cytosine, thymine, and uracil and x = 3-7, (iii) CC  
XX a nucleotide sequence (CG)XRR, where R is as in (i) and x = 3-7, (iv) a CC  
XX nucleotide sequence (CG)XY, where Y is a pyrimidine selected from CC  
XX cytosine, thymine, and uracil and x = 3-7, (v) a nucleotide sequence CC  
XX (CA)XRG, where R is a purine selected from adenine and guanine and x = 6- CC  
XX 16, (vi) a nucleotide sequence (CA)XRY, where R is a purine selected from CC  
XX adenine and guanine and Y is a pyrimidine selected from cytosine, CC

```
XX      Sequence 18 BP; 10 A; 8 C; 0 G; 0 T; 0 U; 0 Other;
SQ
Query Watch          1.6%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1792 TTGCTGTGTGTGTGTG 1808
           |||||
```

RESULT 192.

ID AAX77459 standard; DNA; 18 B  
XX  
AC AAX77459;

XX	US5912147 primer 3.
DE	
XX	Primer; quantitation; genetic instability; tumour cell; detection;
KW	neoplastic transformation; carcinogenesis; ss.
XX	
OS	Synthetic.
XX	
PN	US5912147-A.

PD 15-JUN-1999.  
XX

XX

XX



XXXXXX

**XXXXXXXXXXXX**

XXXXXX  
-----  
XXXXXXXX

2004

CC instability independent

CC comparison from normal cells. The method inv

(CG) xRG, where R is a purine sele

pyrimidine selected from cytosine

```

a nucleotide sequence (CA)XY, where Y is a pyrimidine selected from
CC cytosine, thymine, and uracil and x = 3-7, (v) a nucleotide sequence
CC (CA)XRG, where R is a purine selected from adenine and guanine and x = 6-
CC 16, (vi) a nucleotide sequence (CA)XRY, where R is a purine selected from
CC adenine and guanine and Y is a pyrimidine selected from cytosine,
CC thymine, and uracil, and x = 6-16, (vii) a nucleotide sequence (CA)XRR,
CC where R is a purine selected from adenine and guanine and x = 6-16,
CC (viii) a nucleotide sequence (CA)XY, where Y is a pyrimidine selected
CC from cytosine, thymine, and uracil and x = 6-16, and (ix) a combination
CC of the primers. The method is useful for detecting genomic instability
CC which are commonly associated with the various stages of neoplastic
CC transformation and carcinogenesis. The method is rapid and simple
XX
SQ Sequence 18 BP; 9 A; 9 C; 0 G; 0 T; 0 U; 0 Other;
Query March 1.6k; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Prad. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```



QY 1792 TTGTGTGTGTGTGTGTG 1808  
DB 17 TTGTGTGTGTGTGTGTG 1

RESULT 193  
AAAX77488/c  
ID AAX77488 standard; DNA; 18 BP.

XX AC AAX77488;  
XX DT 05-AUG-1999. (first entry)  
XX DE US5912147 primer 32.  
XX KW Primer; quantitation; genetic instability; tumour cell; detection;  
XX KW neoplastic transformation; carcinogenesis; DNA/RNA hybrid; ss.  
XX OS Synthetic.

XX FH Key Location/Qualifiers  
FT misc\_RNA 18  
FT /\*tag= a  
FT /note= "uracil"

XX PN US5912147-A.  
XX PD 15-JUN-1999.  
XX PF 22-OCT-1996; 96US-00734973.  
XX PR 22-OCT-1996; 96US-00734973.  
XX PA (HEAL-) HEALTH RES INC.  
XX PI Anderson G, Stoler D, Basik M;  
XX WPI; 1999-357197/30.  
XX PT Quantitating genetic instability.  
XX PS Claim 4; Col 29-30; 27pp; English.

XX CC This invention describes a novel method for quantitating genetic  
XX CC instability independent of microsatellite alterations by treating a  
XX CC comparison pair comprising genomic DNA from tumour cells and genomic DNA  
XX CC from normal cells. The method involves the cells from the same individual  
XX CC with oligonucleotide primers selected from (i) a nucleotide sequence  
XX CC (CG)XRG where R is a purine selected from adenine and guanine and x = 3-  
XX CC 7, (ii) a nucleotide sequence (CG)XRY, where R is as in (i) and Y is a  
XX CC pyrimidine selected from cytosine, thymine, and uracil and x = 3-7, (iii)  
XX CC a nucleotide sequence (CG)XRR, where R is as in (i) and x = 3-7, (iv) a  
XX CC nucleotide sequence (CG)XY, where Y is a pyrimidine selected from  
XX CC cytosine, thymine, and uracil and x = 3-7, (v) a nucleotide sequence  
XX CC (CA)XRG, where R is a purine selected from adenine and guanine and x = 6-  
XX CC 16, (vi) a nucleotide sequence (CA)XRY, where R is a purine selected from  
XX CC adenine and guanine and Y is a pyrimidine selected from cytosine,  
XX CC thymine, and uracil, and x = 6-16, (vii) a nucleotide sequence (CA)XRR,  
XX CC where R is a purine selected from adenine and guanine and x = 6-16,  
XX CC (viii) a nucleotide sequence (CA)XY, where Y is a pyrimidine selected  
XX CC from cytosine, thymine, and uracil and x = 6-16, and (ix) a combination  
XX CC of the primers. The method is useful for detecting genomic instability  
XX CC which are commonly associated with the various stages of neoplastic  
XX CC transformation and carcinogenesis. The method is rapid and simple

XX SQ Sequence 18 BP; 8 A; 9 C; 0 G; 0 T; 1 U; 0 Other;  
Query Match 1.6%; Score 17; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTG 1810  
DB 17 TTGTGTGTGTGTGTGTG 1

DB 17 GTGTGTGTGTGTGTGTG 1

RESULT 194  
AAAX77457/c  
ID AAX77457 standard; DNA; 18 BP.

XX AC AAX77457;  
XX DT 05-AUG-1999 (first entry)  
XX DE US5912147 primer 1.  
XX KW Primer; quantitation; genetic instability; tumour cell; detection;  
XX KW neoplastic transformation; carcinogenesis; ss.  
XX OS Synthetic.

XX PN US5912147-A.  
XX PD 15-JUN-1999.  
XX PF 22-OCT-1996; 96US-00734973.  
XX PR 22-OCT-1996; 96US-00734973.  
XX PA (HEAL-) HEALTH RES INC.  
XX PI Anderson G, Stoler D, Basik M;  
XX WPI; 1999-357197/30.  
XX PT Quantitating genetic instability.  
XX PS Claim 4; Col 15-16; 27pp; English.

XX CC This invention describes a novel method for quantitating genetic  
XX CC instability independent of microsatellite alterations by treating a  
XX CC comparison pair comprising genomic DNA from tumour cells and genomic DNA  
XX CC from normal cells. The method involves the cells from the same individual  
XX CC with oligonucleotide primers selected from (i) a nucleotide sequence  
XX CC (CG)XRG, where R is a purine selected from adenine and guanine and x = 3-  
XX CC 7, (ii) a nucleotide sequence (CG)XRY, where R is as in (i) and Y is a  
XX CC pyrimidine selected from cytosine, thymine, and uracil and x = 3-7, (iii)  
XX CC a nucleotide sequence (CG)XRR, where R is as in (i) and x = 3-7, (iv) a  
XX CC nucleotide sequence (CG)XY, where Y is a pyrimidine selected from  
XX CC cytosine, thymine, and uracil and x = 3-7, (v) a nucleotide sequence  
XX CC (CA)XRG, where R is a purine selected from adenine and guanine and x = 6-  
XX CC 16, (vi) a nucleotide sequence (CA)XRY, where R is a purine selected from  
XX CC adenine and guanine and Y is a pyrimidine selected from cytosine,  
XX CC thymine, and uracil, and x = 6-16, (vii) a nucleotide sequence (CA)XRR,  
XX CC where R is a purine selected from adenine and guanine and x = 6-16,  
XX CC (viii) a nucleotide sequence (CA)XY, where Y is a pyrimidine selected  
XX CC from cytosine, thymine, and uracil and x = 6-16, and (ix) a combination  
XX CC of the primers. The method is useful for detecting genomic instability  
XX CC which are commonly associated with the various stages of neoplastic  
XX CC transformation and carcinogenesis. The method is rapid and simple

XX SQ Sequence 18 BP; 9 A; 8 C; 1 G; 0 T; 0 U; 0 Other;  
Query Match 1.6%; Score 17; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1792 TTGTGTGTGTGTGTGTG 1808  
DB 17 TTGTGTGTGTGTGTGTG 1

RESULT 195  
AAQ75581  
ID AAQ75581 standard; DNA; 20 BP.

AC AAQ75581;  
 XX 04-AUG-1995 (first entry)  
 DT  
 XX Reverse transcription primer used in cDNA analysis technique.  
 DE  
 XX Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.  
 XX Synthetic.  
 OS  
 XX JP06303997-A.  
 PN  
 XX 01-NOV-1994.  
 PD  
 XX 16-APR-1993; 93JP-00112515.  
 PF  
 XX 16-APR-1993; 93JP-00112515.  
 PR  
 XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 PA  
 XX WPI; 1995-018287/03.  
 XX  
 XX Analysis of cDNA and gene expression - by amplification of mRNA followed  
 PT by digestion with restriction enzymes.  
 XX  
 XX Disclosure; Page 5; 11pp; Japanese.  
 PS  
 XX A method for the analysis of cDNA comprises (a) preparing an aggregate of  
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
 CC and using the aggregate of mRNAs as the template for each reverse  
 CC transcription primer; (b) digesting each of the prepared aggregates of  
 CC the double-stranded cDNAs with restriction enzyme and; (c)  
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
 CC method can be used to analyse gene expression rapidly and easily  
 XX  
 XX Sequence 20 BP; 2 A; 0 C; 0 G; 18 T; 0 U; 0 Other;  
 SQ  
 Query Match 1.6%; Score 16.8; DB 1; Length 20;  
 Best Local Similarity 90.0%; Pred. No. 1.4e+02;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1865 TTTTATTTTGTGTTTAAAT 1864  
 DB 1 TTTTATTTTGTGTTTAAAT 20  
 RESULT 196  
 ID AAA73096 standard; DNA; 20 BP.  
 XX  
 XX AAA73096;  
 AC  
 XX 24-NOV-2000 (first entry)  
 DT  
 XX Human MC1R gene related TATA box oligonucleotide SEQ ID NO:15.  
 DE  
 XX Human; melanocortin-1 receptor; MC1R; promoter; regulation; detection;  
 KW melanin; ds.  
 XX  
 XX Homo sapiens.  
 OS  
 XX JP2000166563-A.  
 PN  
 XX 20-JUN-2000.  
 PD  
 XX 04-DEC-1998; 98JP-00345881.  
 PF  
 XX 04-DEC-1998; 98JP-00345881.  
 PR  
 XX (SHIS ) SHISEIDO CO LTD.  
 PA  
 XX WPI; 2000-485552/43.  
 XX  
 XX Upstream controlling sequence of melanocortin1 receptor and its  
 PT application.  
 XX  
 XX Disclosure; Page 4; 21pp; Japanese.  
 PS  
 XX The present invention describes a control-active polynucleotide derived  
 CC from the human melanocortin-1 receptor (MC1R) gene upstream controlling  
 CC sequence. Also described is a method for detecting a substance affecting  
 CC synthesis of melanin in which a host transformed by an expression vector,  
 CC comprising a control active polynucleotide derived from MC1R, is cultured  
 CC in the presence of a sample to be tested and a signal formed by the  
 CC expression of said reporter gene is detected. The control-active  
 CC polynucleotide is used for the detection of a substance affecting  
 CC expression of said reporter gene is detected. The control-active  
 CC polynucleotide is used for the detection of a substance affecting  
 CC synthesis of melanin. The present sequence represents a human  
 CC melanocortin-1 receptor gene TATA box oligonucleotide, which is given in  
 CC the exemplification of the present invention

DR WPI; 2000-485552/43.  
 XX Upstream controlling sequence of melanocortin1 receptor and its  
 PT application.  
 XX  
 XX Disclosure; Page 4; 21pp; Japanese.  
 PS  
 XX The present invention describes a control-active polynucleotide derived  
 CC from the human melanocortin-1 receptor (MC1R) gene upstream controlling  
 CC sequence. Also described is a method for detecting a substance affecting  
 CC synthesis of melanin in which a host transformed by an expression vector,  
 CC comprising a control active polynucleotide derived from MC1R, is cultured  
 CC in the presence of a sample to be tested and a signal formed by the  
 CC expression of said reporter gene is detected. The control-active  
 CC polynucleotide is used for the detection of a substance affecting  
 CC expression of said reporter gene is detected. The control-active  
 CC polynucleotide is used for the detection of a substance affecting  
 CC synthesis of melanin. The present sequence represents a human  
 CC melanocortin-1 receptor gene TATA box oligonucleotide, which is given in  
 CC the exemplification of the present invention  
 XX  
 XX Sequence 20 BP; 10 A; 0 C; 0 G; 10 T; 0 U; 0 Other;  
 SQ  
 Query Match 1.6%; Score 16.8; DB 1; Length 20;  
 Best Local Similarity 90.0%; Pred. No. 1.4e+02;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1811 TGTATATATATATATATGTA 1830  
 DB 1 TATATATATATATATATATA 20  
 RESULT 197  
 ID AAA73096 standard; DNA; 20 BP.  
 XX  
 XX AAA73096;  
 AC  
 XX 24-NOV-2000 (first entry)  
 DT  
 XX Human MC1R gene related TATA box oligonucleotide SEQ ID NO:15.  
 DE  
 XX Human; melanocortin-1 receptor; MC1R; promoter; regulation; detection;  
 KW melanin; ds.  
 XX  
 XX Homo sapiens.  
 OS  
 XX JP2000166563-A.  
 PN  
 XX 20-JUN-2000.  
 PD  
 XX 04-DEC-1998; 98JP-00345881.  
 PF  
 XX 04-DEC-1998; 98JP-00345881.  
 PR  
 XX (SHIS ) SHISEIDO CO LTD.  
 PA  
 XX WPI; 2000-485552/43.  
 XX  
 XX Upstream controlling sequence of melanocortin1 receptor and its  
 PT application.  
 XX  
 XX Disclosure; Page 4; 21pp; Japanese.  
 PS  
 XX The present invention describes a control-active polynucleotide derived  
 CC from the human melanocortin-1 receptor (MC1R) gene upstream controlling  
 CC sequence. Also described is a method for detecting a substance affecting  
 CC synthesis of melanin in which a host transformed by an expression vector,  
 CC comprising a control active polynucleotide derived from MC1R, is cultured  
 CC in the presence of a sample to be tested and a signal formed by the  
 CC expression of said reporter gene is detected. The control-active  
 CC polynucleotide is used for the detection of a substance affecting  
 CC expression of said reporter gene is detected. The control-active  
 CC polynucleotide is used for the detection of a substance affecting  
 CC synthesis of melanin. The present sequence represents a human  
 CC melanocortin-1 receptor gene TATA box oligonucleotide, which is given in  
 CC the exemplification of the present invention

XX Sequence 20 BP; 10 A; 0 C; 0 G; 10 T; 0 U; 0 Other;  
SQ  
Query Match 1.6%; Score 16.8; DB 1; Length 20;  
Best Local Similarity 90.0%; Pred. No. 1.4e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1811 TGTATATATATATATATGTA 1830  
DB 20 TATATATATATATATATATA 1  
RESULT 198  
AAL50667  
ID AAL50667 standard; DNA; 20 BP.  
XX  
AC AAL50667;  
XX  
DT 16-JAN-2003 (first entry)  
XX  
DE Human uridine diphosphate glucuronosyltransferase gene polymorphism #1.  
XX  
KW Human; polymorphism; TA repeat; ds; UGT; thymidine-adenine repeat;  
KW uridine diphosphate glucuronosyltransferase gene promoter; UGT1A1;  
KW drug dosage optimisation; xenobiotic sensitivity.  
XX  
OS Homo sapiens.  
XX  
PN US2002115097-A1.  
XX  
PD 22-AUG-2002.  
XX  
PF 01-FEB-2002; 2002US-00061693.  
XX  
PR 16-FEB-1999; 99US-00251274.  
XX  
PA (ARCH-) ARCH DEV CORP.  
XX  
PI Rienzo AD, Iyer L, Ratain MJ;  
XX  
DR WPI; 2002-740095/80.  
XX  
PT Detecting polymorphisms in uridine diphosphate glucuronosyltransferase  
PT gene promoter, useful for optimizing drug dosages for a patient, involves  
PT determining number of thymidine-adenine repeats in the promoter.  
XX  
PS Claim 8; Page 9; 13pp; English.  
XX  
CC The invention comprises a method for detecting polymorphisms in a uridine  
CC diphosphate glucuronosyltransferase (UGT) gene promoter (preferably  
CC UGT1A1). The method involves determining the number of thymidine-adenine  
CC (TA) repeats in the promoter - as the number of TA repeats correlates  
CC with expression of the UGT gene. The method of the invention is useful  
CC for detecting polymorphisms in a UGT gene promoter. The method of the  
CC invention is also useful in optimising drug dosages and predicting an  
CC individual's sensitivity to xenobiotics for drugs and xenobiotics that  
CC are glucuronidated by UGT. The present DNA sequence represents a UGT gene  
CC TA repeat polymorphism  
XX  
SQ Sequence 20 BP; 10 A; 0 C; 0 G; 10 T; 0 U; 0 Other;  
Query Match 1.6%; Score 16.8; DB 1; Length 20;  
Best Local Similarity 90.0%; Pred. No. 1.4e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1811 TGTATATATATATATATGTA 1830  
DB 1 TATATATATATATATATATA 20  
RESULT 199  
AAL50667/c  
ID AAL50667 standard; DNA; 20 BP.

XX AAL50667;  
XX  
DT 16-JAN-2003 (first entry)  
XX  
DE Human uridine diphosphate glucuronosyltransferase gene polymorphism #1.  
XX  
KW Human; polymorphism; TA repeat; ds; UGT; thymidine-adenine repeat;  
KW uridine diphosphate glucuronosyltransferase gene promoter; UGT1A1;  
KW drug dosage optimisation; xenobiotic sensitivity.  
XX  
OS Homo sapiens.  
XX  
PN US2002115097-A1.  
XX  
PD 22-AUG-2002.  
XX  
PF 01-FEB-2002; 2002US-00061693.  
XX  
PR 16-FEB-1999; 99US-00251274.  
XX  
PA (ARCH-) ARCH DEV CORP.  
XX  
PI Rienzo AD, Iyer L, Ratain MJ;  
XX  
DR WPI; 2002-740095/80.  
XX  
PT Detecting polymorphisms in uridine diphosphate glucuronosyltransferase  
PT gene promoter, useful for optimizing drug dosages for a patient, involves  
PT determining number of thymidine-adenine repeats in the promoter.  
XX  
PS Claim 8; Page 9; 13pp; English.  
XX  
CC The invention comprises a method for detecting polymorphisms in a uridine  
CC diphosphate glucuronosyltransferase (UGT) gene promoter (preferably  
CC UGT1A1). The method involves determining the number of thymidine-adenine  
CC (TA) repeats in the promoter - as the number of TA repeats correlates  
CC with expression of the UGT gene. The method of the invention is useful  
CC for detecting polymorphisms in a UGT gene promoter. The method of the  
CC invention is also useful in optimising drug dosages and predicting an  
CC individual's sensitivity to xenobiotics for drugs and xenobiotics that  
CC are glucuronidated by UGT. The present DNA sequence represents a UGT gene  
CC TA repeat polymorphism  
XX  
SQ Sequence 20 BP; 10 A; 0 C; 0 G; 10 T; 0 U; 0 Other;  
Query Match 1.6%; Score 16.8; DB 1; Length 20;  
Best Local Similarity 90.0%; Pred. No. 1.4e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1811 TGTATATATATATATATGTA 1830  
DB 20 TATATATATATATATATATA 1  
RESULT 200  
ABZ91716  
ID ABZ91716 standard; DNA; 20 BP.  
XX  
AC ABZ91716;  
XX  
DT 17-OCT-2003 (first entry)  
XX  
DE Human oligonucleotide sequence.  
XX  
KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
KW antiasthmatic; hypotensive; immunosuppressive; cytosatic; gene therapy;  
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
KW lung inflammation; respiratory disease; ds.  
XX  
OS Homo sapiens.



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FT /mod_base= OTHER
FT /note= "OTHER= phosphorothioate backbone, where 1-5 and
FT 16-20 are 2' methoxyethyl nucleotides. All cytidines are
FT 5-methylcytidines"
XX
XX WO2003053340-A2.
XX
XX 03-JUL-2003.
XX
XX 09-DEC-2002; 2002WO-US038618.
XX
XX 10-DEC-2001; 2001US-00006191.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Gaarde WA, Watt AT;
XX WPI; 2003-559091/52.
XX
XX New antisense oligonucleotides for modulating connective tissue growth
XX factor expression, particularly useful for treating cancers (e.g. breast
XX or prostate cancer), pulmonary or renal fibrosis, scleroderma or
XX atherosclerosis.
XX
XX Claim 3; Page 89; 139pp; English.
XX
XX This invention relates to novel methods for modulating the expression of
XX connective tissue growth factor (CTGF) by antisense oligonucleotides.
XX CTGF has been mapped to human chromosome region 6q23.1, and is also known
XX as ctgfact, fibroblast inducible secreted protein, fisp-12, NOV2,
XX insulin-like growth factor binding protein-related protein 2, IGFBP-rp2,
XX IGFBP-8, Hcs24 and ecogenin. It is known to stimulate DNA synthesis and
XX promote chemotaxis of fibroblasts, however, it is also upregulated in
XX acute lymphoblastic leukemia and in tumour or endothelial cells
XX associated with the vasculature. Accordingly, antisense oligonucleotides
XX that inhibit the expression of CTGF in cells or tissues can be used in
XX gene therapy to treat various conditions including hyperproliferative
XX disorders (particularly cancer, e.g. breast, prostate or renal cancer),
XX pulmonary fibrosis, renal fibrosis, scleroderma and atherosclerosis. As
XX such, the present invention describes these antisense oligos as having
XX cytostatic, dermatological and antiarteriosclerotic activities. This
XX oligonucleotide sequence is a chimeric phosphorothioate antisense oligo
XX with 2' MOE wings and a deoxy gap, which is used to inhibit expression of
XX mouse CTGF of the invention.
XX
XX Sequence 20 BP; 7 A; 3 C; 5 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 1.6%; Score 16.8; DB 1; Length 20;
XX Best Local Similarity 90.0%; Pred. No. 1.4e+02;
XX Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1675 ATTCTGATTCGATGACACT 1694
XX |||||
XX DB 20 ATTCTGATTCGATGACACT 1
XX
XX RESULT 203
XX AAQ75729
XX ID AAQ75729 standard; DNA; 21 BP.
XX
XX AC AAQ75729;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
XX
XX
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PD 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
XX Disclosure; Page 8; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
XX Sequence 21 BP; 2 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
XX
XX Query Match 1.6%; Score 16.8; DB 1; Length 21;
XX Best Local Similarity 90.0%; Pred. No. 1.4e+02;
XX Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1865 TTTTATTTTGTGTTTAAAT 1884
XX |||||
XX DB 1 TTTTATTTTGTGTTTAAAT 20
XX
XX RESULT 204
XX AAQ75730
XX ID AAQ75730 standard; DNA; 21 BP.
XX
XX AC AAQ75730;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
XX Disclosure; Page 8; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
```

CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
 CC method can be used to analyse gene expression rapidly and easily  
 XX  
 SQ Sequence 21 BP; 2 A; 1 C; 0 G; 18 T; 0 U; 0 Other;  
 Query Match 1.6%; Score 16.8; DB 1; Length 21;  
 Best Local Similarity 90.0%; Pred. No. 1.4e+02;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1865 TTTTATTTTGTGTTTAAAT 1884  
 DB 1 TTTTATTTTGTGTTTAAAT 20  
 RESULT 205  
 AAQ75728  
 ID AAQ75728 standard; DNA; 21 BP.  
 AC  
 XX AAQ75728;  
 DT 04-AUG-1995 (first entry)  
 XX  
 DE Reverse transcription primer used in cDNA analysis technique.  
 XX  
 KW Analysis; gene expression; reverse transcription; primer; cDNA;  
 aggregate; restriction enzyme; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN JF06303997-A.  
 XX  
 PD 01-NOV-1994.  
 XX  
 PF 16-APR-1993; 93JP-00112515.  
 XX  
 PR 16-APR-1993; 93JP-00112515.  
 XX  
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.  
 XX  
 DR WPI; 1995-018287/03.  
 XX  
 PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
 by digestion with restriction enzymes.  
 XX  
 PS Disclosure; Page 8; lipp; Japanese.  
 XX  
 CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
 double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
 labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
 and using the aggregate of mRNAs as the template for each reverse  
 transcription primer; (b) digesting each of the prepared aggregates of  
 the double-stranded cDNAs with restriction enzyme and; (c)  
 electrophoresing the digested aggregate of cDNAs in separate lanes. The  
 method can be used to analyse gene expression rapidly and easily  
 XX  
 SQ Sequence 21 BP; 3 A; 0 C; 0 G; 18 T; 0 U; 0 Other;  
 Query Match 1.6%; Score 16.8; DB 1; Length 21;  
 Best Local Similarity 90.0%; Pred. No. 1.4e+02;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1865 TTTTATTTTGTGTTTAAAT 1884  
 DB 1 TTTTATTTTGTGTTTAAAT 20  
 RESULT 206  
 AAZ60082/c  
 ID AAZ60082 standard; DNA; 21 BP.  
 XX  
 AC AAZ60082;  
 XX  
 DT 25-APR-2000 (first entry)

XX Reverse PCR primer -439/MIP-3beta used to amplify MIP-3beta ORF.  
 DE  
 XX Chemokine; PCR primer; macrophage inflammation protein 3beta;  
 dendritic cell; disease treatment; MIP-3beta; infection; cancer; allergy;  
 immune response initiation; autoimmune disease; tissue rejection; ss.  
 KW  
 XX Homo sapiens.  
 OS  
 XX EP974357-A1.  
 FN  
 XX 26-JAN-2000.  
 PD  
 XX 16-JUL-1998; 98EP-00401799.  
 PF  
 XX 16-JUL-1998; 98EP-00401799.  
 PR  
 XX (SCHE) SCHERING-PLOUGH.  
 PA  
 XX Caux C, Vanbervliet B, Lebecque S, Vicari A, Dieu M;  
 FI WPI; 2000-118300/11.  
 DR  
 XX  
 PT Use of chemokines capable of directing migration of dendritic cells.  
 PT useful for treating microbial infections, cancer and autoimmune diseases.  
 PT  
 PS Disclosure; Col 13; lipp; English.  
 XX  
 CC This sequence represents a PCR primer used to amplify the chemokine  
 macrophage inflammation protein 3 beta (MIP 3beta) coding sequence. The  
 PCR product is used in the analysis of dendritic cell response to  
 different chemokines. The invention relates to the use of chemokines  
 which are capable of directing dendritic cells, in the manufacture of a  
 medicament for the treatment of a disease state. Methods are included for  
 treating diseases by facilitating or inhibiting the migration or  
 activation of antigen-presenting dendritic cells. The chemokines can be  
 used to initiate, amplify or modulate an immune response. The chemokines  
 are useful for the treatment of disease states e.g. a bacterial, viral,  
 fungal or parasitic infection, cancer (especially melanoma, breast,  
 pancreatic, colon, lung, glioma, hepatocellular, endometrial, gastric,  
 intestinal, renal, prostate, thyroid, ovarian, testicular, liver, head  
 and neck, colorectal, oesophagus, stomach, eye, bladder, glioblastoma and  
 metastatic carcinomas), autoimmune disease, tissue rejection or an  
 allergy  
 XX  
 SQ Sequence 21 BP; 8 A; 11 C; 0 G; 2 T; 0 U; 0 Other;  
 Query Match 1.6%; Score 16.8; DB 1; Length 21;  
 Best Local Similarity 90.0%; Pred. No. 1.4e+02;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1794 GTGTGTGTGTGTGTGTGTGTGTGTGT 1813  
 DB 21 GTGTGTGTGTGTGTGTGTGTGTGTGT 2  
 RESULT 207  
 ABK47993/c  
 ID ABK47993 standard; DNA; 21 BP.  
 XX  
 AC ABK47993;  
 XX  
 DT 02-JUL-2002 (first entry)  
 XX  
 XX Human MIP-3 beta RT-PCR primer -439/MIP-3 beta.  
 DE  
 XX Human; chemokine; MCP-4; hMCP-4; ss; 6CKine; dendritic cell; renal;  
 autoimmune disease; tissue rejection; allergy; cancer; hepatocellular;  
 melanoma; breast; pancreas; colon; glioma; endometrium; intestine; lung;  
 prostate; thyroid; ovary; testis; liver; head; neck; colorectal; bladder;  
 oesophagus; stomach; eye; glioblastoma; gastric; metastatic carcinoma;  
 immunosuppressive; anti-allergic; cytostatic; rectum; RT-PCR; primer;  
 reverse transcriptase; macrophage inflammatory protein 3 beta;  
 KW

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XX 28-NOV-1994; 94US-00346456.
XX (DUPO ) DU PONT DE NEMOURS & CO E I.
XX PA
XX PI Morgante M, Vogel JM;
XX XX WPI; 1996-277795/28.
XX DR
XX PT Modified amplified fragment length polymorphism assay - for detection of
XX FT polymorphism esp. in micro:satellite regions.
XX PP
XX PS Disclosure; Fig 1c; 173pp; English.
XX CC Detecting polymorphisms between 2 nucleic acid samples, esp. in
XX CC microsatellite regions, comprises digesting the nucleic acid to generate
XX CC fragments, ligating adaptor segments to their ends, amplifying them using
XX CC primer directed amplification and comparing the prods. to detect
XX CC differences. The primers used in the amplification comprise a primer
XX CC consisting of a perfect cpd. simple sequence repeat (SSR), and an adaptor
XX CC directed primer, comprising a sequence complementary to an adaptor
XX CC segment. The present sequence is an example of a compound SSR primer. The
XX CC method represents a modified amplified fragment length polymorphism
XX CC assay, which is partic. useful for genome fingerprinting, i.e. for
XX CC genetic trait marking and germplasm comparisons
XX CC Sequence 24 BP; 12 A; 4 C; 0 G; 8 T; 0 U; 0 Other;
XX SQ
Query Match 1.6%; Score 16.8; DB 1; Length 24;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0
QY 1813 TATATATATATATGACCA 1832
DB 1 TATATATATATATACACA 20
RESULT 209
ADD69518
ID ADD69518 standard; DNA; 17 BP.
AC AC ADD69518;
XX DT 15-JAN-2004 (first entry)
XX DE
XX DE ISSR-related PCR primer 5.
XX KW inter-simple sequence repeat; ISSR; SSR; PCR; primer; genotyping; plant;
XX KW animal; Basmati rice; ss.
XX OS Unidentified.
XX XX WO2003085133-A2.
XX PD 16-OCT-2003.
XX PF 09-JAN-2003; 2003WO-IB000041.
XX XX 08-APR-2002; 2002IN-CH000260.
XX XX (DNAF-) CENT DNA FINGERPRINTING & DIAGNOSTICS.
XX PA Nagaraju JG;
XX PI WPI; 2003-804317/75.
XX DR
XX XX New set of inter-simple sequence repeats (ISSR)-PCR primers for
XX PT genotyping eukaryotes, useful for genotyping diverse genomes of plant and
XX PT animal systems..
XX XX Disclosure; Page 19; 60pp; English.
XX CC The invention relates to a novel set of inter-simple sequence repeats

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CC (ISSR)-PCR primers for genotyping eukaryotes. The primers of the  
 CC invention may be useful for genotyping diverse genomes of plant and  
 CC animal systems, in particular for distinguishing Basmati rice varieties  
 CC from non-Basmati rice varieties and traditional Basmati rice varieties  
 CC from evolved Basmati rice varieties. The current sequence is that of the  
 CC ISSR-related PCR primer of the invention.

XX Sequence 17 BP; 0 A; 0 C; 8 G; 8 T; 0 U; 1 Other;

Query Match 1.6%; Score 16.6; DB 1; Length 17;

Best Local Similarity 94.1%; Pred. No. 1.3e+02; Indels 0; Gaps 0;  
 Matches 16; Conservative 1; Mismatches 0;

QY 1794 GTGTGTGTGTGTGTGTG 1810

DB 1 GTGTGTGTGTGTGTGTG 17

RESULT 210

AAQ33786

ID AAQ33786 standard; DNA; 18 BP.

XX AC AAQ33786;

XX 25-MAR-2003 (revised)

DT 02-FEB-1993 (first entry)

XX Microsatellite sequence from clone TGLA189.

XX PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;

KW genetic mapping; traits; amplification; ss.

XX Bos taurus.

XX W09213102-A1.

XX 06-AUG-1992.

XX 15-JAN-1992; 92WO-US000340.

XX 15-JAN-1991; 91US-00642342.

XX (GENM-) GENMARK.

XX Georges M, Massey JM;

XX WPI; 1992-284684/34.

XX Polymorphic bovine DNA markers - used in genetic identification, gene  
 mapping, and selective breeding.

XX Table 7; Page 244; 517pp; English.

XX The sequence is that of a bovine microsatellite sequence obtd. by  
 CC screening a library of bovine MboI DNA fragments of between 250 and 500  
 CC bp with an (AC)<sub>15</sub> and a (TC)<sub>15</sub> oligonucleotide probe. One out of 50  
 CC clones cross-hybridised. Assuming independent distribution of  
 CC microsatellites and MboI sites, the frequency of (T)<sub>6</sub>n > 9 microsatellites  
 CC in the bovine genome is estimated at >100, 000. The sequence information  
 CC for ca. 230 such bovine microsatellites is summarised in the  
 CC specification and indexed herein (see below). The sequences upstream and  
 CC downstream of the microsatellite sequence were used to generate the  
 CC required PCR primers for in vitro amplification of the corresp.  
 CC microsatellite (using the program OPTIPRIM). The microsatellites may be  
 CC used to identify individuals, for parentage testing, and in the genetic  
 CC mapping of economic trait loci, or genes involved the determination of  
 CC economically important traits esp. in cattle, to allow selective  
 CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN  
 CC field.)

XX Sequence 18 BP; 1 A; 0 C; 9 G; 8 T; 0 U; 0 Other;

Query Match 1.6%; Score 16.4; DB 1; Length 18;

Best Local Similarity 94.4%; Pred. No. 1.4e+02; Indels 0; Gaps 0;  
 Matches 17; Conservative 0; Mismatches 1;

QY 1794 GTGTGTGTGTGTGTGTG 1811

DB 1 GTGTGTGTGTGTGTGTG 18

RESULT 211

AA119941

ID AA119941 standard; DNA; 18 BP.

XX AC AA119941;

XX 14-JUN-1999 (first entry)

XX Primer SEQ ID NO:1 from JP11075880.

XX Primer; oligonucleotide; labelling; detection; self-priming; PCR; ss.

XX Synthetic.

XX JP11075880-A.

XX 23-MAR-1999.

XX 10-JUL-1998; 98JP-00195719.

XX 14-JUL-1997; 97JP-00205378.

XX (KAGA) ZH KAGAKU & KESSEI RYOCHO KENKYUSHO.

XX WPI; 1999-257710/22.

XX Labelling of an oligonucleotide - useful for detecting genes.

XX Example 1; Page 7; 10pp; Japanese.

XX A method has been developed for labelling an oligonucleotide having a  
 CC repeated sequence of (XY)<sub>n</sub> (where X and Y consists of a combination of  
 CC adenine and thymine or uracil or guanine and cytosine, and n is an  
 CC integer of 1 or more) at the 3' terminal side in which the repeated  
 CC sequence is added and extended using a labelled body of the nucleotide  
 CC constituting the repeated sequence and a DNA polymerase lacking in 5' to  
 CC 3' exonuclease activity. The method can be used for detecting a gene. The  
 CC method can detect a gene in a sensitivity up to ten times higher than  
 CC prior art methods. The present sequence represents a primer used in an  
 CC example from the present invention

XX Sequence 18 BP; 9 A; 0 C; 0 G; 9 T; 0 U; 0 Other;

Query Match 1.6%; Score 16.4; DB 1; Length 18;

Best Local Similarity 94.4%; Pred. No. 1.4e+02; Indels 0; Gaps 0;  
 Matches 17; Conservative 0; Mismatches 1;

QY 1813 TATATATATATATATGTA 1830

DB 1 TATATATATATATATATA 18

RESULT 212

AA119941/C

ID AA119941 standard; DNA; 18 BP.

XX AC AA119941;

XX 14-JUN-1999 (first entry)

XX Primer SEQ ID NO:1 from JP11075880.

XX Primer; oligonucleotide; labelling; detection; self-priming; PCR; ss.

XX Synthetic.



XX JP11075880-A.  
XX 23-MAR-1999.  
XX 10-JUL-1998; 98JP-00195719.  
XX 14-JUL-1997; 97JP-00205378.  
XX (KAGA ) ZH KAGAKU & KESSSEI RYOHO KENKYUSHO.  
XX WPI; 1999-357710/22.  
XX Labelling of an oligonucleotide - useful for detecting genes.  
XX Example 1; Page 7; 10pp; Japanese.  
XX A method has been developed for labelling an oligonucleotide having a  
XX repeated sequence of (XY)<sub>n</sub> (where X and Y consists of a combination of  
XX adenine and thymine or uracil or guanine and cytosine, and n is an  
XX integer of 1 or more ) at the 3'-terminal side in which the repeated  
XX sequence is added and extended using a labelled body of the nucleotide  
XX constituting the repeated sequence and a DNA polymerase lacking in 5' to  
XX 3' exonuclease activity. The method can be used for detecting a gene. The  
XX method can detect a gene in a sensitivity up to ten times higher than  
XX prior art methods. The present sequence represents a primer used in an  
XX example from the present invention  
XX  
XX Sequence 18 BP; 9 A; 0 C; 0 G; 9 T; 0 U; 0 Other;  
SQ Query Match 1.6%; Score 16.4; DB 1; Length 18;  
Best Local Similarity 94.4%; Pred. No. 1.4e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1813 TATATATATATATATGTA 1830  
DB 18 TATATATATATATATATA 1  
RESULT 213  
AAAX77485/C  
ID AAX77485 standard; DNA; 18 BP.  
XX AAX77485;  
XX 05-AUG-1999 (first entry)  
XX US5912147 primer 29.  
XX Primer; quantitation; genetic instability; tumour cell; detection;  
XX neoplastic transformation; carcinogenesis; ss.  
XX Synthetic.  
XX US5912147-A.  
XX 15-JUN-1999.  
XX 22-OCT-1996; 96US-00734973.  
XX 22-OCT-1996; 96US-00734973.  
XX (HEAL-) HEALTH RES INC.  
XX Anderson G, Stoler D, Basik M;  
XX WPI; 1999-357197/30.  
XX Quantitating genetic instability.  
XX Claim 4; Col 27-28; 27pp; English.  
XX This invention describes a novel method for quantitating genetic

CC instability independent of microsatellite alterations by treating a  
CC comparison pair comprising genomic DNA from tumour cells and genomic DNA  
CC from normal cells. The method involves the cells from the same individual  
CC with oligonucleotide primers selected from (i) a nucleotide sequence  
CC (CG)xRG, where R is a purine selected from adenine and guanine and x = 3-  
CC 7, (ii) a nucleotide sequence (CG)xRY, where R is as in (i) and Y is a  
CC pyrimidine selected from cytosine, thymine, and uracil and x = 3-7, (iii)  
CC a nucleotide sequence (CG)xRR, where R is as in (i) and x = 3-7, (iv) a  
CC nucleotide sequence (CG)xY, where Y is a pyrimidine selected from  
CC cytosine, thymine, and uracil and x = 3-7, (v) a nucleotide sequence  
CC (CA)xRG, where R is a purine selected from adenine and guanine and x = 6-  
CC 16, (vi) a nucleotide sequence (CA)xRY, where R is a purine selected from  
CC adenine and guanine and Y is a pyrimidine selected from cytosine,  
CC thymine, and uracil, and x = 6-16, (vii) a nucleotide sequence (CA)xRR,  
CC where R is a purine selected from adenine and guanine and x = 6-16,  
CC (viii) a nucleotide sequence (CA)xY, where Y is a pyrimidine selected  
CC from cytosine, thymine, and uracil and x = 6-16, and (ix) a combination  
CC of the primers. The method is useful for detecting genomic instability  
CC which are commonly associated with the various stages of neoplastic  
CC transformation and carcinogenesis. The method is rapid and simple  
XX  
XX Sequence 18 BP; 9 A; 8 C; 1 G; 0 T; 0 U; 0 Other;  
SQ Query Match 1.6%; Score 16.4; DB 1; Length 18;  
Best Local Similarity 94.4%; Pred. No. 1.4e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1793 TGTGTGTGTGTGTGTGTG 1810  
DB 18 TCTGTGTGTGTGTGTGTG 1  
RESULT 214  
AAAX77494/C  
ID AAX77494 standard; DNA; 18 BP.  
XX AAX77494;  
XX 05-AUG-1999 (first entry)  
XX US5912147 primer 38.  
XX Primer; quantitation; genetic instability; tumour cell; detection;  
XX neoplastic transformation; carcinogenesis; DNA/RNA hybrid; ss.  
XX Synthetic.  
XX Key Location/Qualifiers  
XX misc\_RNA 17..18  
XX /\*tag= a  
XX /\*note= "uracil"  
XX US5912147-A.  
XX 15-JUN-1999.  
XX 22-OCT-1996; 96US-00734973.  
XX 22-OCT-1996; 96US-00734973.  
XX (HEAL-) HEALTH RES INC.  
XX Anderson G, Stoler D, Basik M;  
XX WPI; 1999-357197/30.  
XX Quantitating genetic instability.  
XX Claim 4; Col 31-32; 27pp; English.  
XX This invention describes a novel method for quantitating genetic  
XX instability independent of microsatellite alterations by treating a  
XX comparison pair comprising genomic DNA from tumour cells and genomic DNA  
CC

CC from normal cells. The method involves the cells from the same individual  
CC with oligonucleotide primers selected from (i) a nucleotide sequence  
CC (CG)XRG, where R is a purine selected from adenine and guanine and x = 3-  
CC 7, (ii) a nucleotide sequence (CG)XY, where R is as in (i) and Y is a  
CC pyrimidine selected from cytosine, thymine, and uracil and x = 3-7, (iii)  
CC a nucleotide sequence (CG)XRR, where R is as in (i) and x = 3-7, (iv) a  
CC nucleotide sequence (CG)XY, where Y is a pyrimidine selected from  
CC cytosine, thymine, and uracil and x = 3-7, (v) a nucleotide sequence  
CC (CA)XRG, where R is a purine selected from adenine and guanine and x = 6-  
CC 16, (vi) a nucleotide sequence (CA)XY, where R is a purine selected from  
CC adenine and guanine and Y is a pyrimidine selected from cytosine,  
CC thymine, and uracil, and x = 6-16, (vii) a nucleotide sequence (CA)XRR,  
CC where R is a purine selected from adenine and guanine and x = 6-16,  
CC (viii) a nucleotide sequence (CA)XY, where Y is a pyrimidine selected  
CC from cytosine, thymine, and uracil and x = 6-16, and (ix) a combination  
CC of the primers. The method is useful for detecting genomic instability  
CC which are commonly associated with the various stages of neoplastic  
CC transformation and carcinogenesis. The method is rapid and simple  
XX

SQ Sequence 18 BP; 8 A; 8 C; 0 G; 0 T; 2 U; 0 Other;  
Query Match 1.6%; Score 16.4; DB 1; Length 18;  
Best Local Similarity 94.4%; Pred. No. 1.4e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1791 ATTGTGTGTGTGTGTGTG 1808  
| | | | | | | | | | | | | | | | | |  
Db 18 AATGTGTGTGTGTGTGTG 1

RESULT 215  
AAX77493/C  
ID AAX77493 standard; DNA; 18 BP.  
XX AC AAX77493;  
XX DT 05-AUG-1999 (first entry)  
XX DE US912147 primer 37.  
XX KW Primer; quantitation; genetic instability; tumour cell; detection;  
XX KW neoplastic transformation; carcinogenesis; DNA/RNA hybrid; ss.  
XX OS Synthetic.  
XX FH Key Location/Qualifiers  
XX FT misc\_RNA 17 /\*tag= a  
XX FT /\*note= "uracil"  
XX PN US912147-A.  
XX PD 15-JUN-1999.  
XX PF 22-OCT-1996; 96US-00734973.  
XX PR 22-OCT-1996; 96US-00734973.  
XX PA (HEAL-) HEALTH RES INC.  
XX PI Anderson G, Stoler D, Basik M;  
XX DR WPI; 1999-357197/30.  
XX PT Quantitating genetic instability.  
XX PS Claim 4; Col 31-32; 27pp; English.

XX This invention describes a novel method for quantitating genetic  
XX instability independent of microsatellite alterations by treating a  
XX comparison pair comprising genomic DNA from tumour cells and genomic DNA  
XX from normal cells. The method involves the cells from the same individual  
XX with oligonucleotide primers selected from (i) a nucleotide sequence

CC (CG)XRG, where R is a purine selected from adenine and guanine and x = 3-  
CC 7, (ii) a nucleotide sequence (CG)XY, where R is as in (i) and Y is a  
CC pyrimidine selected from cytosine, thymine, and uracil and x = 3-7, (iii)  
CC a nucleotide sequence (CG)XRR, where R is as in (i) and x = 3-7, (iv) a  
CC nucleotide sequence (CG)XY, where Y is a pyrimidine selected from  
CC cytosine, thymine, and uracil and x = 3-7, (v) a nucleotide sequence  
CC (CA)XRG, where R is a purine selected from adenine and guanine and x = 6-  
CC 16, (vi) a nucleotide sequence (CA)XY, where R is a purine selected from  
CC adenine and guanine and Y is a pyrimidine selected from cytosine,  
CC thymine, and uracil, and x = 6-16, (vii) a nucleotide sequence (CA)XRR,  
CC where R is a purine selected from adenine and guanine and x = 6-16,  
CC (viii) a nucleotide sequence (CA)XY, where Y is a pyrimidine selected  
CC from cytosine, thymine, and uracil and x = 6-16, and (ix) a combination  
CC of the primers. The method is useful for detecting genomic instability  
CC which are commonly associated with the various stages of neoplastic  
CC transformation and carcinogenesis. The method is rapid and simple  
XX

SQ Sequence 18 BP; 8 A; 8 C; 0 G; 1 T; 1 U; 0 Other;  
Query Match 1.6%; Score 16.4; DB 1; Length 18;  
Best Local Similarity 94.4%; Pred. No. 1.4e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1791 ATTGTGTGTGTGTGTGTG 1808  
| | | | | | | | | | | | | | | | | |  
Db 18 AATGTGTGTGTGTGTGTG 1

RESULT 216  
AAX77464/C  
ID AAX77464 standard; DNA; 18 BP.  
XX AC AAX77464;  
XX DT 05-AUG-1999 (first entry)  
XX DE US912147 primer 8.  
XX KW Primer; quantitation; genetic instability; tumour cell; detection;  
XX KW neoplastic transformation; carcinogenesis; DNA/RNA hybrid; ss.  
XX OS Synthetic.  
XX FH Key Location/Qualifiers  
XX FT misc\_RNA 18 /\*tag= a  
XX FT /\*note= "uracil"  
XX PN US912147-A.  
XX PD 15-JUN-1999.  
XX PF 22-OCT-1996; 96US-00734973.  
XX PR 22-OCT-1996; 96US-00734973.  
XX PA (HEAL-) HEALTH RES INC.  
XX PI Anderson G, Stoler D, Basik M;  
XX DR WPI; 1999-357197/30.  
XX PT Quantitating genetic instability.  
XX PS Claim 4; Col 19-20; 27pp; English.

XX This invention describes a novel method for quantitating genetic  
XX instability independent of microsatellite alterations by treating a  
XX comparison pair comprising genomic DNA from tumour cells and genomic DNA  
XX from normal cells. The method involves the cells from the same individual  
XX with oligonucleotide primers selected from (i) a nucleotide sequence  
XX (CG)XRG, where R is a purine selected from adenine and guanine and x = 3-  
XX 7, (ii) a nucleotide sequence (CG)XY, where R is as in (i) and Y is a



CC (viii) a nucleotide sequence (CA)xyy, where y is a pyrimidine selected  
 CC from cytosine, thymine, and uracil and x = 6-16, and (ix) a combination  
 CC of the primers. The method is useful for detecting genomic instability  
 CC which are commonly associated with the various stages of neoplastic  
 CC transformation and carcinogenesis. The method is rapid and simple

XX SQ Sequence 18 BP; 8 A; 8 C; 0 G; 2 T; 0 U; 0 Other;  
 Query Match 1.6%; Score 16.4; DB 1; Length 18;  
 Best Local Similarity 94.4%; Pred. No. 1.4e+02;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1791 ATTGTGTGTGTGTGTG 1808  
 Db 18 AATGTGTGTGTGTGTG 1

RESULT 219  
 AAX77463/C  
 ID AAX77463 standard; DNA; 18 BP.  
 XX AAX77463;  
 AC AAX77463;  
 DT 05-AUG-1999 (first entry)  
 XX US5912147 primer 7.  
 DE US5912147 primer 7.  
 XX Primer; quantitation; genetic instability; tumour cell; detection;  
 KW neoplastic transformation; carcinogenesis; ss.  
 XX Synthetic.  
 OS US5912147-A.  
 PN 15-JUN-1999.  
 XX 22-OCT-1996; 96US-00734973.  
 XX 22-OCT-1996; 96US-00734973.  
 PR (HEAL-) HEALTH RES INC.  
 PA Anderson G, Stoler D, Basik M;  
 PI WPI; 1999-357197/30.  
 DR Quantitating genetic instability.  
 XX Claim 4; Col 19-20; 27pp; English.

CC This invention describes a novel method for quantitating genetic  
 CC instability independent of microsatellite alterations by treating a  
 CC comparison pair comprising genomic DNA from tumour cells and genomic DNA  
 CC from normal cells. The method involves the cells from the same individual  
 CC with oligonucleotide primers selected from (i) a nucleotide sequence  
 CC (CG)XRG, where R is a purine selected from adenine and guanine and x = 3-  
 CC 7, (ii) a nucleotide sequence (CG)XYR, where R is as in (i) and Y is a  
 CC pyrimidine selected from cytosine, thymine, and uracil and x = 3-7, (iii)  
 CC a nucleotide sequence (CG)XRR, where R is as in (i) and x = 3-7, (iv) a  
 CC nucleotide sequence (CG)XYR, where Y is a pyrimidine selected from  
 CC cytosine, thymine, and uracil and x = 3-7, (v) a nucleotide sequence  
 CC (CA)XRG, where R is a purine selected from adenine and guanine and x = 6-  
 CC 16, (vi) a nucleotide sequence (CA)XYR, where R is a purine selected from  
 CC adenine and guanine and Y is a pyrimidine selected from cytosine,  
 CC thymine, and uracil, and x = 6-16, (vii) a nucleotide sequence (CA)XRR,  
 CC where R is a purine selected from adenine and guanine and x = 6-16,  
 CC (viii) a nucleotide sequence (CA)xyy, where y is a pyrimidine selected  
 CC from cytosine, thymine, and uracil and x = 6-16, and (ix) a combination  
 CC of the primers. The method is useful for detecting genomic instability  
 CC which are commonly associated with the various stages of neoplastic  
 CC transformation and carcinogenesis. The method is rapid and simple

XX SQ Sequence 18 BP; 8 A; 8 C; 1 G; 1 T; 0 U; 0 Other;

Query Match 1.6%; Score 16.4; DB 1; Length 18;  
 Best Local Similarity 94.4%; Pred. No. 1.4e+02;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1791 ATTGTGTGTGTGTGTG 1808  
 Db 18 ACTGTGTGTGTGTGTG 1

RESULT 220  
 AAS13733/C  
 ID AAS13733 standard; DNA; 18 BP.  
 XX AAS13733;  
 AC AAS13733;  
 DT 08-MAY-2002 (first entry)  
 XX Simple sequence repeat, SSR, #30.  
 DE Simple sequence repeat; plant; ds; SSR; ryegrass; fescue; tandem repeat;  
 KW cereal profiling; grass profiling; seed batch purity testing.  
 XX Poaeae.

OS NZ509193-A.  
 PN 25-MAY-2001.  
 XX 03-JAN-2001; 2001NZ-00509193.  
 XX 24-DEC-1999; 99AU-00004906.  
 PR 04-MAY-2000; 2000AU-00007310.  
 XX (SAUS-) STATE SOUTH AUSTRALIA SOUTH AUSTRALIAN R.  
 PA (UYSC-) UNIV SOUTHERN CROSS.  
 PA (VICT-) STATE VICTORIA DEPT NATURAL RES & ENVIRO.  
 PA (UYAD-) UNIV ADELAIDE.  
 PA (ITMA-) INT MAIZE & WHEAT IMPROVEMENT CENT.

XX Forster JW, Jones ES;  
 DR WPI; 2001-512563/56.  
 XX New simple sequence repeats having 2 or more tandemly repeated nucleotide  
 CC core elements isolated from ryegrass and fescue, useful for selecting of  
 CC genes in grass or cereal breeding or profiling grass or cereal species  
 CC varieties.

XX Claim 6; Page 51; 72pp; English.

CC The invention relates to a substantially purified or isolated nucleic  
 CC acid (i) from ryegrass or fescue species including a simple sequence  
 CC repeat (SSR), having 2 or more tandemly repeated nucleotide core elements  
 CC 2-6 nucleotides in length. Also included are a nucleic acid primer  
 CC suitable for amplifying an SSR, identifying (M1) an SSR by preparing a  
 CC library of ryegrass or fescue genomic DNA enriched for SSRs and  
 CC identifying clones in the library containing SSRs, a library of ryegrass  
 CC or fescue genomic DNA enriched for SSRs prepared by the M1, selecting for  
 CC a gene in grass or cereal breeding by identifying an SSR that is closely  
 CC associated with the gene such that the SSR and the gene are  
 CC preferentially co-inherited, and selecting for the SSR in the breeding, a  
 CC method for DNA profiling grass or cereal species varieties by assessing  
 CC variation between SSR varieties and testing the purity of grass or cereal  
 CC seed batches by assessing variation within seed batch of an SSR. The SSRs  
 CC may be used in the selection of genes in grass or cereal breeding, for  
 CC profiling grass or cereal species varieties, for testing the purity of  
 CC grass or cereal seed batches, and for DNA profiling to establish the  
 CC distinct identity, uniformity and/or stability of a cultivar. The present  
 CC sequence is a ryegrass or fescue SSR

XX SQ Sequence 18 BP; 9 A; 8 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 1.6%; Score 16.4; DB 1; Length 18;  
Best Local Similarity 94.4%; Pred. No. 1.4e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTG 1810  
DB 18 TGTGTGTGTGTGTGTG 1

RESULT 221  
AAS13764  
ID AAS13764 standard; DNA; 18 BP.  
XX AC AAS13764;  
XX AC AAS13764;  
DT 08-MAY-2002 (first entry)  
DE Simple sequence repeat, SSR, #36.  
XX Simple sequence repeat; plant; ds; SSR; ryegrass; fescue; tandem repeat;  
KW cereal profiling; grass profiling; seed batch purity testing.  
XX Lolium rigidum.  
XX NZ509193-A.  
XX PD 25-MAY-2001.  
XX PF 03-JAN-2001; 2001NZ-00509193.  
XX PR 24-DEC-1999; 99AU-00004906.  
XX PR 04-MAY-2000; 2000AU-00007310.  
XX PA (SAUS-) STATE SOUTH AUSTRALIA SOUTH AUSTRALIAN R.  
XX PA (UYSC-) UNIV SOUTHERN CROSS.  
XX PA (VICT-) STATE VICTORIA DEPT NATURAL RES & ENVIRO.  
XX PA (UVAD-) UNIV ADELAIDE.  
XX PA (ITMA-) INT MAIZE & WHEAT IMPROVEMENT CENT.  
XX Forster JW, Jones ES;  
XX WPI; 2001-512563/56.  
XX New simple sequence repeats having 2 or more tandemly repeated nucleotide  
XX core elements isolated from ryegrass and fescue, useful for selecting of  
XX genes in grass or cereal breeding or profiling grass or cereal species  
XX varieties.  
XX Example 1; Fig 6; 72pp; English.  
XX The invention relates to a substantially purified or isolated nucleic  
XX acid (1) from ryegrass or fescue species including a simple sequence  
XX repeat (SSR) having 2 or more tandemly repeated nucleotide core elements  
XX 2-6 nucleotides in length. Also included are a nucleic acid primer  
XX suitable for amplifying an SSR, identifying (M) an SSR by preparing a  
XX library of ryegrass or fescue genomic DNA enriched for SSRs and  
XX identifying clones in the library containing SSRs, a library of ryegrass  
XX or fescue genomic DNA enriched for SSRs prepared by the M, selecting for  
XX a gene in grass or cereal breeding by identifying an SSR that is closely  
XX associated with the gene such that the SSR and the gene are  
XX preferentially co-inherited, and selecting for the SSR in the breeding, a  
XX method for DNA profiling grass or cereal species varieties by assessing  
XX variation between SSR varieties and testing the purity of grass or cereal  
XX seed batches by assessing variation within seed batch of an SSR. The SSRs  
XX may be used in the selection of genes in grass or cereal breeding, for  
XX profiling grass or cereal species varieties, for testing the purity of  
XX grass or cereal seed batches, and for DNA profiling to establish the  
XX distinct identity, uniformity and/or stability of a cultivar. The present  
XX sequence is a ryegrass or fescue SSR  
XX Sequence 18 BP; 0 A; 1 C; 8 G; 9 T; 0 U; 0 Other;  
XX Query Match 1.6%; Score 16.4; DB 1; Length 18;

Best Local Similarity 94.4%; Pred. No. 1.4e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTG 1811  
DB 1 GTGTGTGTGTGTGTGTG 18

RESULT 222  
AAI64450/C  
ID AAI64450 standard; DNA; 18 BP.  
XX AC AAI64450;  
XX AC AAI64450;  
DT 23-NOV-2001 (first entry)  
DE SSR motif #10.  
XX Simple Sequence Repeat; SSR; clover; microsatellite; genome mapping;  
KW trait mapping; marker-assisted selection; gene selection; legume;  
KW DNA profiling; breeding; ds.  
XX Unidentified.  
XX NZ509194-A.  
XX PD 25-MAY-2001.  
XX PF 03-JAN-2001; 2001NZ-00509194.  
XX PR 24-DEC-1999; 99AU-00004907.  
XX PR 28-MAR-2000; 2000AU-00006520.  
XX PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
XX Koelliker R, Forster JW;  
XX WPI; 2001-431058/46.  
XX Novel simple sequence repeats in clover species useful for selection of  
XX genes in legume breeding, for profiling legume species varieties and for  
XX testing the purity of legume seed batches.  
XX Claim 6; Page 35; 52pp; English.  
XX The present invention relates to Simple Sequence Repeats (SSRs) from  
XX clover species. SSRs, also called microsatellites, are based on a 1-7  
XX nucleotide core element which is tandemly repeated. The SSR array is  
XX embedded in complex flanking DNA. SSRs are ideal markers for genome  
XX mapping, trait mapping and marker-assisted selection. The SSRs may be  
XX used in methods for selecting genes in clover/ legume breeding. The SSRs  
XX are also useful for DNA profiling of clover varieties and for testing the  
XX purity of legume seed batches. The present sequence is a SSR motif, which  
XX was used in the present invention  
XX Sequence 18 BP; 8 A; 10 C; 0 G; 0 T; 0 U; 0 Other;  
XX Query Match 1.6%; Score 16.4; DB 1; Length 18;  
XX Best Local Similarity 94.4%; Pred. No. 1.4e+02;  
XX Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTG 1810  
DB 18 TGTGTGTGTGTGTGTG 1

RESULT 223  
ABX79779  
ID ABX79779 standard; cDNA; 18 BP.  
XX AC ABX79779;  
XX AC ABX79779;  
DT 17-APR-2003 (first entry)

XX DE EST polymorphic DNA repeat polynucleotide #104.  
 XX KW EST: expressed sequence tag; ss; polymorphic repeat; tandem repeat;  
 KW polymorphic marker prediction of ubiquitous simple sequences; POMPOUS;  
 KW Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;  
 KW Haw River syndrome; Huntington's disease; fragile-X syndrome;  
 KW Fredreich's ataxia; myotonic dystrophy; hyperandrogenaemia;  
 KW spinal atrophy; bulbar atrophy; spinocerebellar ataxia.  
 XX Homo sapiens.  
 OS US6472154-B1.  
 PN 29-OCT-2002.  
 XX 31-DEC-1999; 99US-00475947.  
 XX 31-DEC-1999; 99US-00475947.  
 XX (TEXA ) UNIV TEXAS SYSTEM.  
 PA Garner HR, Wren JD, Minna JD, Fondon JW;  
 PI WPI; 2003-208818/20.  
 DR Identifying a candidate polymorphic repeat within a coding sequence, for  
 XX understanding or treating genetic disease, comprises detecting tandem  
 XX repeats in a target coding sequence and scoring the repeats for  
 XX polymorphic probability.  
 XX Example; Col 385; 589pp; English.  
 PS The invention discloses a method for identifying a candidate polymorphic  
 XX repeat within a coding sequence (expressed sequence tag, EST), which  
 CC comprises detecting tandem repeats in a target coding sequence, scoring  
 CC the repeats for polymorphic probability and generating a dataset  
 CC correlating the repeats with polymorphic probability to identify a  
 CC candidate polymorphic repeat. The computational methods (polymorphic  
 CC marker prediction of ubiquitous simple sequences, POMPOUS, and Rep-X) are  
 CC useful for identifying and detecting candidate polymorphic repeats in  
 CC human genes, which can be used to understand, treat or eliminate genetic  
 CC diseases, predispositions or adverse drug-treatment reactions. Examples  
 CC of diseases linked to nucleotide repeats are Machado-Joseph, Haw River  
 CC syndrome, Huntington's disease, fragile-X syndrome, Fredreich's ataxia,  
 CC myotonic dystrophy, hyperandrogenaemia, spinal and bulbar atrophy and  
 CC spinocerebellar ataxia. The sequences presented in ABX79676-ABX80022 are  
 CC the polymorphic repeats identified for a search of human ESTs  
 XX Sequence 18 BP; 8 A; 0 C; 1 G; 9 T; 0 U; 0 Other;  
 SQ Query Match 1.6%; Score 16.4; DB 1; Length 18;  
 Best Local Similarity 94.4%; Pred. No. 1.4e+02;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1810 GTGTATATATATATAT 1827  
 DB 1 GTATATATATATATAT 18  
 RESULT 224  
 ABX79779/c  
 ID ABX79779 standard; cDNA; 18 BP.  
 XX ABX79779;  
 AC 17-APR-2003 (first entry)  
 XX EST polymorphic DNA repeat polynucleotide #104.  
 DE EST: expressed sequence tag; ss; polymorphic repeat; tandem repeat;  
 XX polymorphic marker prediction of ubiquitous simple sequences; POMPOUS;  
 KW Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;  
 KW Fredreich's ataxia; myotonic dystrophy; hyperandrogenaemia;  
 KW spinal atrophy; bulbar atrophy; spinocerebellar ataxia.

KW Haw River syndrome; Huntington's disease; fragile-X syndrome;  
 KW Fredreich's ataxia; myotonic dystrophy; hyperandrogenaemia;  
 KW spinal atrophy; bulbar atrophy; spinocerebellar ataxia.  
 XX Homo sapiens.  
 OS US6472154-B1.  
 PN 29-OCT-2002.  
 XX 31-DEC-1999; 99US-00475947.  
 XX 31-DEC-1999; 99US-00475947.  
 XX (TEXA ) UNIV TEXAS SYSTEM.  
 PA Garner HR, Wren JD, Minna JD, Fondon JW;  
 PI WPI; 2003-208818/20.  
 DR Identifying a candidate polymorphic repeat within a coding sequence, for  
 XX understanding or treating genetic disease, comprises detecting tandem  
 XX repeats in a target coding sequence and scoring the repeats for  
 XX polymorphic probability.  
 XX Example; Col 385; 589pp; English.  
 PS The invention discloses a method for identifying a candidate polymorphic  
 XX repeat within a coding sequence (expressed sequence tag, EST), which  
 CC comprises detecting tandem repeats in a target coding sequence, scoring  
 CC the repeats for polymorphic probability and generating a dataset  
 CC correlating the repeats with polymorphic probability to identify a  
 CC candidate polymorphic repeat. The computational methods (polymorphic  
 CC marker prediction of ubiquitous simple sequences, POMPOUS, and Rep-X) are  
 CC useful for identifying and detecting candidate polymorphic repeats in  
 CC human genes, which can be used to understand, treat or eliminate genetic  
 CC diseases, predispositions or adverse drug-treatment reactions. Examples  
 CC of diseases linked to nucleotide repeats are Machado-Joseph, Haw River  
 CC syndrome, Huntington's disease, fragile-X syndrome, Fredreich's ataxia,  
 CC myotonic dystrophy, hyperandrogenaemia, spinal and bulbar atrophy and  
 CC spinocerebellar ataxia. The sequences presented in ABX79676-ABX80022 are  
 CC the polymorphic repeats identified for a search of human ESTs  
 XX Sequence 18 BP; 8 A; 0 C; 1 G; 9 T; 0 U; 0 Other;  
 SQ Query Match 1.6%; Score 16.4; DB 1; Length 18;  
 Best Local Similarity 94.4%; Pred. No. 1.4e+02;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1814 ATATATATATATATGTAC 1831  
 DB 18 ATATATATATATATAC 1  
 RESULT 225  
 AAH91159/c  
 ID AAH91159 standard; DNA; 19 BP.  
 XX AAH91159;  
 AC 09-OCT-2001 (first entry)  
 XX Human inflammatory bowel disease associated polymorphic site #234.  
 DE Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis;  
 KW single nucleotide polymorphism; SNP; chromosome 19p13; paternity test;  
 KW chromosome 5q31-33; forensic test; gene therapy; ds.  
 XX Homo sapiens.  
 OS Key Location/Qualifiers  
 FH misc\_feature 9 /\*tag= a  
 FT

FT /note= "SNP, optional deletion at this position"

XX WO200142511-A2.

XX 14-JUN-2001.

XX 11-DEC-2000; 2000WO-US033632.

XX 10-DEC-1999; 99US-0170257P.

XX 10-APR-2000; 2000US-0196046P.

XX (WHED ) WHITEHEAD INST BIOMEDICAL RES.

XX (ELLI-) ELLIPSIS BIOTHERAPEUTICS CORP.

XX Daly M, Hudson TJ, Lander ES, Rioux J, Siminovitch K;

XX WPI; 2001-367874/38.

XX Testing for the presence of polymorphisms associated with inflammatory

XX bowel disease, using a hybridization assay.

XX Claim 1; Page 48; 463pp; English.

XX The present invention describes a method for detecting the presence of

XX polymorphisms associated with inflammatory bowel diseases such as

XX ulcerative colitis and Crohn's disease. The methods can be used to detect

XX the presence of genetic polymorphisms associated with inflammatory bowel

XX disease and correlating their occurrence with disease states. They may be

XX used in this way for phenotypic correlations, forensics, paternity

XX testing, medicine and genetic analysis. The present sequence is a

XX polymorphic site described in the exemplification of the invention

XX

SQ Sequence 19 BP; 9 A; 4 C; 0 G; 5 T; 0 U; 1 Other;

Query Match 1.6%; Score 16.4; DB 1; Length 19;

Best Local Similarity 89.5%; Pred. No. 1.5e+02;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1802 GTGTGTGTGTGTATATATA 1820

DB 19 GTATGTGTGTATATATA 1

RESULT 226

ABK90423

ID ABK90423 standard; DNA; 19 BP.

XX AC ABK90423;

XX 05-NOV-2002 (first entry)

DT Human UGT1A1 promoter polymorphism (TA)8 repeat region.

DE Human; ds; UGT1A1; promoter; Gilbert's syndrome; hyperbilirubinaemia;

XX uridine diphosphate glucuronosyltransferase; Crigler-Najjar syndrome;

XX UGT; polymorphism detection; TA repeat; glucuronidation; Irinotecan;

XX TAS-103; xenobiotic.

XX Homo sapiens.

OS US6395481-B1.

XX 28-MAY-2002.

XX 16-FEB-1999; 99US-00251274.

XX 16-FEB-1999; 99US-00251274.

XX (ARCH-) ARCH DEV CORP.

XX Di Rienzo A, Iyer L, Ratain MJ;

XX WPI; 2002-588597/63.

DR

XX Detecting polymorphisms in uridine diphosphate glucuronosyltransferase

PT gene promoter, useful for optimizing drug dosages for a patient,

PT comprises determining the presence of five thymidine-adenine repeats in

PT the promoter.

XX Example 6; Col 11; 13pp; English.

XX The invention relates to detecting (M1) polymorphisms in a uridine

XX diphosphate glucuronosyltransferase (UGT) gene promoter by determining

XX the presence of five thymidine-adenine (TA) repeats in the promoter,

XX where the presence of the five TA repeats correlates with increased

XX expression of the gene. The method is used for detecting polymorphisms in

XX a UGT gene promoter, preferably a UGT 1 (UGT1A1) gene promoter. (M1) is

XX useful for screening individuals for variation in glucuronidation

XX activity, for optimizing drug dosages for a patient, where the drugs

XX (e.g. Irinotecan or TAS-103) are glucuronidated by UGT (preferably

XX UGT1A1) and the activity of the drug is effected by its level of

XX glucuronidation. The method preferably involves obtaining DNA from an

XX individual, amplifying all or part of a UGT gene promoter (UGT1A1 gene

XX promoter) contained in the DNA and determining the number of TA repeats

XX in the promoter. Thus the DNA being amplified comprises all or part of

XX UGT1A1 promoter. The DNA is amplified by a polymerase chain reaction and

XX the number of TA repeats is determined by gel electrophoresis or by

XX sequencing the amplified DNA. The polymorphism comprises an allele

XX consisting of five TA repeats (TA)5, six TA repeats (TA)6, or seven TA

XX repeats (TA)7. The promoter has any one of the genotypes (TA)5/(TA)5,

XX (TA)5/(TA)6, (TA)5/(TA)7, (TA)5/(TA)8, (TA)6/(TA)8, (TA)7/(TA)8 or

XX (TA)8/(TA)8. (M1) is also useful for predicting an individual's

XX sensitivity to xenobiotics that are glucuronidated by a UGT (preferably

XX UGT1A1) gene product, the method comprising determining the number of TA

XX repeats in a UGT gene promoter, where the number of TA repeats correlates

XX with expression of the UGT gene, and the individuals sensitivity to

XX xenobiotics is effected by glucuronidation activity. The methods

XX preferably involve determining the presence of five, six or seven TA

XX repeats in the promoter. Defects in glucuronidation is associated with

XX Gilbert's syndrome (hyperbilirubinaemia) and Crigler-Najjar syndrome. The

XX present sequence is the UGT1A1 promoter (TA)8 repeat region

XX

SQ Sequence 19 BP; 10 A; 0 C; 0 G; 9 T; 0 U; 0 Other;

Query Match 1.6%; Score 16.4; DB 1; Length 19;

Best Local Similarity 94.4%; Pred. No. 1.5e+02;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1813 TATATATATATATATGTA 1830

DB 1 TATATATATATATATATA 18

RESULT 227

ABK90423/c

ID ABK90423 standard; DNA; 19 BP.

XX AC ABK90423;

XX 05-NOV-2002 (first entry)

DT Human UGT1A1 promoter polymorphism (TA)8 repeat region.

DE Human; ds; UGT1A1; promoter; Gilbert's syndrome; hyperbilirubinaemia;

XX uridine diphosphate glucuronosyltransferase; Crigler-Najjar syndrome;

XX UGT; polymorphism detection; TA repeat; glucuronidation; Irinotecan;

XX TAS-103; xenobiotic.

XX Homo sapiens.

OS US6395481-B1.

XX 28-MAY-2002.

XX 16-FEB-1999; 99US-00251274.

XX WPI; 2002-588597/63.

DR

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PR 16-FEB-1999; 99US-00251274.
XX (ARCH-) ARCH DEV CORP.
PA Di Rienzo A, Iyer L, Ratain MJ;
XX WPI; 2002-588597/63.
XX
XX Detecting polymorphisms in uridine diphosphate glucuronosyltransferase
XX gene promoter; useful for optimizing drug dosages for a patient,
XX comprises determining the presence of five thymidine-adenine repeats in
XX the promoter.
XX
XX Example 6; Col 11; 13pp; English.
XX
XX The invention relates to detecting (M1) polymorphisms in a uridine
XX diphosphate glucuronosyltransferase (UGT) gene promoter by determining
XX the presence of five thymidine-adenine (TA) repeats in the promoter,
XX where the presence of the five TA repeats correlates with increased
XX expression of the gene. The method is used for detecting polymorphisms in
XX a UGT gene promoter, preferably a UGT1 (UGT1A1) gene promoter. (M1) is
XX useful for screening individuals for variation in glucuronidation
XX activity, for optimising drug dosages for a patient, where the drugs
XX (e.g. Irinotecan or TAS-103) are glucuronidated by UGT (preferably
XX UGT1A1) and the activity of the drug is effected by its level of
XX glucuronidation. The method preferably involves obtaining DNA from an
XX individual, amplifying all or part of a UGT gene promoter (UGT1A1 gene
XX promoter) contained in the DNA and determining the number of TA repeats
XX in the promoter. Thus the DNA being amplified comprises all or part of
XX UGT1A1 promoter. The DNA is amplified by a polymerase chain reaction and
XX the number of TA repeats is determined by gel electrophoresis or by
XX sequencing the amplified DNA. The polymorphism comprises an allele
XX consisting of five TA repeats (TA)5, six TA repeats (TA)6, or seven TA
XX repeats (TA)7. The promoter has any one of the genotypes (TA)5/(TA)5,
XX (TA)5/(TA)6, (TA)5/(TA)7, (TA)5/(TA)8, (TA)6/(TA)8, (TA)7/(TA)8 or
XX (TA)8/(TA)8. (M1) is also useful for predicting an individual's
XX sensitivity to xenobiotics that are glucuronidated by a UGT (preferably
XX UGT1A1) gene product, the method comprising determining the number of TA
XX repeats in a UGT gene promoter, where the number of TA repeats correlates
XX with expression of the UGT gene, and the individuals sensitivity to
XX xenobiotics is effected by glucuronidation activity. The methods
XX preferably involve determining the presence of five, six or seven TA
XX repeats in the promoter. Defects in glucuronidation is associated with
XX Gilbert's syndrome (hyperbilirubinaemia) and Crigler-Najjar syndrome. The
XX present sequence is the UGT1A1 promoter (TA)8 repeat region
XX
XX Sequence 19 BP; 10 A; 0 C; 0 G; 9 T; 0 U; 0 Other;
XX
XX Query Match 1.6%; Score 16.4; DB 1; Length 19;
XX Best Local Similarity 94.4%; Pred. No. 1.5e+02;
XX Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1813 TATATATATATATATGTA 1830
XX Db 18 TATATATATATATATATA 1
XX
XX RESULT 228
XX AAL50681
XX ID AAL50681 standard; DNA; 19 BP.
XX AC AAL50681;
XX
XX DT 16-JAN-2003 (first entry)
XX XX
XX DE Human uridine diphosphate glucuronosyltransferase gene polymorphism #15.
XX
XX KW Human; polymorphism; TA repeat; ds; UGT; thymidine-adenine repeat;
XX uridine diphosphate glucuronosyltransferase gene promoter; UGT1A1;
XX drug dosage optimisation; xenobiotic sensitivity.
XX
XX OS Homo sapiens.
XX
XX PN US2002115097-A1.
XX PD 22-AUG-2002.
XX
XX PF 01-FEB-2002; 2002US-00061693.
XX
XX PR 16-FEB-1999; 99US-00251274.
XX
XX (ARCH-) ARCH DEV CORP.
XX
XX Riienzo AD, Iyer L, Ratain MJ;
XX WPI; 2002-740095/80.
XX
XX Detecting polymorphisms in uridine diphosphate glucuronosyltransferase
XX gene promoter; useful for optimizing drug dosages for a patient, involves
XX determining number of thymidine-adenine repeats in the promoter.
XX
XX Example 6; Page 3; 13pp; English.
XX
XX The invention comprises a method for detecting polymorphisms in a uridine
XX diphosphate glucuronosyltransferase (UGT) gene promoter (preferably
XX UGT1A1). The method involves determining the number of thymidine-adenine
XX (TA) repeats in the promoter - as the number of TA repeats correlates
XX with expression of the UGT gene. The method of the invention is useful
XX for detecting polymorphisms in a UGT gene promoter. The method of the
XX invention is also useful in optimising drug dosages and predicting an
XX individual's sensitivity to xenobiotics for drugs and xenobiotics that
XX are glucuronidated by UGT. The present DNA sequence represents a UGT gene
XX TA repeat polymorphism
XX
XX Sequence 19 BP; 10 A; 0 C; 0 G; 9 T; 0 U; 0 Other;
XX
XX Query Match 1.6%; Score 16.4; DB 1; Length 19;
XX Best Local Similarity 94.4%; Pred. No. 1.5e+02;
XX Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1813 TATATATATATATATGTA 1830
XX Db 1 TATATATATATATATATA 18
XX
XX RESULT 229
XX AAL50681/C
XX ID AAL50681 standard; DNA; 19 BP.
XX AC AAL50681;
XX
XX DT 16-JAN-2003 (first entry)
XX XX
XX DE Human uridine diphosphate glucuronosyltransferase gene polymorphism #15.
XX
XX KW Human; polymorphism; TA repeat; ds; UGT; thymidine-adenine repeat;
XX uridine diphosphate glucuronosyltransferase gene promoter; UGT1A1;
XX drug dosage optimisation; xenobiotic sensitivity.
XX
XX OS Homo sapiens.
XX
XX PN US2002115097-A1.
XX PD 22-AUG-2002.
XX
XX PF 01-FEB-2002; 2002US-00061693.
XX
XX PR 16-FEB-1999; 99US-00251274.
XX
XX (ARCH-) ARCH DEV CORP.
XX
XX Riienzo AD, Iyer L, Ratain MJ;
XX WPI; 2002-740095/80.
XX
XX Detecting polymorphisms in uridine diphosphate glucuronosyltransferase

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PT gene promoter, useful for optimizing drug dosages for a patient, involves  
 PT determining number of thymidine-adenine repeats in the promoter.  
 XX  
 PS Example 6; Page 3; 13pp; English.  
 XX  
 CC The invention comprises a method for detecting polymorphisms in a uridine  
 CC diphosphate glucuronosyltransferase (UGT) gene promoter (preferably  
 CC UGT1A1). The method involves determining the number of thymidine-adenine  
 CC (TA) repeats in the promoter - as the number of TA repeats correlates  
 CC with expression of the UGT gene. The method of the invention is useful  
 CC for detecting polymorphisms in a UGT gene promoter. The method of the  
 CC invention is also useful in optimising drug dosages and predicting an  
 CC individual's sensitivity to xenobiotics for drugs and xenobiotics that  
 CC are glucuronidated by UGT. The present DNA sequence represents a UGT gene  
 CC TA repeat polymorphism  
 XX  
 SQ Sequence 19 BP; 10 A; 0 C; 0 G; 9 T; 0 U; 0 Other;  
 Query Match 1.6%; Score 16.4; DB 1; Length 19;  
 Best Local Similarity 94.4%; Pred. No. 1.5e+02;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1813 TATATATATATATATGTA 1830  
 Db 18 TATATATATATATATA 1  
 RESULT 230  
 ABA99798  
 ID ABA99798 standard; DNA; 20 BP.  
 XX  
 AC ABA99798;  
 XX  
 DT 11-JUN-2002 (first entry)  
 DE Murine capn12 exon 7 splice donor site.  
 XX  
 KW Calpain protease; murine; gene therapy; screening; diagnosis; capn12; ss.  
 XX  
 OS Mus sp.  
 XX  
 FH Key Location/Qualifiers  
 FT exon 1..10  
 FT /\*tag= a  
 FT /number= 7  
 FT intron 11..20  
 FT /\*tag= b  
 FT /number= 7  
 FT  
 FT  
 XX DB10031932-A1.  
 XX  
 PD 10-JAN-2002.  
 XX  
 PF 30-JUN-2000; 2000DE-01031932.  
 XX  
 PR 30-JUN-2000; 2000DE-01031932.  
 XX  
 PA (BADI ) BASF AG.  
 XX  
 DR WPI; 2002-115441/16.  
 XX  
 PT New calpain protein 12 with cysteine protease activity, useful for  
 PT treating specific deficiency disorders.  
 PS Disclosure; Fig 2c; 36pp; German.  
 XX  
 CC This invention describes a novel murine calpain protease 12 (capn12). The  
 CC calpain protease of the invention, related proteins and nucleic acid that  
 CC encodes it, are useful for treatment (including gene therapy) of diseases  
 CC associated with insufficient expression of the calpain protease. The  
 CC protein is also used to screen for calpain protein effectors and to raise  
 CC specific immunoglobulins (Ig) useful for diagnosis. Also the  
 CC polynucleotide encoding capn12 is useful, e.g. as primers and probes, for

CC diagnosis of diseases, or predisposition to them, and for recombinant  
 CC production of capn12. This sequence represents the murine calpain 12,  
 CC capn12 exon 7 splice donor site described in the disclosure of the  
 CC invention  
 XX  
 SQ Sequence 20 BP; 5 A; 2 C; 10 G; 3 T; 0 U; 0 Other;  
 Query Match 1.6%; Score 16.4; DB 1; Length 20;  
 Best Local Similarity 94.4%; Pred. No. 1.5e+02;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1589 AGTGACAGCTAGGATGCTG 1606  
 Db 3 AGTGACAGCTAGGATGGG 20  
 RESULT 231  
 AAQ33743  
 ID AAQ33743 standard; DNA; 16 BP.  
 XX  
 AC AAQ33743;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 02-FEB-1993 (first entry)  
 XX  
 DE Microsatellite sequence from clone TGLA159.  
 XX  
 KW PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;  
 KW genetic mapping; traits; amplification; ss.  
 XX  
 OS Bos taurus.  
 XX  
 PN WO9213102-A1.  
 XX  
 PD 06-AUG-1992.  
 XX  
 PF 15-JAN-1992; 92WO-US000340.  
 XX  
 PR 15-JAN-1991; 91US-00642342.  
 XX  
 PA (GENM-) GENMARK.  
 XX  
 FH Georges M, Massey JM;  
 XX  
 DR WPI; 1992-284684/34.  
 XX  
 PT Polymorphic bovine DNA markers - used in genetic identification, gene  
 PT mapping, and selective breeding.  
 XX  
 PS Table 7; Page 227; 517pp; English.  
 XX  
 CC The sequence is that of a bovine microsatellite sequence obtd. by  
 CC screening a library of bovine MboI DNA fragments of between 250 and 500  
 CC bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50  
 CC clones cross-hybridised. Assuming independent distribution of  
 CC microsatellites and MboI sites, the frequency of (T6)n > 9 microsatellites  
 CC in the bovine genome is estimated at >100, 000. The sequence information  
 CC for ca. 230 such bovine microsatellites is summarised in the  
 CC specification and indexed herein (see below). The sequences upstream and  
 CC downstream of the microsatellite sequence were used to generate the  
 CC required PCR primers for in vitro amplification of the corresp.  
 CC microsatellite (using the program OPTIPRIM). The microsatellites may be  
 CC used to identify individuals, for parentage testing, and in the genetic  
 CC mapping of economic trait loci, or genes involved in the determination of  
 CC economically important traits esp. in cattle, to allow selective  
 CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN  
 CC field.)  
 XX  
 SQ Sequence 16 BP; 0 A; 0 C; 8 G; 8 T; 0 U; 0 Other;  
 Query Match 1.5%; Score 16; DB 1; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1793 TGTGTGTGTGTGTGTGT 1808
DB 1 TGTGTGTGTGTGTGTGT 16

RESULT 232
AAQ33749
ID AAQ33749 standard; DNA; 16 BP.
XX AC AAQ33749;
XX XX
XX 25-MAR-2003 (revised)
DT 02-FEB-1993 (first entry)
XX DE Microsatellite sequence from clone TGLA160.
XX XX
XX PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
KW genetic mapping; traits; amplification; ss.
XX OS Bos taurus.
XX PN WO9213102-A1.
XX PD 06-AUG-1992.
XX PF 15-JAN-1992; 92WO-US000340.
XX PR 15-JAN-1991; 91US-00642342.
XX PA (GENM-) GENMARK.
XX PI Georges M, Massey JM;
XX DR WPI; 1992-284684/34.
XX PT Polymorphic bovine DNA markers - used in genetic identification, gene
XX mapping, and selective breeding.
XX PS Table 7; Page 229; 517pp; English.
XX CC The sequence is that of a bovine microsatellite sequence obtd. by
XX screening a library of bovine MboI DNA fragments of between 250 and 500
XX bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
XX clones cross-hybridised. Assuming independent distribution of
XX microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites
XX in the bovine genome is estimated at >100, 000. The sequence information
XX for ca. 230 such bovine microsatellites is summarised in the
XX specification and indexed herein (see below). The sequences upstream and
XX downstream of the microsatellite sequence were used to generate the
XX required PCR primers for in vitro amplification of the corresp.
XX microsatellite (using the program OPTIPRIM). The microsatellites may be
XX used to identify individuals, for parentage testing, and in the genetic
XX mapping of economic trait loci, or genes involved in the determination of
XX economically important traits esp. in cattle, to allow selective
XX breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
XX field.)
XX SQ Sequence 16 BP; 0 A; 0 C; 8 G; 8 T; 0 U; 0 Other;
XX Query Match 1.5%; Score 16; DB 1; Length 16;
XX Best Local Similarity 100.0%; Fred.No. 1.5e+02; Indels 0; Gaps 0;
XX Matches 16; Conservative 0; Mismatches 0;

QY 1794 GTGTGTGTGTGTGTGT 1809
DB 1 GTGTGTGTGTGTGTGT 16

RESULT 233
AAQ33903
ID AAQ33903 standard; DNA; 16 BP.
XX AC AAQ33903;
XX XX
XX 25-MAR-2003 (revised)
DT 16-FEB-1995 (first entry)
XX DE Purine-pyrimidine contg. ribooligonucleoside R138.
XX XX
XX Purine; pyrimidine; methylphosphonate; MP; triple helix; translation;
KW oligonucleoside; ss.
XX XX

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AC AAQ33903;
XX 25-MAR-2003 (revised)
DT 02-FEB-1993 (first entry)
XX DE Microsatellite sequence from clone TGLA311.
XX XX
XX PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
KW genetic mapping; traits; amplification; ss.
XX OS Bos taurus.
XX PN WO9213102-A1.
XX PD 06-AUG-1992.
XX PF 15-JAN-1992; 92WO-US000340.
XX PR 15-JAN-1991; 91US-00642342.
XX PA (GENM-) GENMARK.
XX PI Georges M, Massey JM;
XX DR WPI; 1992-284684/34.
XX PT Polymorphic bovine DNA markers - used in genetic identification, gene
XX mapping, and selective breeding.
XX PS Table 7; Page 291; 517pp; English.
XX CC The sequence is that of a bovine microsatellite sequence obtd. by
XX screening a library of bovine MboI DNA fragments of between 250 and 500
XX bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
XX clones cross-hybridised. Assuming independent distribution of
XX microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites
XX in the bovine genome is estimated at >100, 000. The sequence information
XX for ca. 230 such bovine microsatellites is summarised in the
XX specification and indexed herein (see below). The sequences upstream and
XX downstream of the microsatellite sequence were used to generate the
XX required PCR primers for in vitro amplification of the corresp.
XX microsatellite (using the program OPTIPRIM). The microsatellites may be
XX used to identify individuals, for parentage testing, and in the genetic
XX mapping of economic trait loci, or genes involved in the determination of
XX economically important traits esp. in cattle, to allow selective
XX breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
XX field.)
XX SQ Sequence 16 BP; 0 A; 0 C; 8 G; 8 T; 0 U; 0 Other;
XX Query Match 1.5%; Score 16; DB 1; Length 16;
XX Best Local Similarity 100.0%; Fred.No. 1.5e+02; Indels 0; Gaps 0;
XX Matches 16; Conservative 0; Mismatches 0;

QY 1794 GTGTGTGTGTGTGTGT 1809
DB 1 GTGTGTGTGTGTGTGT 16

RESULT 234
AAQ68236/c
ID AAQ68236 standard; RNA; 16 BP.
XX AC AAQ68236;
XX XX
XX 25-MAR-2003 (revised)
DT 16-FEB-1995 (first entry)
XX DE Purine-pyrimidine contg. ribooligonucleoside R138.
XX XX
XX Purine; pyrimidine; methylphosphonate; MP; triple helix; translation;
KW oligonucleoside; ss.
XX XX

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Best Local Similarity 50.0%; Pred. No. 1.5e+02; Indels 0; Gaps 0;
Matches 8; Conservative 8; Mismatches 0;

QY 1793 TGTGTGTGTGTGTGTG 1808
    .|.|.|.|.|.|.|.|.|.
Db 1 UGUGUGUGUGUGUGUG 16

RESULT 237
AAQ68237/C
ID AAQ68237 standard; DNA; 16 BP.
AC AAQ68237;
XX
XX 25-MAR-2003 (revised)
DT 16-FEB-1995 (first entry)
XX
XX Purine-pyrimidine contg. methylphosphonate oligonucleoside G2018.
XX
XX Purine; pyrimidine; methylphosphonate; MP; triple helix; translation;
KW oligonucleoside; ss.
XX
XX Synthetic.
XX
XX WO9413326-A1.
XX
XX 23-JUN-1994.
XX
XX 08-DEC-1993; 93WO-US011986.
XX
XX 08-DEC-1992; 92US-00987746.
XX
XX (GENT-) GENTA INC.
XX
XX Arnold LJ, Reynolds MA;
XX
XX WPI; 1994-217542/26.
XX
XX Detection, recognition, inhibition and alteration of single and double
PT stranded target nucleic acid sequences - by formation of a triple helix
PT structure using 2 oligomers which block translation.
XX
XX Example 2; Page 37; 67pp; English.
XX
XX Two sets of methylphosphonate oligonucleosides ("MP oligomers") and
CC complementary ribooligonucleosides ("RNA oligomers") contg. alternating
CC purines and pyrimidines were examined for their ability to form triple
CC helix complexes. (Set 1:G2019 and R138; Set 2:G2018 and R139 - see
CC AAQ68235-38). It was shown that MP oligomers contg. alternating purines
CC and pyrimidines are capable of forming triple stranded complexes with
CC complementary RNA oligomers. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
XX Sequence 16 BP; 8 A; 8 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.5%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGT 1809
    |||||
Db 16 GTGTGTGTGTGTGTGT 1

RESULT 238
AAT66090/C
ID AAT66090 standard; DNA; 16 BP.
XX
XX AAT66090;
XX
XX 25-MAR-2003 (revised)
DT 18-JUN-1997 (first entry)
XX
XX

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DE Repeat sequence found in ADP/ATP translocase gene.
XX Polymorphism; repeat sequence; genetic marker; primer; amplification;
KW PCR; polymerase chain reaction; paternity; maternity; human; pedigree;
KW linkage analysis; genetic disease; animal; plant; breeding; locus;
KW hybridisation; chromosome; ds.
XX
XX Homo sapiens.
XX
XX US5582979-A.
XX
XX 10-DEC-1996.
XX
XX 04-APR-1994; 94US-00222177.
XX
XX 21-APR-1989; 89US-00341562.
PR 05-SEP-1991; 91US-00754351.
XX
XX (MARS-) MARSHFIELD CLINIC.
XX
XX Weber JL;
XX
XX WPI; 1997-042299/04.
XX
XX Detection of polymorphic genetic markers of the form (dc-da)n(dg-dt)n -
PT using novel nucleic acid mols. as primers.
XX
XX Example 9; Col 59-60; 186pp; English.
XX
XX The invention relates to the isolation of polymorphic repeat sequences
CC having the sequence (dc-da)n.(dg-dt)n which can be used as genetic
CC markers. Primers based on these sequences can be used to detect these
CC repeats, especially for use in e.g. paternity or maternity testing, human
CC genetic analysis such as linkage analysis of genetic disease, commercial
CC animal or plant breeding or pedigree analysis. The sequences AAT66084-
CC T66107 represent repeat sequences of low informativeness found in
CC specific human genes. This repeat sequence is found in the ADP/ATP
CC translocase gene. The sequence is amplified by primers AAT66091-2.
CC (Updated on 25-MAR-2003 to correct PF field.)
XX
XX Sequence 16 BP; 8 A; 8 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.5%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTG 1808
    |||||
Db 16 TGTGTGTGTGTGTGTG 1

RESULT 239
AAZ98508/C
ID AAZ98508 standard; DNA; 16 BP.
XX
XX AAZ98508;
XX
XX 19-JUN-2000 (first entry)
XX
XX H. discus derived sequence #26.
XX
XX Satellite sequence; DNA fragmentation; microsatellite DNA; DNA marker;
KW Haliotis discus; ss.
XX
XX Haliotis discus.
OS
XX WO200011156-A1.
XX
XX 02-MAR-2000.
XX
XX 01-JUL-1999; 99WO-JP003551.
XX
XX 18-AUG-1998; 98JP-00232153.
PR

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XX PA (NORQ) JAPAN MIN AGRIC FORESTRY & FISHERIES.

XX PI Takahashi H, Sekino M;

XX DR WPI; 2000-224592/19.

XX PT Isolation of satellite sequences from genomic DNA for use as DNA markers

XX PT comprises isolating a library with high homogeneity by DNA fragmentation.

XX PS Example 5; Page 14; 35pp; Japanese.

XX CC The invention provides a novel method for isolation of satellite  
sequences from genomic DNA that comprises fragmentation of the DNA by a  
method which is not dependent on base sequence; then selection of the  
satellite sequences from the obtained genomic library of high  
homogeneity. The method is useful for the isolation of microsatellite DNA  
homogeneity which can be used as DNA markers. The new method markedly  
improves the efficiency of isolation of satellite sequences in comparison  
to prior art methods which are reliant on base sequences. Sequences  
AAZ98483-514 represent sequences from *Halotis* discus, used in the method  
of the invention

XX SQ Sequence 16 BP; 8 A; 8 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.5%; Score 16; DB 1; Length 16;

Best Local Similarity 100.0%; Pred. No. 1.5e+02;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTG 1808

Db 16 TGTGTGTGTGTGTGTG 1

RESULT 240

AAAD17599/c

ID AAAD17599 standard; DNA; 17 BP.

XX AC AAAD17599;

XX DT 10-DEC-2001 (first entry)

XX DE 5' variation generator oligonucleotide PCR primer #14.

XX KW Genomic DNA analysis; 5' variation generator; 3' fragment generator;

XX KW endangered animal identification; PCR primer; ss.

XX OS Unidentified.

XX PN EP1130114-A1.

XX PD 05-SEP-2001.

XX PF 03-MAR-2000; 2000EP-00200757.

XX PR 03-MAR-2000; 2000EP-00200757.

XX PA (VHAE-) VAN HAERINGEN LAB BV.

XX PI Van Haringen H, Van Haringen WA;

XX DR WPI; 2001-572636/65.

XX DR Analyzing genomic DNA in a sample, useful for analyzing genes of

XX PT organisms (e.g. a species or individual) or identifying endangered

XX PT animals or plants, by using oligonucleotide primers comprising universal

XX PT variable fragments.

XX PS Example 1; Page 6; 23pp; English.

XX CC The patent discloses a method and associated kit for analysing genomic

XX CC DNA in a sample. The method comprises conducting a nucleic acid

XX CC amplification on the genomic DNA in the sample using both first and

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CC second oligonucleotide primer to produce DNA fragments based on repeat  
sequences on at least one end of the genomic DNA. The first primer is a  
5' variation generator including a repeat sequence and at least one non-  
repeat nucleotide. The second oligonucleotide primer is a 3' fragment  
generator starting within such a genetic distance that amplification of  
the genomic DNA can be performed and preferably includes inosine. The  
method is useful for the genetic analysis of an individual organism,  
particularly of a species or individual. It is also useful for the rapid  
and straight forward identification of endangered animals or plants. The  
present DNA sequence is a 5' variation generator oligonucleotide PCR  
primer

XX SQ Sequence 17 BP; 8 A; 8 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 1.5%; Score 16; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 1.5e+02;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTG 1808

Db 17 TGTGTGTGTGTGTGTG 2

RESULT 241

AAAD17597/c

ID AAAD17597 standard; DNA; 17 BP.

XX AC AAAD17597;

XX DT 10-DEC-2001 (first entry)

XX DE 5' variation generator oligonucleotide PCR primer #12.

XX KW Genomic DNA analysis; 5' variation generator; 3' fragment generator;

XX KW endangered animal identification; PCR primer; ss.

XX OS Unidentified.

XX PN EP1130114-A1.

XX PD 05-SEP-2001.

XX PF 03-MAR-2000; 2000EP-00200757.

XX PR 03-MAR-2000; 2000EP-00200757.

XX PA (VHAE-) VAN HAERINGEN LAB BV.

XX PI Van Haringen H, Van Haringen WA;

XX DR WPI; 2001-572636/65.

XX DR Analyzing genomic DNA in a sample, useful for analyzing genes of

XX PT organisms (e.g. a species or individual) or identifying endangered

XX PT animals or plants, by using oligonucleotide primers comprising universal

XX PT variable fragments.

XX PS Example 1; Page 6; 23pp; English.

XX CC The patent discloses a method and associated kit for analysing genomic

XX CC DNA in a sample. The method comprises conducting a nucleic acid

XX CC amplification on the genomic DNA in the sample using both first and

XX CC second oligonucleotide primer to produce DNA fragments based on repeat

XX CC sequences on at least one end of the genomic DNA. The first primer is a

XX CC 5' variation generator including a repeat sequence and at least one non-

XX CC repeat nucleotide. The second oligonucleotide primer is a 3' fragment

XX CC generator starting within such a genetic distance that amplification of

XX CC the genomic DNA can be performed and preferably includes inosine. The

XX CC method is useful for the genetic analysis of an individual organism,

XX CC particularly of a species or individual. It is also useful for the rapid

XX CC and straight forward identification of endangered animals or plants. The

XX CC present DNA sequence is a 5' variation generator oligonucleotide PCR

XX CC primer

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XX SQ Sequence 17 BP; 8 A; 9 C; 0 G; 0 T; 0 U; 0 Other;
Query Match 1.5%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTG 1808
Db 17 TGTGTGTGTGTGTGTG 2

RESULT 242
AAD17595
ID AAD17595 standard; DNA; 17 BP.
XX AC AAD17595;
XX DT 10-DEC-2001 (first entry)
XX DE 5' variation generator oligonucleotide PCR primer #10.
XX KW Genomic DNA analysis; 5' variation generator; 3' fragment generator;
XX KW endangered animal identification; PCR primer; ss.
XX OS Unidentified.
XX PN EP1130114-A1.
XX PD 05-SEP-2001.
XX PF 03-MAR-2000; 2000EP-00200757.
XX PR 03-MAR-2000; 2000EP-00200757.
XX PA (VHAE-) VAN HAERINGEN LAB BV.
XX PI Van Haringen H, Van Haringen WA;
XX DR WPI; 2001-572636/65.
XX PT Analyzing genomic DNA in a sample, useful for analyzing genes of
XX PT organisms (e.g. a species or individual) or identifying endangered
XX PT animals or plants, by using oligonucleotide primers comprising universal
XX PT variable fragments.
XX PS Example 1; Page 6; 23pp; English.
XX CC The patent discloses a method and associated kit for analysing genomic
XX CC DNA in a sample. The method comprises conducting a nucleic acid
XX CC amplification on the genomic DNA in the sample using both first and
XX CC second oligonucleotide primer to produce DNA fragments based on repeat
XX CC sequences on at least one end of the genomic DNA. The first primer is a
XX CC 5' variation generator including a repeat sequence and at least one non-
XX CC repeat nucleotide. The second oligonucleotide primer is a 3' fragment
XX CC generator starting within such a genetic distance that amplification of
XX CC the genomic DNA can be performed and preferably includes inosine. The
XX CC method is useful for the genetic analysis of an individual organism,
XX CC particularly of a species or individual. It is also useful for the rapid
XX CC and straight forward identification of endangered animals or plants. The
XX CC present DNA sequence is a 5' variation generator oligonucleotide PCR
XX CC primer
XX SQ Sequence 17 BP; 1 A; 0 C; 8 G; 8 T; 0 U; 0 Other;
Query Match 1.5%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTG 1808
Db 2 TGTGTGTGTGTGTGTG 17

RESULT 244
AAD17598/c
ID AAD17598 standard; DNA; 17 BP.
XX AC AAD17598;
XX DT 10-DEC-2001 (first entry)
XX DE 5' variation generator oligonucleotide PCR primer #13.
XX
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RESULT 243
AAD17596
ID AAD17596 standard; DNA; 17 BP.
XX AC AAD17596;
XX DT 10-DEC-2001 (first entry)
XX DE 5' variation generator oligonucleotide PCR primer #11.
XX KW Genomic DNA analysis; 5' variation generator; 3' fragment generator;
XX KW endangered animal identification; PCR primer; ss.
XX OS Unidentified.
XX PN EP1130114-A1.
XX PD 05-SEP-2001.
XX PF 03-MAR-2000; 2000EP-00200757.
XX PR 03-MAR-2000; 2000EP-00200757.
XX PA (VHAE-) VAN HAERINGEN LAB BV.
XX PI Van Haringen H, Van Haringen WA;
XX DR WPI; 2001-572636/65.
XX PT Analyzing genomic DNA in a sample, useful for analyzing genes of
XX PT organisms (e.g. a species or individual) or identifying endangered
XX PT animals or plants, by using oligonucleotide primers comprising universal
XX PT variable fragments.
XX PS Example 1; Page 6; 23pp; English.
XX CC The patent discloses a method and associated kit for analysing genomic
XX CC DNA in a sample. The method comprises conducting a nucleic acid
XX CC amplification on the genomic DNA in the sample using both first and
XX CC second oligonucleotide primer to produce DNA fragments based on repeat
XX CC sequences on at least one end of the genomic DNA. The first primer is a
XX CC 5' variation generator including a repeat sequence and at least one non-
XX CC repeat nucleotide. The second oligonucleotide primer is a 3' fragment
XX CC generator starting within such a genetic distance that amplification of
XX CC the genomic DNA can be performed and preferably includes inosine. The
XX CC method is useful for the genetic analysis of an individual organism,
XX CC particularly of a species or individual. It is also useful for the rapid
XX CC and straight forward identification of endangered animals or plants. The
XX CC present DNA sequence is a 5' variation generator oligonucleotide PCR
XX CC primer
XX SQ Sequence 17 BP; 0 A; 1 C; 8 G; 8 T; 0 U; 0 Other;
Query Match 1.5%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTG 1808
Db 2 TGTGTGTGTGTGTGTG 17

RESULT 244
AAD17598/c
ID AAD17598 standard; DNA; 17 BP.
XX AC AAD17598;
XX DT 10-DEC-2001 (first entry)
XX DE 5' variation generator oligonucleotide PCR primer #13.
XX
```

KW Genomic DNA analysis; 5' variation generator; 3' fragment generator;  
 KW endangered animal identification; PCR primer; ss.  
 OS Unidentified.  
 XX EP1130114-A1.  
 PN  
 XX 05-SEP-2001.  
 PD  
 XX 03-MAR-2000; 2000EP-00200757.  
 PF  
 XX 03-MAR-2000; 2000EP-00200757.  
 PR  
 XX (VZAE-) VAN HAERINGEN LAB BV.  
 PA  
 XX Van Haringen H, Van Haringen WA;  
 PI  
 XX WPI; 2001-572636/65.  
 DR  
 XX Analyzing genomic DNA in a sample, useful for analyzing genes of  
 PT organisms (e.g. a species or individual) or identifying endangered  
 PT animals or plants, by using oligonucleotide primers comprising universal  
 PT variable fragments.  
 XX  
 XX Example 1; Page 6; 23pp; English.  
 PS  
 XX The patent discloses a method and associated kit for analysing genomic  
 CC DNA in a sample. The method comprises conducting a nucleic acid  
 CC amplification on the genomic DNA in the sample using both first and  
 CC second oligonucleotide primer to produce DNA fragments based on repeat  
 CC sequences on at least one end of the genomic DNA. The first primer is a  
 CC 5' variation generator including a repeat sequence and at least one non-  
 CC repeat nucleotide. The second oligonucleotide primer is a 3' fragment  
 CC generator starting within such a genetic distance that amplification of  
 CC the genomic DNA can be performed and preferably includes inosine. The  
 CC method is useful for the genetic analysis of an individual organism,  
 CC particularly of a species or individual. It is also useful for the rapid  
 CC and straight forward identification of endangered animals or plants. The  
 CC present DNA sequence is a 5' variation generator oligonucleotide PCR  
 CC primer.  
 XX  
 XX Sequence 17 BP; 8 A; 8 C; 1 G; 0 T; 0 U; 0 Other;  
 SQ Query Match 1.5%; Score 16; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1793 TGTGTGTGTGTGTGTG 1808  
 DB 17 TGTGTGTGTGTGTGTG 2  
 RESULT 245  
 AAX77462/C  
 ID AAX77462 standard; DNA; 18 BP.  
 XX  
 AC AAX77462;  
 XX  
 DT 05-AUG-1999 (first entry)  
 XX  
 DE US5912147 primer 6.  
 XX  
 XX Primer; quantitation; genetic instability; tumour cell; detection;  
 KW neoplastic transformation; carcinogenesis; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN US5912147-A.  
 XX  
 PD 15-JUN-1999.  
 XX  
 PF 22-OCT-1996; 96US-00734973.  
 XX  
 PR (HEAL-) HEALTH RES INC.  
 XX  
 PA Anderson G, Stoler D, Basik M;  
 PI  
 XX WPI; 1999-357197/30.  
 DR

PR 22-OCT-1996; 96US-00734973.  
 XX (HEAL-) HEALTH RES INC.  
 PA  
 XX Anderson G, Stoler D, Basik M;  
 PI  
 XX WPI; 1999-357197/30.  
 DR  
 XX Quantitating genetic instability.  
 PT  
 XX Claim 4; Col 17-18; 27pp; English.  
 PS  
 XX This invention describes a novel method for quantitating genetic  
 CC instability independent of microsatellite alterations by treating a  
 CC comparison pair comprising genomic DNA from tumour cells and genomic DNA  
 CC from normal cells. The method involves the cells from the same individual  
 CC with oligonucleotide primers selected from (i) a nucleotide sequence  
 CC (CG)XRG, where R is a purine selected from adenine and guanine and x = 3-  
 CC 7, (ii) a nucleotide sequence (CG)XY, where R is as in (i) and Y is a  
 CC pyrimidine selected from cytosine, thymine, and uracil and x = 3-7, (iii)  
 CC a nucleotide sequence (CG)XRR, where R is as in (i) and x = 3-7, (iv) a  
 CC nucleotide sequence (CG)XY, where Y is a pyrimidine selected from  
 CC cytosine, thymine, and uracil and x = 3-7, (v) a nucleotide sequence  
 CC (CA)XRG, where R is a purine selected from adenine and guanine and x = 6-  
 CC 16, (vi) a nucleotide sequence (CA)XY, where R is a purine selected from  
 CC adenine and guanine and Y is a pyrimidine selected from cytosine,  
 CC thymine, and uracil, and x = 6-16, (vii) a nucleotide sequence (CA)XRR,  
 CC where R is a purine selected from adenine and guanine and x = 6-16,  
 CC (viii) a nucleotide sequence (CA)XY, where Y is a pyrimidine selected  
 CC from cytosine, thymine, and uracil and x = 6-16, and (ix) a combination  
 CC of the primers. The method is useful for detecting genomic instability  
 CC which are commonly associated with the various stages of neoplastic  
 CC transformation and carcinogenesis. The method is rapid and simple  
 XX  
 SQ Sequence 18 BP; 8 A; 9 C; 1 G; 0 T; 0 U; 0 Other;  
 Query Match 1.5%; Score 16; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1793 TGTGTGTGTGTGTGTG 1808  
 DB 16 TGTGTGTGTGTGTGTG 1  
 RESULT 246  
 AAX77458/C  
 ID AAX77458 standard; DNA; 18 BP.  
 XX  
 AC AAX77458;  
 XX  
 DT 05-AUG-1999 (first entry)  
 XX  
 DE US5912147 primer 2.  
 XX  
 XX Primer; quantitation; genetic instability; tumour cell; detection;  
 KW neoplastic transformation; carcinogenesis; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN US5912147-A.  
 XX  
 PD 15-JUN-1999.  
 XX  
 PF 22-OCT-1996; 96US-00734973.  
 XX  
 PR 22-OCT-1996; 96US-00734973.  
 XX  
 PA (HEAL-) HEALTH RES INC.  
 XX  
 PI Anderson G, Stoler D, Basik M;  
 XX  
 XX WPI; 1999-357197/30.  
 DR

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XX Quantitating genetic instability.
PT Claim 4; Col 17-18; 27pp; English.
PS
XX
XX This invention describes a novel method for quantitating genetic
XX instability independent of microsatellite alterations by treating a
XX comparison pair comprising genomic DNA from tumour cells and genomic DNA
XX from normal cells. The method involves the cells from the same individual
XX with oligonucleotide primers selected from (i) a nucleotide sequence
XX (CG)XRG, where R is a purine selected from adenine and guanine and x = 3-
XX 7, (ii) a nucleotide sequence (CG)XY, where R is as in (i) and Y is a
XX pyrimidine selected from cytosine, thymine, and uracil and x = 3-7, (iii)
XX a nucleotide sequence (CG)XRY, where R is as in (i) and x = 3-7, (iv) a
XX nucleotide sequence (CG)XY, where Y is a pyrimidine selected from
XX cytosine, thymine, and uracil and x = 3-7, (v) a nucleotide sequence
XX (CA)XRG, where R is a purine selected from adenine and guanine and x = 6-
XX 16, (vi) a nucleotide sequence (CA)XY, where R is a purine selected from
XX adenine and guanine and Y is a pyrimidine selected from cytosine,
XX thymine, and uracil, and x = 6-16, (vii) a nucleotide sequence (CA)XRR,
XX where R is a purine selected from adenine and guanine and x = 6-16,
XX (viii) a nucleotide sequence (CA)XY, where Y is a pyrimidine selected
XX from cytosine, thymine, and uracil and x = 6-16, and (ix) a combination
XX of the primers. The method is useful for detecting genomic instability
XX which are commonly associated with the various stages of neoplastic
XX transformation and carcinogenesis. The method is rapid and simple
XX
SQ Sequence 18 BP; 8 A; 8 C; 2 G; 0 T; 0 U; 0 Other;
Query Match 1.5%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1793 TGTGTGTGTGTGTGTG 1808
DB 16 TGTGTGTGTGTGTGTG 1
RESULT 247
AAX77492/C
ID AAX77492 standard; DNA; 18 BP.
XX
XX AAX77492;
XX
XX 05-AUG-1999 (first entry)
XX
XX US5912147 primer 36.
XX
XX Primer; quantitation; genetic instability; tumour cell; detection;
XX neoplastic transformation; carcinogenesis; DNA/RNA hybrid; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX misc_RNA 17
XX /tag= a
XX /note= "uracil"
XX
XX US5912147-A.
XX
XX 15-JUN-1999.
XX
XX 22-OCT-1996; 96US-00734973.
XX
XX 22-OCT-1996; 96US-00734973.
XX
XX (HEAL-) HEALTH RES INC.
XX
XX Anderson G, Stoler D, Basik M;
XX
XX WPI; 1999-357197/30.
XX
XX Quantitating genetic instability.
XX
XX This invention describes a novel method for quantitating genetic
XX instability independent of microsatellite alterations by treating a
XX comparison pair comprising genomic DNA from tumour cells and genomic DNA
XX from normal cells. The method involves the cells from the same individual
XX with oligonucleotide primers selected from (i) a nucleotide sequence
XX (CG)XRG, where R is a purine selected from adenine and guanine and x = 3-
XX 7, (ii) a nucleotide sequence (CG)XY, where R is as in (i) and Y is a
XX pyrimidine selected from cytosine, thymine, and uracil and x = 3-7, (iii)
XX a nucleotide sequence (CG)XRY, where R is as in (i) and x = 3-7, (iv) a
XX nucleotide sequence (CG)XY, where Y is a pyrimidine selected from
XX cytosine, thymine, and uracil and x = 3-7, (v) a nucleotide sequence
XX (CA)XRG, where R is a purine selected from adenine and guanine and x = 6-
XX 16, (vi) a nucleotide sequence (CA)XY, where R is a purine selected from
XX adenine and guanine and Y is a pyrimidine selected from cytosine,
XX thymine, and uracil, and x = 6-16, (vii) a nucleotide sequence (CA)XRR,
XX where R is a purine selected from adenine and guanine and x = 6-16,
XX (viii) a nucleotide sequence (CA)XY, where Y is a pyrimidine selected
XX from cytosine, thymine, and uracil and x = 6-16, and (ix) a combination
XX of the primers. The method is useful for detecting genomic instability
XX which are commonly associated with the various stages of neoplastic
XX transformation and carcinogenesis. The method is rapid and simple
XX
SQ Sequence 18 BP; 8 A; 8 C; 2 G; 0 T; 0 U; 0 Other;
Query Match 1.5%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1793 TGTGTGTGTGTGTGTG 1808
DB 16 TGTGTGTGTGTGTGTG 1

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XX Claim 4; Col 31-32; 27pp; English.
XX
XX This invention describes a novel method for quantitating genetic
XX instability independent of microsatellite alterations by treating a
XX comparison pair comprising genomic DNA from tumour cells and genomic DNA
XX from normal cells. The method involves the cells from the same individual
XX with oligonucleotide primers selected from (i) a nucleotide sequence
XX (CG)XRG, where R is a purine selected from adenine and guanine and x = 3-
XX 7, (ii) a nucleotide sequence (CG)XY, where R is as in (i) and Y is a
XX pyrimidine selected from cytosine, thymine, and uracil and x = 3-7, (iii)
XX a nucleotide sequence (CG)XRY, where R is as in (i) and x = 3-7, (iv) a
XX nucleotide sequence (CG)XY, where Y is a pyrimidine selected from
XX cytosine, thymine, and uracil and x = 3-7, (v) a nucleotide sequence
XX (CA)XRG, where R is a purine selected from adenine and guanine and x = 6-
XX 16, (vi) a nucleotide sequence (CA)XY, where R is a purine selected from
XX adenine and guanine and Y is a pyrimidine selected from cytosine,
XX thymine, and uracil, and x = 6-16, (vii) a nucleotide sequence (CA)XRR,
XX where R is a purine selected from adenine and guanine and x = 6-16,
XX (viii) a nucleotide sequence (CA)XY, where Y is a pyrimidine selected
XX from cytosine, thymine, and uracil and x = 6-16, and (ix) a combination
XX of the primers. The method is useful for detecting genomic instability
XX which are commonly associated with the various stages of neoplastic
XX transformation and carcinogenesis. The method is rapid and simple
XX
SQ Sequence 18 BP; 8 A; 9 C; 0 G; 0 T; 1 U; 0 Other;
Query Match 1.5%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1793 TGTGTGTGTGTGTGTG 1808
DB 16 TGTGTGTGTGTGTGTG 1
RESULT 248
AAX77490/C
ID AAX77490 standard; DNA; 18 BP.
XX
XX AAX77490;
XX
XX 05-AUG-1999 (first entry)
XX
XX US5912147 primer 34.
XX
XX Primer; quantitation; genetic instability; tumour cell; detection;
XX neoplastic transformation; carcinogenesis; ss.
XX
XX Synthetic.
XX
XX US5912147-A.
XX
XX 15-JUN-1999.
XX
XX 22-OCT-1996; 96US-00734973.
XX
XX 22-OCT-1996; 96US-00734973.
XX
XX (HEAL-) HEALTH RES INC.
XX
XX Anderson G, Stoler D, Basik M;
XX
XX WPI; 1999-357197/30.
XX
XX Quantitating genetic instability.
XX
XX Claim 4; Col 29-30; 27pp; English.
XX
XX This invention describes a novel method for quantitating genetic
XX instability independent of microsatellite alterations by treating a
XX comparison pair comprising genomic DNA from tumour cells and genomic DNA
XX from normal cells. The method involves the cells from the same individual
XX

```



CC with oligonucleotide primers selected from (i) a nucleotide sequence  
 CC (CG)XRG, where R is a purine selected from adenine and guanine and x = 3-  
 CC 7, (ii) a nucleotide sequence (CG)XYR, where R is as in (i) and Y is a  
 CC pyrimidine selected from cytosine, thymine, and uracil and x = 3-7, (iii)  
 CC a nucleotide sequence (CG)XRR, where R is as in (i) and x = 3-7, (iv) a  
 CC nucleotide sequence (CG)XXY, where Y is a pyrimidine selected from  
 CC cytosine, thymine, and uracil and x = 3-7, (v) a nucleotide sequence  
 CC (CA)XRG, where R is a purine selected from adenine and guanine and x = 6-  
 CC 16, (vi) a nucleotide sequence (CA)XYR, where R is a purine selected from  
 CC adenine and guanine and Y is a pyrimidine selected from cytosine,  
 CC thymine, and uracil, and x = 6-16, (vii) a nucleotide sequence (CA)XRR,  
 CC where R is a purine selected from adenine and guanine and x = 6-16,  
 CC (viii) a nucleotide sequence (CA)XXY, where Y is a pyrimidine selected  
 CC from cytosine, thymine, and uracil and x = 6-16, and (ix) a combination  
 CC of the primers. The method is useful for detecting genomic instability  
 CC which are commonly associated with the various stages of neoplastic  
 CC transformation and carcinogenesis. The method is rapid and simple  
 XX  
 SQ Sequence 18 BP; 8 A; 9 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 1.5%; Score 16; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTG 1808  
 DB 16 TGTGTGTGTGTGTGTG 1

RESULT 249  
 ABZ89513  
 ID ABZ89513 standard; DNA; 20 BP.

AC ABZ89513;  
 DT 17-OCT-2003 (first entry)

DE Human oligonucleotide sequence.

KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
 KW lung inflammation; respiratory disease; ds.

OS Homo sapiens.

FN WO200285308-A2.

PD 31-OCT-2002.

PF 23-APR-2002; 2002WO-US013135.

PR 24-APR-2001; 2001US-0286137P.

PA (EPTG-) EPIGENESIS PHARM INC.

PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;

PI Miller S, Tang L, Shahabuddin S;

DR WPI; 2003-229219/22.

PT Pharmaceutical composition for treating ailments associated with impaired  
 PT respiration, has oligo(s) antisense to specific gene(s) or its  
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
 PT ubiquinone.

PS Disclosure; SEQ ID NO 4755; 872pp; English.

CC The invention relates to a novel pharmaceutical composition, which has a  
 CC first active agent comprising an oligonucleotide antisense to the  
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,

CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
 CC junctions of genes encoding a polypeptide associated with lung and/or  
 CC nasal airway dysfunction and a second active agent comprising an  
 CC antiinflammatory steroid and ubiquinone. A composition of the invention  
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
 CC immunosuppressive, and cytostatic activity. The composition may have a  
 CC use in antisense gene therapy. The composition is useful for treating or  
 CC preventing a respiratory, lung or malignant disease or condition, also  
 CC for enhancing the prophylactic or therapeutic respiratory effect of an  
 CC antiinflammatory steroid in a subject, for reducing or depleting levels  
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
 CC lung inflammation, lung allergies, or a respiratory disease or condition.  
 CC Note: The sequence data for this patent is not represented in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences

SQ Sequence 20 BP; 3 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 1.5%; Score 16; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTT 1880  
 DB 1 TTTTATTTTGTGTTT 16

RESULT 250  
 AAQ75552  
 ID AAQ75552 standard; DNA; 19 BP.

AC AAQ75552;  
 DT 04-AUG-1995 (first entry)

DE Reverse transcription primer used in cDNA analysis technique.

KW Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.  
 OS Synthetic.

PN JP06303997-A.

PD 01-NOV-1994.

PF 16-APR-1993; 93JP-00112515.

PR 16-APR-1993; 93JP-00112515.

PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

DR WPI; 1995-018287/03.

PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
 PT by digestion with restriction enzymes.

PS Disclosure; Page 5; 11pp; Japanese.

CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
 CC labelled reverse transcription primers (GENSEQ files AAQ75547-Q75798)  
 CC and using the aggregate of mRNAs as the template for each reverse  
 CC transcription primer; (b) digesting each of the prepared aggregates of  
 CC the double-stranded cDNAs with restriction enzyme and; (c)  
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
 CC method can be used to analyse gene expression rapidly and easily

SQ Sequence 19 BP; 2 A; 0 C; 0 G; 17 T; 0 U; 0 Other;

Query Match 1.5%; Score 15.8; DB 1; Length 19;

Best Local Similarity 89.5%; Pred. No. 1.7e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTATTTCTTTTAA 1883  
1 TTTTATTTTATTTTAA 19

Db  
|||||  
1 TTTTATTTTATTTTAA 19

RESULT 251  
AAQ34094/C  
ID AAQ34094 standard; DNA; 40 BP.  
XX  
AC AAQ34094;  
XX  
AC  
XX 25-MAR-2003 (revised)  
DT 02-FEB-1993 (first entry)  
XX  
XX Sequence of a microsatellite from clone TGLA53.  
DE  
XX PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;  
KW genetic mapping; traits; amplification; ss.  
XX  
XX Bos taurus.  
OS  
XX WO9213102-A1.  
PN  
XX  
XX 06-AUG-1992.  
PD  
XX  
XX 15-JAN-1992; 92WO-US000340.  
PF  
XX  
XX 15-JAN-1991; 91US-00642342.  
PR  
XX  
XX (GENM-) GENMARK.  
PA  
XX  
XX Georges M, Massey JM;  
PI  
XX WPI; 1992-284684/34.  
DR  
XX Polymorphic bovine DNA markers - used in genetic identification, gene  
PT mapping, and selective breeding.  
PT  
XX  
XX Table 7; Page 369; 517pp; English.  
PS  
XX The sequence is that of a bovine microsatellite sequence obtd. by  
CC screening a library of bovine MboI DNA fragments of between 250 and 500  
CC bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50  
CC clones cross-hybridised. Assuming independent distribution of  
CC microsatellites and MboI sites, the frequency of (T6)n > 9 microsatellites  
CC in the bovine genome is estimated at >100, 000. The sequence information  
CC for ca. 230 such bovine microsatellites is summarised in the  
CC specification and indexed herein (see below). The sequences upstream and  
CC downstream of the microsatellite sequence were used to generate the  
CC required PCR primers for in vitro amplification of the corresp.  
CC microsatellite (using the program OPTIPRIM). The microsatellites may be  
CC used to identify individuals, for parentage testing, and in the genetic  
CC mapping of economic trait loci, or genes involved the determinism of  
CC economically important traits esp. in cattle, to allow selective  
CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN  
CC field.)  
XX  
XX Sequence 40 BP; 7 A; 1 C; 13 G; 19 T; 0 U; 0 Other;  
SQ

Query Match 1.5%; Score 15.8; DB 1; Length 40;  
Best Local Similarity 89.5%; Pred. No. 2.5e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1814 ATATATATATATATCTACA 1832  
39 ATATATATATATATACACA 21

Db  
|||||  
39 ATATATATATATATACACA 21

RESULT 252  
AAT27914

ID AAT27914 standard; DNA; 18 BP.  
XX  
AC AAT27914;  
XX  
DT 28-JAN-1997 (first entry)  
XX  
DE 5'-anchored simple sequence repeat primer HVH(TG)7.5.  
XX  
XX Detection; polymorphism; perfect compound simple sequence repeat;  
KW adaptor directed primer; genome; genetic; fingerprinting;  
KW amplified fragment length polymorphism assay; microsatellite region;  
XX genetic trait marking; germplasm comparisons; 5'-anchored; ss.  
XX  
OS Synthetic.  
XX  
XX WO9617082-A2.  
FN  
XX 06-JUN-1996.  
PD  
XX  
XX 21-NOV-1995; 95WO-US015150.  
PF  
XX 28-NOV-1994; 94US-00346456.  
PR  
XX (DUFO) DU PONT DE NEMOURS & CO E I.  
PA  
XX Morgante M, Vogel JM;  
PI  
XX WPI; 1996-277795/28.  
DR  
XX Modified amplified fragment length polymorphism assay - for detection of  
PT polymorphism esp. in microsatellite regions.  
PT  
XX  
XX Example 1; Page 77; 173pp; English.  
PS  
XX Detecting polymorphisms between 2 nucleic acid samples, esp. in  
CC microsatellite regions, comprises digesting the nucleic acid to generate  
CC fragments, ligating adaptor segments to their ends, amplifying them using  
CC primer directed amplification and comparing the prods. to detect  
CC differences. The primers used in the amplification comprise a primer  
CC consisting of a perfect cpd. simple sequence complementary to an adaptor  
CC directed primer, comprising a sequence complementary to a SSR primer, which is  
CC segment. The present sequence is an example of a SSR primer, which is  
CC flanked at its 5'-end by degenerate nucleotides. The method represents a  
CC modified amplified fragment length polymorphism assay, which is partic.  
CC useful for genome fingerprinting, i.e. for genetic trait marking and  
CC germplasm comparisons  
XX  
XX Sequence 18 BP; 0 A; 0 C; 7 G; 8 T; 0 U; 3 Other;  
SQ

Query Match 1.5%; Score 15.6; DB 1; Length 18;  
Best Local Similarity 83.3%; Pred. No. 1.8e+02;  
Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1790 TATTGTGTGTGTGTGTGT 1807  
1 HVHTGTGTGTGTGTGTGT 18

Db  
|||||  
1 HVHTGTGTGTGTGTGTGT 18

RESULT 253  
AAV91399  
ID AAV91399 standard; RNA; 17 BP.  
XX  
AC AAV91399;  
XX  
DT 18-FEB-1999 (first entry)  
XX  
XX Human C-raf target site nucleotide position 2899.  
DE  
XX Human; c-raf; A-raf; B-raf; hammerhead ribozyme; hairpin ribozyme;  
KW target; substrate; catalyst; modulation; expression; Raf gene; delivery;  
KW screening; identification; synthesis; deprotection; purification; cancer;  
KW inflammation; psoriasis; non-hepatic ascites; infection; genetic drift;  
KW restenosis; rheumatoid arthritis; ss.

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XX OS Homo sapiens.
XX KW WO9850530-A2.
XX PN 12-NOV-1998.
XX PD 05-MAY-1998; 98WO-US009249.
XX PF 09-MAY-1997; 97US-0046059P.
XX PR 09-JUN-1997; 97US-0049002P.
XX PR 03-JUL-1997; 97US-0051718P.
XX PR 22-AUG-1997; 97US-0056808P.
XX PR 02-OCT-1997; 97US-0061321P.
XX PR 02-OCT-1997; 97US-0061324P.
XX PR 05-NOV-1997; 97US-0064866P.
XX PR 19-DEC-1997; 97US-0068212P.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PI Jarvis T, Metulic-Adamic J, Reynolds M, Kisich K, Bellon L;
XX PI Parry T, Beigelman L, Meswiggen JA, Karpelisky A, Burgin A;
XX PI Thompson J, Workman CT, Beaudry A, Sweedler D;
XX DR WPI; 1999-009494/01.
XX PS Identifying new catalytic nucleic acid that modulates selected processes
XX PT - especially ribozymes that cleave Raf RNA for treating cancer.
XX PT restenosis, and also new ribozymes and modified nucleoside triphosphates
XX PT used as antiviral agents and synthons.
XX PS Claim 177; Page 154; 259pp; English.
XX CC A method has been developed for the identification of a nucleic acid
XX CC capable of modulating a process in a biological system. The method
XX CC comprises: (a) introducing into the system a random library of nucleic
XX CC acid catalysts (NAC) having a substrate binding domain (SBD), comprising
XX CC a random sequence, and a catalytic domain (CD); and (b) identifying NAC
XX CC in systems where modulation has occurred and/or determining the sequence
XX CC of at least part of the SBDs in such systems. Nucleic acid molecules with
XX CC endonuclease activity and catalytic activity, from the present invention,
XX CC are used to modulate gene expression in plant and mammalian cells and to
XX CC cleave target nucleic acid, particularly for treating systemic diseases
XX CC caused by specific RNA, e.g. cancer, inflammation, psoriasis, non-hepatic
XX CC ascites and infection. They may also be used to detect genetic drift and
XX CC mutations in diseased cells and to determine c-rat RNA. Specifically NACs
XX CC with RNA-cleaving activity that modulate expression of the Raf gene, are
XX CC used to treat cancer, restenosis, psoriasis or rheumatoid arthritis, or
XX CC generally any condition associated with the level of c-rat. Introduction
XX CC of sugar/phosphate modifications increases stability against nuclease and
XX CC activity. AAV90922 to AAV93877 represent NACs that can be used in the
XX CC method, specifically for modulating the expression of a Raf gene
XX SQ Sequence 17 BP; 3 A; 0 C; 1 G; 0 T; 13 U; 0 Other;

Query Match 1.5%; Score 15.4; DB 1; Length 17;
Best Local Similarity 17.6%; Pred. No. 1.8e+02;
Matches 3; Conservative 13; Mismatches 1; Indels 0; Gaps 0;

QY 1866 TTTTATTTTGTGTTTA 1882
DB 1 UUUUAAUUUUUUUUU 17

RESULT 254
AAV21967
ID AAV21967 standard; DNA; 18 BP.
XX AC AAV21967;
XX DE 14-JUL-1998 (first entry)
XX DT Nuclease resistant antisense oligo NBT 140 targeted against (AT)9.
XX DE Nuclease resistant antisense oligo NBT 140 targeted against (AT)9.

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XX KW Nuclease resistant; bacterial infection; antibiotic; target;
XX KW veterinary medicine; treatment; human; industrial process;
XX KW bacterial control; ss.
XX OS Synthetic.
XX PN WO9803533-A1.
XX PD 29-JAN-1998.
XX PF 23-JUL-1997; 97WO-US012961.
XX PR 24-JUL-1996; 96US-00685575.
XX PA (OLIG-) OLIGOS ETC & OLIGOS THERAPEUTICS INC.
XX PI Arrow A, Dale RMK, Thompson TL;
XX PI WPI; 1998-120687/11.
XX DR Treating bacterial infections in humans or animals with
XX PT oligonucleotide(s) resistant to nuclease and targeted to bacterial
XX PT nucleic acid or proteins, also conjugates of these oligonucleotide(s)
XX PT with antibiotics.
XX PS Claim 49; Page 87; 163pp; English.
XX CC This antisense oligonucleotide is nuclease resistant and can be used in
XX CC the treatment of animals, including humans, having a bacterial infection.
XX CC The treatment comprises administration of such nuclease resistant
XX CC oligonucleotides, targeted to a nucleic acid or protein of the bacterium,
XX CC and formulated with a carrier. A compound comprising this nuclease
XX CC resistant oligonucleotide can be covalently linked to an antibiotic. The
XX CC method is used to treat infections by a wide variety of Gram-positive and
XX CC Gram-negative or acid-fast, bacteria, in human and veterinary medicine.
XX CC The methods are particularly used in immuno-compromised individuals (e.g.
XX CC patients with acquired immunodeficiency syndrome or those receiving
XX CC chemotherapy or radiation therapy), optionally in combination with, or
XX CC fused to, antiviral or other antimicrobial oligonucleotides. Apart from
XX CC therapeutic use, the oligonucleotides can be used to control bacteria in
XX CC laboratory cultures, foods, beverages and industrial processes. The
XX CC oligonucleotides are specific for bacteria, without affecting metabolism
XX CC in mammalian cells. They may also activate RNase H and have a general,
XX CC non-specific immune-stimulating effect. The oligonucleotides can be
XX CC administered orally, intranasally, rectally, topically or by injection,
XX CC optionally coupled to an agent (e.g. carbohydrate or polyamine) that
XX CC enhances cellular uptake
XX SQ Sequence 18 BP; 9 A; 0 C; 0 G; 9 T; 0 U; 0 Other;

Query Match 1.5%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1814 ATATATATATATATGTA 1830
DB 1 ATATATATATATATATA 17

RESULT 255
AAV21967/c
ID AAV21967 standard; DNA; 18 BP.
XX AC AAV21967;
XX DE 14-JUL-1998 (first entry)
XX DT Nuclease resistant antisense oligo NBT 140 targeted against (AT)9.
XX DE Nuclease resistant; bacterial infection; antibiotic; target;
XX KW veterinary medicine; treatment; human; industrial process;
XX KW bacterial control; ss.

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XX OS Synthetic.  
 XX PN WO9803533-A1.  
 XX PD 29-JAN-1998.  
 XX PF 23-JUL-1997; 97WO-US012961.  
 XX PR 24-JUL-1996; 96US-00685575.  
 XX PA (OLIG-) OLIGOS ETC & OLIGOS THERAPEUTICS INC.  
 XX PI Arrow A, Dale RMK, Thompson TL;  
 XX DR WPI; 1998-120687/11.  
 XX PT Treating bacterial infections in humans or animals with  
 PT oligonucleotide(s) - resistant to nuclease and targetted to bacterial  
 PT nucleic acid or proteins, also conjugates of these oligo:nucleotide(s)  
 PT with antibiotics.  
 XX PS Claim 49; Page 87; 163pp; English.  
 XX CC This antisense oligonucleotide is nuclease resistant and can be used in  
 CC the treatment of animals, including humans, having a bacterial infection.  
 CC The treatment comprises administration of such nuclease resistant  
 CC oligonucleotides, targeted to a nucleic acid or protein of the bacterium,  
 CC and formulated with a carrier. A compound comprising this nucleic  
 CC resistant oligonucleotide can be covalently linked to an antibiotic. The  
 CC method is used to treat infections by a wide variety of Gram-positive and  
 CC Gram-negative, or acid-fast, bacteria, in human and veterinary medicine.  
 CC The methods are particularly used in immuno-compromised individuals (e.g.  
 CC patients with acquired immunodeficiency syndrome or those receiving  
 CC chemotherapy or radiation therapy), optionally in combination with, or  
 CC fused to, antiviral or other antimicrobial oligonucleotides. Apart from  
 CC therapeutic use, the oligonucleotides can be used to control bacteria in  
 CC laboratory cultures, foods, beverages and industrial processes. The  
 CC oligonucleotides are specific for bacteria, without affecting metabolism  
 CC in mammalian cells. They may also activate RNase H and have a general,  
 CC non-specific immune-stimulating effect. The oligonucleotides can be  
 CC administered orally, intranasally, rectally, topically or by injection,  
 CC optionally coupled to an agent (e.g. carbohydrate or polyamine) that  
 CC enhances cellular uptake  
 XX SQ Sequence 18 BP; 9 A; 0 C; 0 G; 9 T; 0 U; 0 Other;  
 Query Match 1.5%; Score 15.4; DB 1; Length 18;  
 Best Local Similarity 94.1%; Pred. No. 1.9e+02;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1814 ATATATATATATATATGTA 1830  
 DB 18 ATATATATATATATATA 2  
 RESULT 256  
 AAH37514  
 ID AAH37514 standard; DNA; 18 BP.  
 XX AC AAH37514;  
 XX DT 14-AUG-2001 (first entry)  
 XX DE SNP specific lower PCR primer SEQ ID 310.  
 XX KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;  
 KW SNPs; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;  
 KW Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;  
 KW polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;  
 KW acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;  
 KW inflammation; forensic investigation; paternity analysis; PCR primer; ss.

OS Homo sapiens.  
 XX PN WO200129262-A2.  
 XX PD 26-APR-2001.  
 XX PF 13-OCT-2000; 2000WO-US028436.  
 XX PR 15-OCT-1999; 99US-0160096P.  
 XX PA (ORCH-) ORCHID BIOSCIENCES INC.  
 XX PI Picoult-Newburg L, Pohl M;  
 XX DR WPI; 2001-290930/30.  
 XX PT New genotyping oligonucleotide, useful for detecting the presence,  
 PT absence or identity of single polynucleotide polymorphism in a nucleic  
 PT acid sample.  
 XX PS Claim 1; Page 51; 83pp; English.  
 XX CC Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide  
 CC primer extension (SNPE) primers, and the sequences of regions flanking  
 CC sites of single nucleotide polymorphisms SNPs. The present invention  
 CC includes kits for determining the presence or absence of a SNP, using the  
 CC oligonucleotides of the invention. The PCR primers are used to amplify a  
 CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.  
 CC The oligonucleotides are useful for genotyping a nucleic acid sample by  
 CC performing a single-nucleotide primer extension reaction. The  
 CC oligonucleotides are useful for determining the presence, absence or  
 CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to  
 CC assess by association analysis the genotype of an individual or group of  
 CC individuals, having a pathological phenotypic trait suspected of being  
 CC caused by one or more SNPs. Phenotypic traits include diseases e.g.  
 CC agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular  
 CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,  
 CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic  
 CC traits also include symptoms of or susceptibility to multifactorial  
 CC disease of which a component is or may be genetic such as autoimmune  
 CC diseases, including, rheumatoid arthritis, multiple sclerosis, pathogenic  
 CC inflammation, cancer, nervous system diseases and infection by pathogenic  
 CC microorganism. The method is also useful in forensic investigations and  
 CC paternity analysis. The present sequence represents a PCR primer specific  
 CC for a human SNP containing DNA sequence  
 XX SQ Sequence 18 BP; 0 A; 2 C; 9 G; 7 T; 0 U; 0 Other;  
 Query Match 1.5%; Score 15.4; DB 1; Length 18;  
 Best Local Similarity 94.1%; Pred. No. 1.9e+02;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1794 GTGTGTGTGTGTGTGTG 1810  
 DB 1 GTGTGTGTGTGTGTGCG 17  
 RESULT 257  
 ABL38718  
 ID ABL38718 standard; DNA; 18 BP.  
 XX AC ABL38718;  
 XX DT 16-APR-2002 (first entry)  
 XX DE Immunostimulatory nucleic acid SEQ ID NO: 85.  
 XX KW Antibody-induced cell lysis; cancer; immunostimulatory; CD20;  
 KW angiogenesis; metastasis; cytostatic; phosphorothioate backbone; ss.  
 XX OS Synthetic.  
 XX PH Key Location/Qualifiers

modified\_base 1..18  
 /\*tag= a  
 /mod\_base= OTHER  
 /note= "phosphorothioate backbone"

WO200197843-A2.  
 27-DEC-2001.  
 22-JUN-2001; 2001WO-US020154.  
 22-JUN-2000; 2000US-0213346P.  
 (IOWA ) UNIV IOWA RES FOUND.  
 Weiner G, Hartmann G;  
 WPI; 2002-154611/20.

Treating or preventing cancer, such as basal cell carcinoma, comprises administering immunostimulatory nucleic acids that induce expression of cell surface antigens and antibodies to a subject having or at risk of developing cancer.

Disclosure; Page 116; 312pp; English.

The present invention relates to methods for treating or preventing cancer, involving administering to a subject having or at risk of developing cancer immunostimulatory nucleic acids that induce expression of cell surface antigens and antibodies. The methods are useful for treating or preventing cancer such as basal cell carcinoma, bladder cancer, bone cancer, brain and central nervous system (CNS) cancer, breast cancer, cervical cancer, colon and rectum cancer, connective tissue cancer, oesophageal cancer, eye cancer, kidney cancer, larynx cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin cancer, stomach cancer, testicular cancer, and uterine cancer. The present sequence is an immunostimulatory oligonucleotide described in the exemplification of the invention

Sequence 18 BP; 9 A; 0 C; 0 G; 9 T; 0 U; 0 Other;

Query Match 1.5%; Score 15.4; DB 1; Length 18;  
 Best Local Similarity 94.1%; Pred. No. 1.9e+02;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1814 ATATATATATATATGTA 1830  
 |||||  
 Db 1 ATATATATATATATA 17

RESULT 258  
 ABL38718/c  
 ID ABL38718 standard; DNA; 18 BP.  
 AC ABL38718;  
 DT 16-APR-2002 (first entry)  
 DE Immunostimulatory nucleic acid SEQ ID NO: 85.  
 KW Antibody-induced cell lysis; cancer; immunostimulatory; CD20;  
 KW angiogenesis; metastasis; cytostatic; phosphorothioate backbone; ss.  
 OS Synthetic.  
 FH Key Location/Qualifiers  
 modified\_base 1..18  
 /\*tag= a  
 /mod\_base= OTHER  
 /note= "phosphorothioate backbone"

PN WO200197843-A2.  
 XX 27-DEC-2001.  
 PD 22-JUN-2001; 2001WO-US020154.  
 XX 22-JUN-2000; 2000US-0213346P.  
 PF (IOWA ) UNIV IOWA RES FOUND.  
 XX Weiner G, Hartmann G;  
 XX WPI; 2002-154611/20.  
 DR Treating or preventing cancer, such as basal cell carcinoma, comprises administering immunostimulatory nucleic acids that induce expression of cell surface antigens and antibodies to a subject having or at risk of developing cancer.

Disclosure; Page 116; 312pp; English.

The present invention relates to methods for treating or preventing cancer, involving administering to a subject having or at risk of developing cancer immunostimulatory nucleic acids that induce expression of cell surface antigens and antibodies. The methods are useful for treating or preventing cancer such as basal cell carcinoma, bladder cancer, bone cancer, brain and central nervous system (CNS) cancer, breast cancer, cervical cancer, colon and rectum cancer, connective tissue cancer, oesophageal cancer, eye cancer, kidney cancer, larynx cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin cancer, stomach cancer, testicular cancer, and uterine cancer. The present sequence is an immunostimulatory oligonucleotide described in the exemplification of the invention

Sequence 18 BP; 9 A; 0 C; 0 G; 9 T; 0 U; 0 Other;

Query Match 1.5%; Score 15.4; DB 1; Length 18;  
 Best Local Similarity 94.1%; Pred. No. 1.9e+02;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1814 ATATATATATATATGTA 1830  
 |||||  
 Db 18 ATATATATATATATA 2

RESULT 259  
 AAT27912/c  
 ID AAT27912 standard; DNA; 18 BP.  
 XX AAT27912;  
 AC AAT27912;  
 DT 28-JAN-1997 (first entry)  
 DE 5'-anchored simple sequence repeat primer DBD(AC)7.5.  
 KW Detection; polymorphism; perfect compound simple sequence repeat;  
 KW adaptor directed primer; genome; genetic; fingerprinting;  
 KW amplified fragment length polymorphism assay; microsatellite region;  
 KW genetic trait marking; germplasm comparisons; 5'-anchored; ss.  
 OS Synthetic.  
 XX WO9617082-A2.  
 XX 06-JUN-1996.  
 PD 21-NOV-1995; 95WO-US015150.  
 XX 28-NOV-1994; 94US-00346456.  
 XX (DUPO ) DU PONT DE NEMOURS & CO E I.

XX PI Morgante M, Vogel JM;  
 XX DR WPI; 1996-277795/28.  
 XX PT Modified amplified fragment length polymorphism assay - for detection of  
 XX PT polymorphism esp. in microsatellite regions.  
 XX PS Example 1; Page 76; 173pp; English.  
 XX CC Detecting polymorphisms between 2 nucleic acid samples, esp. in  
 XX CC microsatellite regions, comprises digesting the nucleic acid to generate  
 XX CC fragments, ligating adaptor segments to their ends, amplifying them using  
 XX CC primer directed amplification and comparing the prods. to detect  
 XX CC differences. The primers used in the amplification comprise a primer  
 XX CC consisting of a perfect cpd. simple sequence repeat (SSR), and an adaptor  
 XX CC directed primer, comprising a sequence complementary to an adaptor  
 XX CC segment. The present sequence is an example of a SSR primer, which is  
 XX CC flanked at its 5'-end by degenerate nucleotides. The method represents a  
 XX CC modified amplified fragment length polymorphism assay, which is partic.  
 XX CC useful for genome fingerprinting, i.e. for genetic trait marking and  
 XX CC germplasm comparisons  
 XX SQ Sequence 18 BP; 8 A; 7 C; 0 G; 0 T; 0 U; 3 Other;  
 Query Match 1.4%; Score 15.2; DB 1; Length 18;  
 Best Local Similarity 93.8%; Pred. No. 2e+02;  
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1799 TGTGTGTGTGTGTGTA 1814  
 Db 18 TGTGTGTGTGTGTGTH 3  
 RESULT 260  
 AAH77495/c  
 ID AAH77495 standard; DNA; 41 BP.  
 AC AAH77495;  
 XX 20-NOV-2001 (first entry)  
 XX Human zinc finger protein 14 coding sequence probe #1.  
 XX Human; zinc finger protein 14; cancer; haemopathy; HIV infection;  
 XX immunological disease; inflammation; gene therapy; probe; ss.  
 XX Homo sapiens.  
 XX WO200166583-A1.  
 XX 13-SEP-2001.  
 XX 26-FEB-2001; 2001WO-CN000187.  
 XX 10-MAR-2000; 2000CN-00111978.  
 XX (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.  
 XX Mao Y, Xie Y;  
 XX WPI; 2001-565570/63.  
 XX New human zinc finger protein 14 for diagnosing and treating malignant  
 XX neoplasm, hemopathy, human immunodeficiency virus infection,  
 XX immunological diseases and various inflammations.  
 XX Example 6; Page 20; 37pp; Chinese.  
 XX The present invention provides the protein and coding sequences of human  
 XX zinc finger protein 14. The sequences can be used in the treatment of  
 XX cancer, haemopathy, HIV infection, immunological diseases and  
 XX inflammation. The present sequence is a probe for the coding sequence of

CC the invention  
 XX SQ Sequence 41 BP; 9 A; 0 C; 11 G; 21 T; 0 U; 0 Other;  
 Query Match 1.4%; Score 15.2; DB 1; Length 41;  
 Best Local Similarity 85.0%; Pred. No. 2.8e+02;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1813 TATATATATATATGTACA 1832  
 Db 40 TATAAATTTATATATACA 21  
 RESULT 261  
 AAQ33764  
 ID AAQ33764 standard; DNA; 15 BP.  
 AC AAQ33764;  
 XX 25-MAR-2003 (revised)  
 XX 02-FEB-1993 (first entry)  
 XX Microsatellite sequence from clone TGLA171.  
 XX PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;  
 XX genetic mapping; traits; amplification; ss.  
 XX Bos taurus.  
 XX WO3213102-A1.  
 XX 06-AUG-1992.  
 XX 15-JAN-1992; 92WO-US000340.  
 XX 15-JAN-1991; 91US-00642342.  
 XX (GENM-) GENMARK.  
 XX Georges M, Massey JM;  
 XX WPI; 1992-284684/34.  
 XX Polymorphic bovine DNA markers - used in genetic identification, gene  
 XX mapping, and selective breeding.  
 XX Table 7; Page 235; 517pp; English.  
 XX The sequence is that of a bovine microsatellite sequence obt'd. by  
 XX screening a library of bovine MboI DNA fragments of between 250 and 500  
 XX bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50  
 XX clones cross-hybridised. Assuming independent distribution of  
 XX microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites  
 XX in the bovine genome is estimated at >100, 000. The sequence information  
 XX for ca. 230 such bovine microsatellites is summarised in the  
 XX specification and indexed herein (see below). The sequences upstream and  
 XX downstream of the microsatellite sequence were used to generate the  
 XX required PCR primers for in vitro amplification of the corresp.  
 XX microsatellite (using the program OPLPRIM). The microsatellites may be  
 XX used to identify individuals, for parentage testing, and in the genetic  
 XX mapping of economic trait loci, or genes involved in the determination of  
 XX economically important traits esp. in cattle, to allow selective  
 XX breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN  
 XX field.)  
 XX SQ Sequence 15 BP; 0 A; 0 C; 8 G; 7 T; 0 U; 0 Other;  
 Query Match 1.4%; Score 15; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1794 GGTGTGTGTGTGTG 1808  
 |||||

Synthetic oligonucleotide; dinucleotide repeat; cytostatic; apoptosis;  
cell cycle arrest; cell proliferation; caspase; cytokine; interleukin;  
tumour necrosis factor; TNF; cancer; carcinoma; sarcoma; leukemia;  
lymphoma; ss.

Synthetic.

WO200144465-A2.  
21-JUN-2001.  
12-DEC-2000; 2000WO-CA001467.  
13-DEC-1999; 99US-0170325P.  
29-AUG-2000; 2000US-0228925P.  
(BION-) BIONICHE LIFE SCI INC.  
Phillips NC, Filion MC;  
WPI; 2001-398150/42.  
Composition comprising synthetic oligonucleotides which comprise multiple  
repeats of dinucleotides such as GT, TG useful for treating cancer by  
inducing cell cycle arrest, inhibiting proliferation, activating  
caspases.

Claim 5; Page 17; 77pp; English.

The present sequence is that of a synthetic oligonucleotide useful to the  
invention. The invention relates to a composition, comprising a 2 to 20  
base 3'-OH, 5'-OH synthetic oligonucleotide which comprises multiple  
repeats of dinucleotides such as GT, TG, etc., according to specific  
formula and having cytostatic activity. The oligonucleotide compositions  
are useful for inducing cell cycle arrest, inhibition of proliferation,  
activation of caspases and induction of apoptosis or production of  
cytokines such as interleukin (IL)-1-beta, IL-6, IL-10, IL-12 and tumour  
necrosis factor (TNF)-alpha by immune system cells, in an animal having  
cancer such as primary carcinoma, secondary carcinoma, primary sarcoma  
and secondary sarcoma such as, leukemia, lymphoma, breast, prostate,  
colorectal, ovarian or bone cancer. The compositions induce apoptosis  
independent of Fas, p53/p21, p21/waf-1/CIP, pl5(ink4B), pl6(ink4), drug  
resistance, caspase 3, transforming growth factor (TGF)-beta 1 receptor  
and hormone dependence

Sequence 15 BP; 0 A; 0 C; 8 G; 7 T; 0 U; 0 Other;

Query Match 1.4%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. NO. 1.8e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTCGTGTGTG 1808  
1 GTGTGTCGTGTGTG 15

Db

RESULT 264  
ABK32632  
ID ABK32632 standard; DNA; 15 BP.  
XX AC ABK32632;  
XX DT  
XX DE 23-APR-2002 (first entry)  
DE Human pancreatic cancer SAGE tag #184.  
XX Human; colon cancer; colorectal cancer; pancreatic cancer; SAGE tag;  
KW serial analysis of gene expression; diagnostic; prognostic; probe;  
KW cancer marker; ss.  
XX Homo sapiens.  
OS  
XX US6333152-B1.  
PN

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XX PD 25-DEC-2001.
XX PF 20-MAY-1998; 98US-00081645.
XX PR 20-MAY-1998; 98US-00081645.
XX PA (UYJO ) UNIV JOHNS HOPKINS.
XX PI Vogelstein B, Kinzler KW, Zhang L, Zhou W;
XX DR WPI; 2002-153921/20.
XX PT New human nucleic acid containing specific SAGE tags, useful as
XX PT diagnostic markers for cancer, also derived probes.
XX PS Disclosure; Col 83; 161pp; English.
XX CC The invention relates to an isolated, purified human nucleic acid (I)
XX CC that has the same sequence as a mRNA found in humans and is a SAGE
XX CC (serial analysis of gene expression) tag comprising a single stranded
XX CC probe containing at least 10 consecutive nucleotides. SAGE tags, are
XX CC diagnostic and prognostic markers of cancer, especially of the colon and
XX CC pancreas. ABK1900-ABK3270 represent human colon and pancreatic cancer
XX CC SAGE tags of the invention
XX CC
XX CC Sequence 15 BP; 2 A; 4 C; 2 G; 7 T; 0 U; 0 Other;
XX
XX Query Match 1.4%; Score 15; DB 1; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 1.8e+02;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 2231 CATGTTGCACCTTT 2245
XX DB 1 CATGTTGCACCTTT 15
XX
XX RESULT 265
XX ABK90419
XX ID ABK90419 standard; DNA; 16 BP.
XX AC ABK90419;
XX DT 05-NOV-2002 (first entry)
XX DE Human UGT1A1 promoter polymorphism (TA)8 repeat.
XX KW Human; ds; UGT1A1; promoter; Gilbert's syndrome; hyperbilirubinaemia;
XX KW uridine diphosphate glucuronosyltransferase; Crigler-Najjar syndrome;
XX KW UGT; polymorphism detection; TA repeat; glucuronidation; Irinotecan;
XX KW TAS-103; xenobiotic.
XX OS Homo sapiens.
XX PN US6395481-B1.
XX XX 28-MAY-2002.
XX PF 16-FEB-1999; 99US-00251274.
XX PR 16-FEB-1999; 99US-00251274.
XX PA (ARCH-) ARCH DEV CORP.
XX PI Di Rienzo A, Iyer L, Ratain MJ;
XX DR WPI; 2002-588597/63.
XX PT Detecting polymorphisms in uridine diphosphate glucuronosyltransferase
XX PT gene promoter, useful for optimizing drug dosages for a patient,
XX PT comprises determining the presence of five thymidine-adenine repeats in
XX PT the promoter.

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PS Claim 7; Col 17; 13pp; English.
XX
XX CC The invention relates to detecting (M1) polymorphisms in a uridine
XX CC diphosphate glucuronosyltransferase (UGT) gene promoter by determining
XX CC the presence of five thymidine-adenine (TA) repeats in the promoter,
XX CC where the presence of the five TA repeats correlates with increased
XX CC expression of the gene. The method is used for detecting polymorphisms in
XX CC a UGT gene promoter, preferably a UGT 1 (UGT1A1) gene promoter. (M1) is
XX CC useful for screening individuals for variation in glucuronidation
XX CC activity, for optimising drug dosages for a patient, where the drugs
XX CC (e.g. Irinotecan or TAS-103) are glucuronidated by UGT (preferably
XX CC UGT1A1) and the activity of the drug is effected by its level of
XX CC glucuronidation. The method preferably involves obtaining DNA from an
XX CC individual, amplifying all or part of a UGT gene promoter (UGT1A1 gene
XX CC promoter) contained in the DNA and determining the number of TA repeats
XX CC in the promoter. Thus the DNA being amplified comprises all or part of
XX CC UGT1A1 promoter. The DNA is amplified by a polymerase chain reaction and
XX CC the number of TA repeats is determined by gel electrophoresis or by
XX CC sequencing the amplified DNA. The polymorphism comprises an allele
XX CC consisting of five TA repeats (TA)5, six TA repeats (TA)6, or seven TA
XX CC repeats (TA)7. The promoter has any one of the genotypes (TA)5/(TA)5,
XX CC (TA)5/(TA)6, (TA)5/(TA)7, (TA)5/(TA)8, (TA)6/(TA)8, (TA)7/(TA)8 or
XX CC (TA)8/(TA)8. (M1) is also useful for predicting an individual's
XX CC sensitivity to xenobiotics that are glucuronidated by a UGT (preferably
XX CC UGT1A1) gene product, the method comprising determining the number of TA
XX CC repeats in a UGT gene promoter, where the number of TA repeats correlates
XX CC with expression of the UGT gene, and the individual's sensitivity to
XX CC xenobiotics is effected by glucuronidation activity. The methods
XX CC preferably involve determining the presence of five, six or seven TA
XX CC repeats in the promoter. Defects in glucuronidation is associated with
XX CC Gilbert's syndrome (hyperbilirubinaemia) and Crigler-Najjar syndrome. The
XX CC present sequence is the UGT1A1 promoter (TA)8 repeat
XX
XX CC Sequence 16 BP; 8 A; 0 C; 0 G; 8 T; 0 U; 0 Other;
XX
XX Query Match 1.4%; Score 15; DB 1; Length 16;
XX Best Local Similarity 100.0%; Pred. No. 1.9e+02;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1813 TATATATATATATAT 1827
XX DB 1 TATATATATATATAT 15
XX
XX RESULT 266
XX ABK90419/C
XX ID ABK90419 standard; DNA; 16 BP.
XX AC ABK90419;
XX DT 05-NOV-2002 (first entry)
XX DE Human UGT1A1 promoter polymorphism (TA)8 repeat.
XX KW Human; ds; UGT1A1; promoter; Gilbert's syndrome; hyperbilirubinaemia;
XX KW uridine diphosphate glucuronosyltransferase; Crigler-Najjar syndrome;
XX KW UGT; polymorphism detection; TA repeat; glucuronidation; Irinotecan;
XX KW TAS-103; xenobiotic.
XX OS Homo sapiens.
XX PN US6395481-B1.
XX XX 28-MAY-2002.
XX PF 16-FEB-1999; 99US-00251274.
XX PR 16-FEB-1999; 99US-00251274.
XX PA (ARCH-) ARCH DEV CORP.
XX PI Di Rienzo A, Iyer L, Ratain MJ;
XX DR WPI; 2002-588597/63.
XX PT Detecting polymorphisms in uridine diphosphate glucuronosyltransferase
XX PT gene promoter, useful for optimizing drug dosages for a patient,
XX PT comprises determining the presence of five thymidine-adenine repeats in
XX PT the promoter.

```



DR WPI; 2002-598597/63.  
 XX  
 PT Detecting polymorphisms in uridine diphosphate glucuronosyltransferase  
 PT gene promoter, useful for optimizing drug dosages for a patient,  
 PT comprises determining the presence of five thymidine-adenine repeats in  
 PT the promoter.  
 XX  
 XX Claim 7; Col 17; 13pp; English.  
 XX  
 CC The invention relates to detecting (M1) polymorphisms in a uridine  
 CC diphosphate glucuronosyltransferase (UGT) gene promoter by determining  
 CC the presence of five thymidine-adenine (TA) repeats in the promoter,  
 CC where the presence of the five TA repeats correlates with increased  
 CC expression of the gene. The method is used for detecting polymorphisms in  
 CC a UGT gene promoter, preferably a UGT 1 (UGT1A1) gene promoter. (M1) is  
 CC useful for screening individuals for variation in glucuronidation  
 CC activity, for optimising drug dosages for a patient, where the drugs  
 CC (e.g. Irinotecan or TAS-103) are glucuronidated by UGT (preferably  
 CC UGT1A1) and the activity of the drug is effected by its level of  
 CC glucuronidation. The method preferably involves obtaining DNA from an  
 CC individual, amplifying all or part of a UGT gene promoter (UGT1A1 gene  
 CC promoter) contained in the DNA and determining the number of TA repeats  
 CC in the promoter. Thus the DNA being amplified comprises all or part of  
 CC UGT1A1 promoter. The DNA is amplified by a polymerase chain reaction and  
 CC the number of TA repeats is determined by gel electrophoresis or by  
 CC sequencing the amplified DNA. The polymorphism comprises an allele  
 CC consisting of five TA repeats (TA)5, six TA repeats (TA)6, or seven TA  
 CC repeats (TA)7. The promoter has any one of the genotypes (TA)5/(TA)5,  
 CC (TA)5/(TA)6, (TA)5/(TA)7, (TA)6/(TA)8, (TA)7/(TA)8 or  
 CC (TA)8/(TA)8. (M1) is also useful for predicting an individual's  
 CC sensitivity to xenobiotics that are glucuronidated by a UGT (preferably  
 CC UGT1A1) gene product, the method comprising determining the number of TA  
 CC repeats in a UGT gene promoter, where the number of TA repeats correlates  
 CC with expression of the UGT gene, and the individuals sensitivity to  
 CC xenobiotics is effected by glucuronidation activity. The methods  
 CC preferably involve determining the presence of five, six or seven TA  
 CC repeats in the promoter. Defects in glucuronidation is associated with  
 CC Gilbert's syndrome (hyperbilirubinaemia) and Crigler-Najjar syndrome. The  
 CC present sequence is the UGT1A1 promoter (TA)8 repeat  
 XX  
 XX Sequence 16 BP; 8 A; 0 C; 0 G; 8 T; 0 U; 0 Other;  
 SQ  
 Query Match 1.4%; Score 15; DB 1; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1813 TATATATATATAT 1827  
 DB 16 TATATATATATAT 2  
 RESULT 267  
 AAL50677  
 ID AAL50677 standard; DNA; 16 BP.  
 AC AAL50677;  
 XX  
 XX 16-JAN-2003 (first entry)  
 XX  
 XX Human uridine diphosphate glucuronosyltransferase gene polymorphism #11.  
 DE  
 KW Human; polymorphism; TA repeat; ds; UGT; thymidine-adenine repeat;  
 KW uridine diphosphate glucuronosyltransferase gene promoter; UGT1A1;  
 KW drug dosage optimisation; xenobiotic sensitivity.  
 XX  
 OS Homo sapiens.  
 XX  
 XX US2002115097-A1.  
 PN  
 XX 22-AUG-2002.  
 PD  
 XX 01-FEB-2002; 2002US-00061693.  
 PF  
 XX 16-FEB-1999; 99US-00251274.  
 XX  
 XX (ARCH-) ARCH DEV CORP.  
 PA  
 XX Rienzo AD, Iyer L, Ratain MJ;  
 PI  
 XX WPI; 2002-740095/80.  
 XX  
 XX Detecting polymorphisms in uridine diphosphate glucuronosyltransferase  
 XX gene promoter, useful for optimizing drug dosages for a patient, involves  
 XX determining number of thymidine-adenine repeats in the promoter.  
 XX  
 XX Claim 7; Page 9; 13pp; English.  
 XX  
 CC The invention comprises a method for detecting polymorphisms in a uridine

PR 16-FEB-1999; 99US-00251274.  
 XX  
 XX (ARCH-) ARCH DEV CORP.  
 XX  
 PI Rienzo AD, Iyer L, Ratain MJ;  
 XX  
 XX WPI; 2002-740095/80.  
 DR  
 XX  
 XX Detecting polymorphisms in uridine diphosphate glucuronosyltransferase  
 PT gene promoter, useful for optimizing drug dosages for a patient, involves  
 PT determining number of thymidine-adenine repeats in the promoter.  
 PT  
 XX Claim 7; Page 9; 13pp; English.  
 PS  
 XX The invention comprises a method for detecting polymorphisms in a uridine  
 CC diphosphate glucuronosyltransferase (UGT) gene promoter (preferably  
 CC UGT1A1). The method involves determining the number of thymidine-adenine  
 CC (TA) repeats in the promoter - as the number of TA repeats correlates  
 CC with expression of the UGT gene. The method of the invention is useful  
 CC for detecting polymorphisms in a UGT gene promoter. The method of the  
 CC invention is also useful in optimising drug dosages and predicting an  
 CC individual's sensitivity to xenobiotics for drugs and xenobiotics that  
 CC are glucuronidated by UGT. The present DNA sequence represents a UGT gene  
 CC TA repeat polymorphism  
 XX  
 SQ Sequence 16 BP; 8 A; 0 C; 0 G; 8 T; 0 U; 0 Other;  
 Query Match 1.4%; Score 15; DB 1; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1813 TATATATATATAT 1827  
 DB 1 TATATATATATAT 15  
 RESULT 268  
 AAL50677/c  
 ID AAL50677 standard; DNA; 16 BP.  
 XX  
 XX AAL50677;  
 AC  
 XX  
 XX 16-JAN-2003 (first entry)  
 DT  
 XX  
 XX Human uridine diphosphate glucuronosyltransferase gene polymorphism #11.  
 DE  
 KW Human; polymorphism; TA repeat; ds; UGT; thymidine-adenine repeat;  
 KW uridine diphosphate glucuronosyltransferase gene promoter; UGT1A1;  
 KW drug dosage optimisation; xenobiotic sensitivity.  
 XX  
 OS Homo sapiens.  
 XX  
 XX US2002115097-A1.  
 PN  
 XX 22-AUG-2002.  
 PD  
 XX 01-FEB-2002; 2002US-00061693.  
 PF  
 XX 16-FEB-1999; 99US-00251274.  
 XX  
 XX (ARCH-) ARCH DEV CORP.  
 PA  
 XX Rienzo AD, Iyer L, Ratain MJ;  
 PI  
 XX WPI; 2002-740095/80.  
 XX  
 XX Detecting polymorphisms in uridine diphosphate glucuronosyltransferase  
 PT gene promoter, useful for optimizing drug dosages for a patient, involves  
 PT determining number of thymidine-adenine repeats in the promoter.  
 PT  
 XX Claim 7; Page 9; 13pp; English.  
 XX  
 CC The invention comprises a method for detecting polymorphisms in a uridine

CC diphosphate glucuronosyltransferase (UGT) gene promoter (preferably  
 CC UGT1A1). The method involves determining the number of thymidine-adenine  
 CC (TA) repeats in the promoter - as the number of TA repeats correlates  
 CC with expression of the UGT gene. The method of the invention is useful  
 CC for detecting polymorphisms in a UGT gene promoter. The method of the  
 CC invention is also useful in optimizing drug dosages and predicting an  
 CC individual's sensitivity to xenobiotics for drugs and xenobiotics that  
 CC are glucuronidated by UGT. The present DNA sequence represents a UGT gene  
 CC TA repeat polymorphism

XX  
 SQ Sequence 16 BP; 8 A; 0 C; 0 G; 8 T; 0 U; 0 Other;  
 Query Match 1.4%; Score 15; DB 1; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1813 TATATATATATATAT 1827  
 DB 16 TATATATATATATAT 2  
 |||||

RESULT 269  
 ABK90422  
 ID ABK90422 standard; DNA; 17 BP.  
 XX AC ABK90422;  
 XX 05-NOV-2002 (first entry)  
 XX Human UGT1A1 promoter polymorphism (TA)7 repeat region.  
 XX Human; ds; UGT1A1; promoter; Gilbert's syndrome; hyperbilirubinaemia;  
 KW uridine diphosphate glucuronosyltransferase; Crigler-Najjar syndrome;  
 KW UGT; polymorphism detection; TA repeat; glucuronidation; irinotecan;  
 KW TAS-103; xenobiotic.  
 XX Homo sapiens.  
 OS US6395481-B1.  
 PN 28-MAY-2002.  
 XX 16-FEB-1999; 99US-00251274.  
 XX 16-FEB-1999; 99US-00251274.  
 XX (ARCH-) ARCH DEV CORP.  
 PA Di Rienzo A, Iyer L, Ratain MJ;  
 PI WPI; 2002-588597/63.  
 XX Detecting polymorphisms in uridine diphosphate glucuronosyltransferase  
 PT gene promoter, useful for optimizing drug dosages for a patient,  
 PT comprises determining the presence of five thymidine-adenine repeats in  
 PT the promoter.  
 XX Example 6; Col 11; 13pp; English.

CC The invention relates to detecting (M1) polymorphisms in a uridine  
 CC diphosphate glucuronosyltransferase (UGT) gene promoter by determining  
 CC the presence of five thymidine-adenine (TA) repeats in the promoter,  
 CC where the presence of the five TA repeats correlates with increased  
 CC expression of the gene. The method is used for detecting polymorphisms in  
 CC a UGT gene promoter, preferably a UGT 1 (UGT1A1) gene promoter. (M1) is  
 CC useful for screening individuals for variation in glucuronidation  
 CC activity, for optimising drug dosages for a patient, where the drugs  
 CC (e.g. irinotecan or TAS-103) are glucuronidated by UGT (preferably  
 CC UGT1A1) and the activity of the drug is affected by its level of  
 CC glucuronidation. The method preferably involves obtaining DNA from an  
 CC individual, amplifying all or part of a UGT gene promoter (UGT1A1 gene  
 CC promoter) contained in the DNA and determining the number of TA repeats  
 CC in the promoter. Thus the DNA being amplified comprises all or part of

CC UGT1A1 promoter. The DNA is amplified by a polymerase chain reaction and  
 CC the number of TA repeats is determined by gel electrophoresis or by  
 CC sequencing the amplified DNA. The polymorphism comprises an allele  
 CC consisting of five TA repeats (TA)5, six TA repeats (TA)6, or seven TA  
 CC repeats (TA)7. The promoter has any one of the genotypes (TA)5/(TA)5,  
 CC (TA)5/(TA)6, (TA)5/(TA)7, (TA)5/(TA)8, (TA)6/(TA)8, (TA)7/(TA)8 or  
 CC (TA)8/(TA)8. (M1) is also useful for predicting an individual's  
 CC sensitivity to xenobiotics that are glucuronidated by a UGT (preferably  
 CC UGT1A1) gene product, the method comprising determining the number of TA  
 CC repeats in a UGT gene promoter, where the number of TA repeats correlates  
 CC with expression of the UGT gene, and the individual's sensitivity to  
 CC xenobiotics is affected by glucuronidation activity. The methods  
 CC preferably involve determining the presence of five, six or seven TA  
 CC repeats in the promoter. Defects in glucuronidation is associated with  
 CC Gilbert's syndrome (hyperbilirubinaemia) and Crigler-Najjar syndrome. The  
 CC present sequence is the UGT1A1 promoter (TA)7 repeat region

XX  
 SQ Sequence 17 BP; 9 A; 0 C; 0 G; 8 T; 0 U; 0 Other;  
 Query Match 1.4%; Score 15; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 2e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1813 TATATATATATATAT 1827  
 DB 1 TATATATATATATAT 15  
 |||||

RESULT 270  
 ABK90422/c  
 ID ABK90422 standard; DNA; 17 BP.  
 XX AC ABK90422;  
 XX 05-NOV-2002 (first entry)  
 XX Human UGT1A1 promoter polymorphism (TA)7 repeat region.  
 XX Human; ds; UGT1A1; promoter; Gilbert's syndrome; hyperbilirubinaemia;  
 KW uridine diphosphate glucuronosyltransferase; Crigler-Najjar syndrome;  
 KW UGT; polymorphism detection; TA repeat; glucuronidation; irinotecan;  
 KW TAS-103; xenobiotic.  
 XX Homo sapiens.  
 OS US6395481-B1.  
 PN 28-MAY-2002.  
 XX 16-FEB-1999; 99US-00251274.  
 XX 16-FEB-1999; 99US-00251274.  
 XX (ARCH-) ARCH DEV CORP.  
 PA Di Rienzo A, Iyer L, Ratain MJ;  
 PI WPI; 2002-588597/63.  
 XX Detecting polymorphisms in uridine diphosphate glucuronosyltransferase  
 PT gene promoter, useful for optimizing drug dosages for a patient,  
 PT comprises determining the presence of five thymidine-adenine repeats in  
 PT the promoter.  
 XX Example 6; Col 11; 13pp; English.

CC The invention relates to detecting (M1) polymorphisms in a uridine  
 CC diphosphate glucuronosyltransferase (UGT) gene promoter by determining  
 CC the presence of five thymidine-adenine (TA) repeats in the promoter,  
 CC where the presence of the five TA repeats correlates with increased  
 CC expression of the gene. The method is used for detecting polymorphisms in  
 CC a UGT gene promoter, preferably a UGT 1 (UGT1A1) gene promoter. (M1) is  
 CC useful for screening individuals for variation in glucuronidation

CC activity, for optimising drug dosages for a patient, where the drugs  
 CC (e.g. Irinotecan or TAS-103) are glucuronidated by UGT (preferably  
 CC UGT1A1) and the activity of the drug is affected by its level of  
 CC glucuronidation. The method preferably involves obtaining DNA from an  
 CC individual, amplifying all or part of a UGT gene promoter (UGT1A1 gene  
 CC promoter) contained in the DNA and determining the number of TA repeats  
 CC in the promoter. Thus the DNA being amplified comprises all or part of  
 CC UGT1A1 promoter. The DNA is amplified by a polymerase chain reaction and  
 CC the number of TA repeats is determined by gel electrophoresis or by  
 CC sequencing the amplified DNA. The polymorphism comprises an allele  
 CC consisting of five TA repeats (TA)5, six TA repeats (TA)6, or seven TA  
 CC repeats (TA)7. The promoter has any one of the genotypes (TA)5/(TA)5,  
 CC (TA)5/(TA)6, (TA)5/(TA)7, (TA)6/(TA)8, (TA)7/(TA)8 or  
 CC (TA)8/(TA)8. (M1) is also useful for predicting an individual's  
 CC sensitivity to xenobiotics that are glucuronidated by a UGT (preferably  
 CC UGT1A1) gene product, the method comprising determining the number of TA  
 CC repeats in a UGT gene promoter, where the number of TA repeats correlates  
 CC with expression of the UGT gene, and the individuals sensitivity to  
 CC xenobiotics is affected by glucuronidation activity. The methods  
 CC preferably involve determining the presence of five, six or seven TA  
 CC repeats in the promoter. Defects in glucuronidation is associated with  
 CC Gilbert's syndrome (hyperbilirubinaemia) and Crigler-Najjar syndrome. The  
 CC present sequence is the UGT1A1 promoter (TA)7 repeat region  
 CC  
 XX Sequence 17 BP; 9 A; 0 C; 0 G; 8 T; 0 U; 0 Other;

Query Match 1.4%; Score 15; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 2e+02; 0; Indels 0; Gaps 0;  
 Matches 15; Conservative 0; Mismatches 0;

QY 1813 TATATATATATATAT 1827  
 DB 15 TATATATATATATAT 2

RESULT 271  
 AAL50679  
 ID AAL50679 standard; DNA; 17 BP.  
 XX  
 AC AAL50679;  
 XX  
 DT 16-JAN-2003 (first entry)  
 XX  
 DE Human uridine diphosphate glucuronosyltransferase gene polymorphism #13.  
 XX  
 KW Human; polymorphism; TA repeat; ds; UGT; thymidine-adenine repeat;  
 KW uridine diphosphate glucuronosyltransferase gene promoter; UGT1A1;  
 KW drug dosage optimisation; xenobiotic sensitivity.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2002115097-A1.  
 XX  
 PD 22-AUG-2002.  
 XX  
 PF 01-FEB-2002; 2002US-00061693.  
 XX  
 PR 16-FEB-1999; 99US-00251274.  
 XX  
 PA (ARCH-) ARCH DEV CORP.  
 XX  
 PI Rienzo AD, Iyer L, Ratain MJ;  
 XX  
 DR WPI; 2002-740095/80.  
 XX  
 PS Example 6; Page 2; 13pp; English.

The invention comprises a method for detecting polymorphisms in a uridine  
 PT gene promoter, useful for optimizing drug dosages for a patient, involves  
 PT determining number of thymidine-adenine repeats in the promoter.

XX  
 PS Example 6; Page 2; 13pp; English.  
 XX  
 CC The invention comprises a method for detecting polymorphisms in a uridine  
 CC diphosphate glucuronosyltransferase (UGT) gene promoter (preferably

CC UGT1A1). The method involves determining the number of thymidine-adenine  
 CC (TA) repeats in the promoter - as the number of TA repeats correlates  
 CC with expression of the UGT gene. The method of the invention is useful  
 CC for detecting polymorphisms in a UGT gene promoter. The method of the  
 CC invention is also useful in optimising drug dosages and predicting an  
 CC individual's sensitivity to xenobiotics for drugs and xenobiotics that  
 CC are glucuronidated by UGT. The present DNA sequence represents a UGT gene  
 CC TA repeat polymorphism  
 XX  
 SQ Sequence 17 BP; 9 A; 0 C; 0 G; 8 T; 0 U; 0 Other;

Query Match 1.4%; Score 15; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 2e+02; 0; Indels 0; Gaps 0;  
 Matches 15; Conservative 0; Mismatches 0;

QY 1813 TATATATATATATAT 1827  
 DB 1 TATATATATATATAT 15

RESULT 272  
 AAL50679/c  
 ID AAL50679 standard; DNA; 17 BP.  
 XX  
 AC AAL50679;  
 XX

DT 16-JAN-2003 (first entry)

DE Human uridine diphosphate glucuronosyltransferase gene polymorphism #13.

KW Human; polymorphism; TA repeat; ds; UGT; thymidine-adenine repeat;  
 KW uridine diphosphate glucuronosyltransferase gene promoter; UGT1A1;  
 KW drug dosage optimisation; xenobiotic sensitivity.

OS Homo sapiens.

PN US2002115097-A1.

PD 22-AUG-2002.

PF 01-FEB-2002; 2002US-00061693.

PR 16-FEB-1999; 99US-00251274.

PA (ARCH-) ARCH DEV CORP.

PI Rienzo AD, Iyer L, Ratain MJ;

DR WPI; 2002-740095/80.

PT Detecting polymorphisms in uridine diphosphate glucuronosyltransferase  
 PT gene promoter, useful for optimizing drug dosages for a patient, involves  
 PT determining number of thymidine-adenine repeats in the promoter.

PS Example 6; Page 2; 13pp; English.

XX The invention comprises a method for detecting polymorphisms in a uridine  
 CC diphosphate glucuronosyltransferase (UGT) gene promoter (preferably  
 CC UGT1A1). The method involves determining the number of thymidine-adenine  
 CC (TA) repeats in the promoter - as the number of TA repeats correlates  
 CC with expression of the UGT gene. The method of the invention is useful  
 CC for detecting polymorphisms in a UGT gene promoter. The method of the  
 CC invention is also useful in optimising drug dosages and predicting an  
 CC individual's sensitivity to xenobiotics for drugs and xenobiotics that  
 CC are glucuronidated by UGT. The present DNA sequence represents a UGT gene  
 CC TA repeat polymorphism  
 XX  
 SQ Sequence 17 BP; 9 A; 0 C; 0 G; 8 T; 0 U; 0 Other;

Query Match 1.4%; Score 15; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 2e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

[illegible]

PD 06-JUN-1996.  
 XX 21-NOV-1995; 95WO-US015150.  
 XX 28-NOV-1994; 94US-00346456.  
 XX (DUPO ) DU PONT DE NEMOURS & CO E I.  
 XX Morgante M, Vogel JM;  
 PI WPI; 1996-277795/28.  
 DR Modified amplified fragment length polymorphism assay - for detection of  
 PT polymorphism esp. in micro:satellite regions.  
 XX Example 1; Page 77; 173pp; English.  
 CC Detecting polymorphisms between 2 nucleic acid samples, esp. in  
 CC microsatellite regions, comprises digesting the nucleic acid to generate  
 CC fragments, ligating adaptor segments to their ends, amplifying them using  
 CC primer directed amplification and comparing the prods. to detect  
 CC differences. The primers used in the amplification comprise a primer  
 CC consisting of a perfect cpd. simple sequence repeat (SSR), and an adaptor  
 CC directed primer, comprising a sequence complementary to an adaptor  
 CC segment. The present sequence is an example of a SSR primer, which is  
 CC flanked at its 5'-end by degenerate nucleotides. The method represents a  
 CC modified amplified fragment length polymorphism assay, which is partic.  
 CC useful for genome fingerprinting, i.e. for genetic trait marking and  
 CC germplasm comparisons  
 XX Sequence 18 BP; 0 A; 0 C; 8 G; 7 T; 0 U; 3 Other;  
 XX  
 Query Match 1.4%; Score 15; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1794 GTGTGTGTGTGTGTG 1808  
 Db 4 GTGTGTGTGTGTGTG 18  
 RESULT 276  
 ABZ11102  
 ID ABZ11102 standard; DNA; 18 BP.  
 XX ABZ11102;  
 AC  
 XX 16-JAN-2003 (first entry)  
 DT  
 XX Haematopoietic cell proliferation disorder related oligonucleotide #1242.  
 DE  
 XX Human; haematopoietic cell proliferation disorder; cytostatic;  
 KW gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia;  
 KW cytosine methylation state; probe; primer; ss.  
 XX Homo sapiens.  
 OS Synthetic.  
 XX WO200277272-A2.  
 PN  
 XX 03-OCT-2002.  
 PD  
 XX 26-MAR-2002; 2002WO-EP003401.  
 PF  
 XX 26-MAR-2001; 2001US-0278333P.  
 PR  
 XX (EPIG-) EPIGENOMICS AG.  
 PA  
 XX Berlin K, Braun A, Distler J, Guefig D, Howe A, Mueller J;  
 PI Olek A, Piepenbrock C, Adorjan P, Grabs G, Lesche R, Leu E;  
 PI Lewin A, Lipscher E, Maier S, Model F, Mueller V, Otto T, Pelet C;  
 PI Schwope I, Ziebarth H;  
 XX

DR WPI; 2003-018942/01.  
 XX Detecting and differentiating between hematopoietic cell proliferative  
 PT disorders, comprises contacting a target nucleic acid with a reagent that  
 PT distinguishes between methylated and non-methylated CpG dinucleotides.  
 XX Claim 15; Page 69; 117pp; English.  
 XX The present invention describes a method for detecting and  
 CC differentiating between haematopoietic cell proliferative disorders  
 CC associated with at least 1 gene and/or their regulatory regions in a  
 CC subject. The method comprises contacting a target nucleic acid in a  
 CC biological sample obtained from the subject with at least 1 reagent,  
 CC which distinguishes between methylated and non-methylated CpG  
 CC dinucleotides within the target nucleic acid. ABZ09861 to ABZ11118  
 CC represent specifically claimed nucleotide sequences from the present  
 CC invention. Oligonucleotides from the present invention can be used: for  
 CC differentiating between healthy haematopoietic cells and proliferative  
 CC disorder haematopoietic cells; for differentiating between acute  
 CC lymphocytic leukaemia and acute myelogenous leukaemia; as probes for  
 CC determining the cytosine methylation state and/or single nucleotide  
 CC polymorphisms (SNPs) of haematopoietic cell proliferation disorder  
 CC related sequences and their complements; and as primers for the  
 CC amplification of haematopoietic cell proliferation disorder related DNA  
 CC sequences. The nucleotide sequences from the present invention can also  
 CC be used for detecting a predisposition to, differentiation between  
 CC subclasses, diagnosis, prognosis, treatment and/or monitoring of  
 CC haematopoietic cell proliferative disorders. The present method enables a  
 CC highly specific classification of haematopoietic cell proliferative  
 CC disorders allowing for improved and informed treatment of patients  
 XX Sequence 18 BP; 1 A; 0 C; 4 G; 13 T; 0 U; 0 Other;  
 XX  
 Query Match 1.4%; Score 15; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1867 TTTATTTTGTGTTT 1881  
 Db 1 TTTATTTTGTGTTT 15  
 RESULT 277  
 ABZ10510  
 ID ABZ10510 standard; DNA; 18 BP.  
 XX ABZ10510;  
 AC  
 XX 16-JAN-2003 (first entry)  
 DT  
 XX Haematopoietic cell proliferation disorder related oligonucleotide #650.  
 DE  
 XX Human; haematopoietic cell proliferation disorder; cytostatic;  
 KW gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia;  
 KW cytosine methylation state; probe; primer; ss.  
 XX Homo sapiens.  
 OS Synthetic.  
 XX WO200277272-A2.  
 PN  
 XX 03-OCT-2002.  
 PD  
 XX 26-MAR-2002; 2002WO-EP003401.  
 PF  
 XX 26-MAR-2001; 2001US-0278333P.  
 PR  
 XX (EPIG-) EPIGENOMICS AG.  
 PA  
 XX Berlin K, Braun A, Distler J, Guefig D, Howe A, Mueller J;  
 PI Olek A, Piepenbrock C, Adorjan P, Grabs G, Lesche R, Leu E;  
 PI Lewin A, Lipscher E, Maier S, Model F, Mueller V, Otto T, Pelet C;  
 PI Schwope I, Ziebarth H;  
 XX

XX WPI; 2003-018942/01.  
 XX  
 PT Detecting and differentiating between hematopoietic cell proliferative  
 PT disorders, comprises contacting a target nucleic acid with a reagent that  
 PT distinguishes between methylated and non-methylated CpG dinucleotides.  
 XX  
 XX Claim 15; Page 47; 117pp; English.  
 XX  
 CC The present invention describes a method for detecting and  
 CC differentiating between haematopoietic cell proliferative disorders  
 CC associated with at least 1 gene and/or their regulatory regions in a  
 CC subject. The method comprises contacting a target nucleic acid in a  
 CC biological sample obtained from the subject with at least 1 reagent,  
 CC which distinguishes between methylated and non-methylated CpG  
 CC dinucleotides within the target nucleic acid. ABZ09861 to ABZ11118  
 CC represent specifically claimed nucleotide sequences from the present  
 CC invention. Oligonucleotides from the present invention can be used: for  
 CC differentiating between healthy haematopoietic cells and proliferative  
 CC disorder haematopoietic cells; for differentiating between acute  
 CC lymphocytic leukaemia and acute myelogenous leukaemia; as probes for  
 CC determining the cytosine methylation state and/or single nucleotide  
 CC polymorphisms (SNPs) of haematopoietic cell proliferation disorder  
 CC related sequences and their complements; and as primers for the  
 CC amplification of haematopoietic cell proliferation disorder related DNA  
 CC sequences. The nucleotide sequences from the present invention can also  
 CC be used for detecting a predisposition to, differentiation between  
 CC subclasses, diagnosis, prognosis, treatment and/or monitoring of  
 CC haematopoietic cell proliferative disorders. The present method enables a  
 CC highly specific classification of haematopoietic cell proliferative  
 CC disorders allowing for improved and informed treatment of patients  
 XX  
 XX Sequence 18 BP; 1 A; 0 C; 4 G; 13 T; 0 U; 0 Other;  
 SQ  
 Query Match 1.4%; Score 15; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1867 TTTATTTTGTGTTTT 1881  
 DB 1 TTTATTTTGTGTTTT 15  
 RESULT 278  
 ADC70018  
 ID ADC70018 standard; DNA; 18 BP.  
 AC  
 AC ADC70018;  
 XX  
 DT 18-DEC-2003 (first entry)  
 DE  
 DE Primer oligo used for analysing CpG islands in genomic DNA (SeqID 507).  
 XX  
 XX PCR; primer; ss; lung cell proliferative disorder; CpG dinucleotide;  
 KW adenocarcinoma; squamous cell carcinoma; cytostatic; probe; PNA-oligomer;  
 KW cytosine methylation state.  
 XX  
 OS Unidentified.  
 OS  
 XX WO2003052135-A2.  
 XX  
 XX 26-JUN-2003.  
 PD  
 XX 10-DEC-2002; 2002WO-EP014026.  
 PF  
 XX 14-DEC-2001; 2001DE-01061625.  
 PR  
 XX (EPIG-) EPIGENOMICS AG.  
 PA  
 PI Burger M, Field JK, Genc B, Liloglou T, Lipscher E, Maier S;  
 PI Nimmrich I;  
 XX  
 XX WPI; 2003-533029/50.

XX Detecting and differentiating cytosine methylation state of genomic DNA,  
 PT useful for diagnosing, treating prognosticating and/or monitoring lung  
 PT cell proliferative disorders e.g. adenocarcinoma and squamous cell  
 PT carcinoma.  
 XX  
 XX Claim 15; SEQ ID NO 507; 58pp; English.  
 PS  
 XX This invention relates to a novel method for detecting and  
 CC differentiating between lung cell proliferative disorders associated with  
 CC at least one gene and/or their regulatory regions. Specifically, it  
 CC refers to a method comprising contacting a target nucleic acid in a  
 CC biological sample with at least one reagent, wherein the reagent is able  
 CC to distinguish between methylated and non-methylated CpG dinucleotides  
 CC present in the target DNA. As such, it is possible to further  
 CC differentiate and diagnose medical conditions including adenocarcinoma  
 CC and squamous cell carcinoma, and their respective adjacent lung tissue.  
 CC The present invention describes cytostatic oligomers and PNA-oligomers  
 CC that are useful as probes for determining the cytosine methylation state  
 CC or single nucleotide polymorphisms (SNPs) of the target sequence. This  
 CC oligonucleotide sequence is a primer oligomer used for the analysis of  
 CC CpG positions within genomic DNA, used in an exemplification of the  
 CC invention.  
 XX  
 XX Sequence 18 BP; 1 A; 0 C; 4 G; 13 T; 0 U; 0 Other;  
 SQ  
 Query Match 1.4%; Score 15; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1867 TTTATTTTGTGTTTT 1881  
 DB 1 TTTATTTTGTGTTTT 15  
 RESULT 279  
 ADE84378  
 ID ADE84378 standard; DNA; 18 BP.  
 AC  
 AC ADE84378;  
 XX  
 DT 29-JAN-2004 (first entry)  
 DE  
 DE Human lymphoid cell proliferative disorder gene CpG analysis oligo #84.  
 XX  
 XX lymphoid cell proliferative disorder; methylation;  
 KW methylated CpG dinucleotide; single nucleotide polymorphism; SNP;  
 KW diffuse large B-cell lymphoma; mantle cell lymphoma;  
 KW chronic lymphocytic leukemia; small lymphocytic lymphoma;  
 KW follicular lymphoma; diagnosis; prognosis; primer; ss.  
 XX  
 XX Homo sapiens.  
 OS  
 XX WO2003044226-A2.  
 PN  
 XX 30-MAY-2003.  
 PD  
 XX 25-NOV-2002; 2002WO-EP013265.  
 PF  
 XX 23-NOV-2001; 2001DE-01057491.  
 PR  
 XX 28-DEC-2001; 2001DE-01064501.  
 XX  
 XX (EPIG-) EPIGENOMICS AG.  
 PA  
 XX Burger M, Caldwell C, Genc B, Becker E, Maier S, Nimmrich I;  
 PI  
 XX WPI; 2003-457621/43.  
 DR  
 XX Detecting and differentiating between lymphoid cell proliferative  
 PT disorders comprises contacting a target nucleic acid with at least one  
 PT reagent that distinguishes between methylated and non-methylated CpG  
 PT dinucleotides.  
 XX



CC flavonoid 3' hydroxylase (see AAW35704) was isolated using a differential  
CC display approach. This can be used to manipulate the pigmentation of  
CC transgenic plants  
XX  
SQ Sequence 18 BP; 1 A; 0 C; 0 G; 17 T; 0 U; 0 Other;

Query Match 1.4%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 2.2e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTTAA 1882  
|||||  
Db 1 TTTTATTTTGTGTTTAA 18

RESULT 282  
AAAX18372  
ID AAX18372 standard; DNA; 18 BP.  
XX  
AC AAX18372;  
XX  
DT 11-MAY-1999 (first entry)  
DE RT-PCR primer of the invention SEQ ID 13.  
XX  
KW RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.  
OS Synthetic.  
XX  
PN JPI1032765-A.  
XX  
PD 09-FEB-1999.  
XX  
PF 18-JUL-1997; 97JP-00208312.  
XX  
PR 18-JUL-1997; 97JP-00208312.  
XX  
PA (TAKI) TAKARA SHUZO CO LTD.  
XX  
DR WPI; 1999-183822/16.  
XX  
PT Peptides having at least two new nucleotides - useful as primers in RT-PCR.  
XX  
PS Disclosure; Page 11; 19pp; Japanese.

CC This sequence represents a primer of the invention. The invention relates  
CC to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta  
CC -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or  
CC a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =  
CC natural number indicating the repetition of alpha, beta, delta = V or N;  
CC V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or  
CC thymine; gamma = thymine; k = natural number of 3 or over indicating the  
CC repetition of gamma, in which thymine expressed by gamma is composed of  
CC 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are  
CC useful as primers for RT-PCR and determination of base sequences. The new  
CC sequences allow for reproductive and highly efficient analysis of gene  
CC sequences

SQ Sequence 18 BP; 2 A; 0 C; 0 G; 16 T; 0 U; 0 Other;  
Query Match 1.4%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 2.2e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1866 TTTTATTTTGTGTTTAA 1883  
|||||  
Db 1 TTTTATTTTGTGTTTAA 18

RESULT 283  
AAA07067/C  
ID AAA07067 standard; DNA; 18 BP.

XX AAA07067;  
AC  
XX  
DT 03-JUL-2000 (first entry)  
DE  
XX  
DE Human integrin beta 3 antisense oligonucleotide, SEQ ID NO:40.  
XX  
KW Integrin beta 3; human endothelial glycoprotein; GP3A; GPIIa; ITGB3;  
KW CD61; platelet glycoprotein 3a; cellular adhesion; vitronectin receptor;  
KW fibronectin receptor; expression inhibition; antisense; tumour formation;  
KW cancer invasion; bleeding disorder; inflammation; ss.  
XX  
OS Homo sapiens.  
XX  
PN US6037176-A.  
XX  
PD 14-MAR-2000.  
XX  
PF 25-JUN-1999; 99US-00344520.  
XX  
PR 25-JUN-1999; 99US-00344520.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Bennett CP, Cowsert LM, Monia BP;  
XX  
DR WPI; 2000-246189/21.  
XX  
PT New antisense compound that inhibits human integrin beta3, useful e.g.  
XX for treating or preventing infection, inflammation and tumors.  
XX  
PS Example 15; Col 40; 3pp; English.

CC Sequences AAA07035-A07074 represent antisense oligonucleotides targetted  
CC to the human integrin beta 3 gene, which inhibit its expression. The  
CC antisense oligonucleotides were designed to target different regions of  
CC the human integrin beta 3 RNA, and were analysed for their effect on  
CC integrin beta 3 mRNA levels by quantitative real-time PCR. GAPDH  
CC (glyceraldehyde-3-phosphate) mRNA levels were measured as a control.  
CC Integrins constitute one of four classes of cellular adhesion molecules,  
CC and play an important role in cell migration, cell anchorage to  
CC substrates and cytoadhesion signalling pathways. They are heterodimeric  
CC cation-dependent membrane glycoproteins composed of an alpha and beta  
CC subunit. Integrin beta 3 (also known as human endothelial glycoprotein,  
CC GP3A, GPIIa, ITGB3, CD61 and platelet glycoprotein 3a) is the common  
CC beta subunit partner of the members of the beta-3 subfamily of integrins.  
CC This family consists of the vitronectin receptor (alpha-v-beta-3) and the  
CC fibronectin receptor (alpha-1b-beta-3). Cells expressing this class of  
CC integrin can adhere to various matrix proteins and participate in various  
CC cytoadhesion-driven cellular responses. Integrin beta 3 is implicated in  
CC conditions such as vascular restenosis, excessive bone resorption,  
CC angiogenesis (in melanoma), tumour invasion, platelet aggregation and  
CC Glanzmann's thrombasthenia. The oligonucleotides of the invention are  
CC useful for diagnosis, prevention and treatment of conditions associated  
CC with integrin beta 3 expression, such as tumour formation, inflammation,  
CC infections and the diseases mentioned above

SQ Sequence 18 BP; 10 A; 7 C; 0 G; 1 T; 0 U; 0 Other;  
Query Match 1.4%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 2.2e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTGT 1811  
|||||  
Db 18 GTGTGTGTGTGTGTGTGT 1

RESULT 284  
ADD69515  
ID ADD69515 standard; DNA; 15 BP.  
XX  
AC ADD69515;



XX 15-JAN-2004 (first entry)  
 XX ISSR-related PCR primer 2.  
 XX inter-simple sequence repeat; ISSR, SSR, PCR; primer; genotyping; plant;  
 XX animal; Basmati rice; ss.  
 XX Unidentified.  
 OS WO2003085133-A2.  
 XX 16-OCT-2003.  
 XX 09-JAN-2003; 2003WO-IB000041.  
 XX 08-APR-2002; 2002IN-CH000260.  
 XX (DNAF-) CENT DNA FINGERPRINTING & DIAGNOSTICS.  
 PI Nagaraju JG;  
 XX WPI; 2003-804317/75.  
 XX New set of inter-simple sequence repeats (ISSR)-PCR primers for  
 PT genotyping eukaryotes, useful for genotyping diverse genomes of plant and  
 PT animal systems.  
 PS Disclosure; Page 19; 60pp; English.  
 CC The invention relates to a novel set of inter-simple sequence repeats  
 CC (ISSR)-PCR primers for genotyping eukaryotes. The primers of the  
 CC invention may be useful for genotyping diverse genomes of plant and  
 CC animal systems, in particular for distinguishing Basmati rice varieties  
 CC from non-Basmati rice varieties and traditional Basmati rice varieties  
 CC from evolved Basmati rice varieties. The current sequence is that of the  
 CC ISSR-related PCR primer of the invention.  
 XX Sequence 15 BP; 0 A; 0 C; 7 G; 7 T; 0 U; 1 Other;  
 SQ Query Match 1.4%; Score 14.6; DB 1; Length 15;  
 Best Local Similarity 93.3%; Pred. No. 2e+02;  
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 XX 1792 TTGTGTGTGTGTGTG 1806  
 :|||||  
 1 TTGTGTGTGTGTGTG 15  
 RESULT 285  
 ADD69514  
 ID ADD69514 standard; DNA; 15 BP.  
 AC ADD69514;  
 XX 15-JAN-2004 (first entry)  
 XX ISSR-related PCR primer 1.  
 XX inter-simple sequence repeat; ISSR, SSR, PCR; primer; genotyping; plant;  
 XX animal; Basmati rice; ss.  
 XX Unidentified.  
 OS WO2003085133-A2.  
 XX 16-OCT-2003.  
 XX 09-JAN-2003; 2003WO-IB000041.  
 XX 08-APR-2002; 2002IN-CH000260.  
 XX (DNAF-) CENT DNA FINGERPRINTING & DIAGNOSTICS.

XX Nagaraju JG;  
 PI WPI; 2003-804317/75.  
 XX New set of inter-simple sequence repeats (ISSR)-PCR primers for  
 PT genotyping eukaryotes, useful for genotyping diverse genomes of plant and  
 PT animal systems.  
 XX Disclosure; Page 19; 60pp; English.  
 CC The invention relates to a novel set of inter-simple sequence repeats  
 CC (ISSR)-PCR primers for genotyping eukaryotes. The primers of the  
 CC invention may be useful for genotyping diverse genomes of plant and  
 CC animal systems, in particular for distinguishing Basmati rice varieties  
 CC from non-Basmati rice varieties and traditional Basmati rice varieties  
 CC from evolved Basmati rice varieties. The current sequence is that of the  
 CC ISSR-related PCR primer of the invention.  
 XX Sequence 15 BP; 0 A; 0 C; 7 G; 7 T; 0 U; 1 Other;  
 SQ Query Match 1.4%; Score 14.6; DB 1; Length 15;  
 Best Local Similarity 93.3%; Pred. No. 2e+02;  
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1794 GTGTGTGTGTGTGTG 1808  
 :|||||  
 1 TTGTGTGTGTGTGTG 15  
 Db  
 RESULT 286  
 AAQ51146  
 ID AAQ51146 standard; DNA; 16 BP.  
 XX AAQ51146;  
 AC AAQ51146;  
 XX 27-AUG-2003 (revised)  
 DT 25-MAR-2003 (revised)  
 DT 02-JUN-1994 (first entry)  
 XX S. cerevisiae telomeric sequence.  
 XX Telomere; budding yeast; eukaryotic; conserved region;  
 KW phylogenetic relationship; ss.  
 XX Saccharomyces cerevisiae.  
 OS Key Location/Qualifiers  
 FT misc\_feature 4  
 FT /\*tag= a  
 FT /note= "May be absent"  
 FT misc\_feature 5..16  
 FT /\*tag= b  
 FT /note= "May be truncated by multiples of 2 bp"  
 XX WO9323572-A1.  
 XX 25-NOV-1993.  
 XX 13-MAY-1993; 93WO-US004546.  
 XX 13-MAY-1992; 92US-00892438.  
 XX 24-MAR-1993; 93US-00038766.  
 XX (GERO-) GERON CORP.  
 XX (UYCA-) UNIV CALIFORNIA SAN FRANCISCO.  
 XX West MD, Shay J, Wright W, Blackburn EH;  
 XX WPI; 1993-386602/48.  
 XX Therapy and diagnosis of conditions involving telomerase using inhibitor  
 PT - partic. for neoplasia, infection with pathogenic parasites and age-

PT related diseases.  
 PS Disclosure; Fig 30; 186pp; English.  
 XX  
 CC The sequences given in AA051138-46 represent telomeric sequences derived from various budding yeast species. There is a great variety in the length and sequence complexity of these sequences compared to those of other eukaryotes, yet they all have a 6 base conserved region at the 3' end. The telomeric relationships between these yeasts is fairly consistent with the phylogenetic relationship and it has been shown that C. tropicalis contains at least two forms of telomeric sequences. CC (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR-2003 to correct PA field.) (Updated on 27-AUG-2003 to correct OS field.)  
 XX  
 SQ Sequence 16 BP; 0 A; 0 C; 9 G; 7 T; 0 U; 0 Other;  
 Query Match 1.4%; Score 14.4; DB 1; Length 16;  
 Best Local Similarity 93.8%; Pred. No. 2.2e+02;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1793 TGTGTGTGTGTGTGTG 1808  
 Db 1 TGGGTGTGTGTGTGTG 16  
 RESULT 287  
 AA096310  
 ID AA096310 standard; DNA; 16 BP.  
 AC AA096310;  
 XX  
 XX 25-MAR-2003 (revised)  
 DT 08-APR-1998 (first entry)  
 XX  
 DE Fungal telomeric nucleic acid sequence.  
 XX  
 KW Detection; eukaryotic pathogen; telomeric nucleic acid sequence;  
 KW telomerase activity; diagnosis; fungal infection; fungus; fungi;  
 KW malarial infection; malaria; ss.  
 XX  
 OS Saccharomyces cerevisiae.  
 XX  
 PN US5695932-A.  
 XX  
 PD 09-DEC-1997.  
 XX  
 PF 13-MAY-1993; 93US-00060952.  
 XX  
 PR 13-MAY-1992; 92US-00882438.  
 PR 24-MAR-1993; 93US-00038766.  
 XX  
 XX (UYCA-) UNIV CALIFORNIA SAN FRANCISCO.  
 PA (TEXA) UNIV TEXAS SYSTEM.  
 PI Blackburn EH, Shay J, Meeachern MJ, West MD, Wright W;  
 XX  
 DR WPI; 1998-041292/04.  
 XX  
 PT Detection of eukaryotic pathogens, especially fungal or Plasmodium spp. -  
 PT by detecting telomerase activity.  
 XX  
 PS Claim 5; Col 95-96; 82pp; English.  
 XX  
 CC The present sequence can be used in a novel method for detecting a eukaryotic pathogen in a patient. The method comprises obtaining a sample of somatic tissue or cells from the patient, determining if telomerase activity is present and correlating this with the presence of the pathogen. The method is useful for diagnosis of fungal infections, especially a fungus of the genus Candida, Kluyveromyces, Saccharomyces, Sporothrix, Coccidioides, Histoplasma, Blastomyces, Paracoccidioides, Cryptococcus, Aspergillus, Mucor or Rhizopus, or malarial infections, especially Plasmodium vivax, P. ovale, P. malariae or P. falciparum. CC (Updated on 25-MAR-2003 to correct PA field.)

XX  
 SQ Sequence 16 BP; 0 A; 0 C; 9 G; 7 T; 0 U; 0 Other;  
 Query Match 1.4%; Score 14.4; DB 1; Length 16;  
 Best Local Similarity 93.8%; Pred. No. 2.2e+02;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1793 TGTGTGTGTGTGTGTG 1808  
 Db 1 TGGGTGTGTGTGTGTG 16  
 RESULT 288  
 AA013770  
 ID AA013770 standard; DNA; 16 BP.  
 XX  
 AC AA013770;  
 XX  
 DT 08-MAY-2002 (first entry)  
 XX  
 DE Simple sequence repeat, SSR, #42.  
 XX  
 KW Simple sequence repeat; plant; ds; SSR; ryegrass; fescue; tandem repeat;  
 KW cereal profiling; grass profiling; seed batch purity testing.  
 XX  
 OS Phalaris aquatica.  
 XX  
 PN NZ509193-A.  
 XX  
 PD 25-MAY-2001.  
 XX  
 PF 03-JAN-2001; 2001NZ-00509193.  
 XX  
 PR 24-DEC-1999; 99AU-00004906.  
 PR 04-MAY-2000; 2000AU-00007310.  
 XX  
 PA (SAUS-) STATE SOUTH AUSTRALIA SOUTH AUSTRALIAN R.  
 PA (UNSC-) UNIV SOUTHERN CROSS.  
 PA (VICT-) STATE VICTORIA DEPT NATURAL RES & ENVIRO.  
 PA (UYAD-) UNIV ADELAIDE.  
 PA (ITMA-) INT MAIZE & WHEAT IMPROVEMENT CENT.  
 XX  
 PI Forster JW, Jones ES;  
 XX  
 DR WPI; 2001-512563/56.  
 XX  
 PT New simple sequence repeats having 2 or more tandemly repeated nucleotide core elements isolated from ryegrass and fescue, useful for selecting of genes in grass or cereal breeding or profiling grass or cereal species varieties.  
 PT  
 XX  
 PS Example 1; Fig 6; 72pp; English.  
 XX  
 CC The invention relates to a substantially purified or isolated nucleic acid (I) from ryegrass or fescue species including a simple sequence repeat (SSR), having 2 or more tandemly repeated nucleotide core elements 2-6 nucleotides in length. Also included are a nucleic acid primer suitable for amplifying an SSR identifying (M) an SSR by preparing a library of ryegrass or fescue genomic DNA enriched for SSRs and identifying clones in the library containing SSRs, a library of ryegrass or fescue genomic DNA enriched for SSRs prepared by the M1, selecting for a gene in grass or cereal breeding by identifying an SSR that is closely associated with the gene such that the SSR and the gene are preferentially co-inherited, and selecting for the SSR in the breeding, a method for DNA profiling grass or cereal species varieties by assessing variation between SSR varieties and testing the purity of grass or cereal seed batches by assessing variation within seed batch of an SSR. The SSRs may be used in the selection of genes in grass or cereal breeding, for profiling grass or cereal species varieties, for testing the purity of grass or cereal seed batches, and for DNA profiling to establish the distinct identity, uniformity and/or stability of a cultivar. The present sequence is a ryegrass or fescue SSR

SQ Sequence 16 BP; 0 A; 1 C; 7 G; 8 T; 0 U; 0 Other;

Query Match 1.4%; Score 14.4; DB 1; Length 16;  
Best Local Similarity 93.8%; Pred. No. 2.2e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1794 GTGCTGTGTGTGTGT 1809  
DB 1 GTCTGTGTGTGTGTGT 16

RESULT 289

ABX50034  
ID ABX50034 standard; DNA; 16 BP.

AC XX

AC XX

DT 12-FEB-2003 (first entry)

DE Telomere length and/or telomerase activity related polynucleotide #57.

XX Cell proliferation; cell senescence; telomere length;

KW telomerase activity; cell replication; neoplasia; cancer;

KW age-related macular degeneration; Alzheimer's disease; atherosclerosis;

KW telomerase; telomerase inhibitor; immortalised cell; ss.

XX Synthetic.

OS US2002127634-A1.

PN 12-SEP-2002.

PD 05-JUN-1995; 95US-00463404.

PF 13-MAY-1992; 92US-00882438.

PR 24-MAR-1993; 93US-00038766.

PR 13-MAY-1993; 93US-00060952.

XX (WEST/) WEST M D.

PA (SHAY/) SHAY J.

PA (WRIGHT/) WRIGHT W.

PA (BLAC/) BLACKBURN E H.

XX West MD, Shay J, Wright W, Blackburn EH;

PI WPI; 2003-066896/06.

DR Treating condition associated with cell senescence or increased rate of

XX cell proliferation, by administering to cell an agent that derepresses

PT telomerase in the senescing cells or that reduces loss of telomere

PT length.

PT Disclosure; Page 51; 86pp; English.

PS The invention describes a method use for treating increased rate of

XX proliferation of a cell or extending the ability of a cell to replicate,

XX or treating a disease associated with cell senescence. The method

XX comprises administering an agent to reduce loss of telomere length within

XX the cell during proliferation or replication, or to derepress telomerase

XX in the senescing cells. The method is useful for treating a condition

XX associated with an increased rate of proliferation of a cell extending

XX the ability of a cell to replicate, or for treating a disease or

XX condition associated with cell senescence e.g. neoplasia. A second method

XX disclosed in the invention is useful for treating a condition associated

XX with an elevated level of telomerase activity within a cell e.g. cancer.

XX Also disclosed is a method useful for diagnosis of an individual e.g.

XX with an increased rate of proliferation in a cell in an individual e.g.

XX age-related macular degeneration, astrocytes associated with Alzheimer's

XX disease and endothelial cells associated with atherosclerosis. This

XX sequence represents a polynucleotide used in the study of telomere length

XX and telomerase activity described in the invention

SQ Sequence 16 BP; 0 A; 0 C; 9 G; 7 T; 0 U; 0 Other;

Query Match 1.4%; Score 14.4; DB 1; Length 16;  
Best Local Similarity 93.8%; Pred. No. 2.2e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTG 1808  
DB 1 TGGGTGTGTGTGTGTG 16

RESULT 290

ADC06894  
ID ADC06894 standard; DNA; 16 BP.

XX AC

AC ADC06894;

DT 18-DEC-2003 (first entry)

DE Saccharomyces cerevisiae telomere repeat sequence DNA.

XX nanocircle; telomere repeat sequence; cytostatic; ophthalmological;

KW cancer; liver degeneration; macular; skin aging; gene therapy; yeast.

KW biomedical research; tissue engineering; transplantation; ds; yeast.

XX Saccharomyces cerevisiae.

OS Saccharomyces cerevisiae.

XX Key Location/Qualifiers

FT misc\_difference 4 /\*tag= a

FT /note= "Optionally absent"

FT misc\_difference 7.16

FT /\*tag= b

FT /note= "Each TG unit may be optionally absent"

XX WO2003057849-A2.

PN 17-JUL-2003.

XX 03-JAN-2003; 2003WO-US000109.

XX 04-JAN-2002; 2002US-0345056P.

XX (STRD ) UNIV STANFORD.

XX Kool ET;

XX WPI; 2003-697275/66.

XX Novel nucleic acid nanocircle comprising at least 2 repeats of a telomere

PT repeat sequence, useful for extending length of telomere in vitro or in

PT vivo, and for treating macular degeneration, and cancer in mammals.

XX Disclosure; Page; 81pp; English.

XX The invention relates to a novel nucleic acid nanocircle comprising at

XX least two repeats of a telomere repeat sequence. The nanocircle of the

XX invention demonstrates cytostatic and ophthalmological activities and may

XX be useful during the diagnosis and treatment of cancer, liver

XX degeneration, macular degeneration and skin aging, as well as during gene

XX therapy procedures. Furthermore, the nanocircle may be used to extend the

XX lifespan of non-cancerous cell populations in culture, providing enhanced

XX materials for biomedical research, tissue engineering and

XX transplantation. The current sequence is that of the Saccharomyces

XX cerevisiae telomere repeat sequence DNA of the invention. Note: this

XX sequence is not displayed within the specification per se but was created

XX by the indexer.

XX Sequence 16 BP; 0 A; 0 C; 9 G; 7 T; 0 U; 0 Other;

Query Match 1.4%; Score 14.4; DB 1; Length 16;  
Best Local Similarity 93.8%; Pred. No. 2.2e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTG 1808  
 DB 1 TGGGTGTGTGTGTGTG 16

RESULT 291  
 AAQ35687  
 ID AAQ35687 standard; DNA; 17 BP.

XX AC AAQ35687;  
 XX 25-MAR-2003 (revised)  
 DT 24-FEB-1993 (first entry)  
 XX 42kD promoter element primer RG286.

XX NYVAC; EHV-1; GB; GC; GP; glycoprotein; homolog; vaccinia virus; ATI;  
 KW I3L promoter; H6 promoter; entomopox virus; 42 kD gene promoter; HA;  
 KW deletion loci; Copenhagen vaccine; virulence factors; deletion loci;  
 KW recipient loci; polymerase chain reaction; PCR; amplify; ss.

XX Synthetic.

XX WO9215672-A1.

XX 17-SEP-1992.

XX 09-MAR-1992; 92WO-US001906.

XX 07-MAR-1991; 91US-00666056.

XX 11-JUN-1991; 91US-00713967.

XX 06-MAR-1992; 92US-00847951.

XX (VIRO-) VIROGENETICS CORP.

XX Paoletti E, Perkus ME, Taylor J, Tartaglia J, Norton EK;

PI Riviere M, De Taisne C, Limbach KJ, Johnson GP, Pincus SZ, Cox WI;

PI Francis J, Gettig RR;

XX WPI; 1992-331718/40.

XX Vaccine comprises recombinant, attenuated pox-virus - use for vaccinating  
 PT against viral infections such as rabies, hepatitis B, HIV, HSV, EBV, CMV,  
 PT mumps etc.

XX Disclosure; Page 182; 456pp; English.

XX The sequences given in AAQ35675-90 were used in the construction of NYVAC  
 CC -based recombinants expressing the EHV-1 GB, GC and GP glycoprotein  
 CC homologs. Expression of the EHV-1 GB glycoprotein was accomplished by  
 CC putting the EHV-1 GB homolog gene under the control of the vaccinia virus  
 CC I3L promoter. The EHV-1 GC gene was expressed by placing the homolog gene  
 CC under the control of the vaccinia virus H6 promoter and the EHV-GD  
 CC glycoprotein was expressed by putting the homolog gene under the control  
 CC of the entomopox virus 42 kD gene promoter. The homolog genes were  
 CC derived by polymerase chain reaction (PCR) and were inserted into the ATI  
 CC and HA deletion loci of NYVAC. NYVAC is a Copenhagen vaccine strain of  
 CC vaccinia virus which has been modified by deletion of six non-essential  
 CC regions of the genome encoding known or potential virulence factors. The  
 CC deletion loci were engineered as recipient loci for the insertion of  
 CC foreign genes. See also AAQ35501-864. (Updated on 25-MAR-2003 to correct  
 CC PN field.)

XX Sequence 17 BP; 6 A; 0 C; 1 G; 10 T; 0 U; 0 Other;

Query Match 1.4%; Score 14.4; DB 1; Length 17;  
 Best Local Similarity 93.8%; Pred. No. 2.3e+02;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1777 TTTATATTGTAATAT 1792

DB 1 TTTATATTGTAATAT 16

RESULT 292  
 AAT81558/C  
 ID AAT81558 standard; RNA; 17 BP.

XX AC AAT81558;

XX 14-DEC-1997 (first entry)

XX Human c-myb hammerhead ribozyme target sequence (nt. position 2896).

XX Enzymatic nucleic acid; hammerhead; ribozyme; cleavage; human;  
 KW smooth muscle cell; hyperproliferation; restenosis; cancer; c-myb;  
 KW coronary angioplasty; ss.

XX Homo sapiens.

XX WO9531541-A2.

XX 23-NOV-1995.

XX 18-MAY-1995; 95WO-US006368.

XX 18-MAY-1994; 94US-00245466.

XX 13-JAN-1995; 95US-00373124.

XX (RIBO-) RIBOZYME PHARM INC.

XX Stinchcomb DT, Draper K, Mcswiggen J, Jarvis T;

XX WPI; 1996-010927/01.

XX New enzymatic nucleic acid molecules - cleave RNA produced by e.g. c-myb,  
 PT for treating restenosis or cancer.

XX Claim 1; Page 78; 128pp; English.

XX The present sequence represents the preferred target sequence for an  
 CC enzymatic nucleic acid, especially a hammerhead ribozyme, which cleaves  
 CC the human c-myb sequence at the base position indicated in the descriptor  
 CC line. The c-myb sequence was screened for optimal ribozyme target sites  
 CC using a computer folding algorithm, and regions of the mRNA which did not  
 CC form secondary folding structures and contained potential ribozyme  
 CC cleavage sites were identified. Ribozymes were synthesised and their  
 CC activities optimised by either varying the length of the binding arms or  
 CC by modification to prevent degradation by nucleases. The ribozymes cleave  
 CC the c-myb sequence and can be used to prevent smooth muscle cell  
 CC hyperproliferation in restenosis, especially after coronary angioplasty,  
 CC and in cancers

XX Sequence 17 BP; 7 A; 1 C; 0 G; 0 T; 9 U; 0 Other;

Query Match 1.4%; Score 14.4; DB 1; Length 17;  
 Best Local Similarity 93.8%; Pred. No. 2.3e+02;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1811 TGTATATATATATA 1826

DB 17 TGTATATATATAAA 2

RESULT 293

AAK71409

ID AAK71409 standard; RNA; 17 BP.

XX AC AAK71409;

XX 28-JUL-1999 (first entry)

XX Human KDR VEGF receptor hammerhead ribozyme substrate #421.

XX Vascular endothelial growth factor receptor; VEGF receptor; flk-1;  
 KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;

KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;  
 KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;  
 KW foetal liver kinase 1; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FN WO9715662-A2.  
 XX  
 PD 01-MAY-1997.  
 XX  
 PF 25-OCT-1996; 96WO-US017480.  
 XX  
 PR 26-OCT-1995; 95US-0005974P.  
 PR 11-JAN-1996; 96US-00584040.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 PA (CHIR ) CHIRON CORP.  
 XX  
 PI Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;  
 XX WPI; 1997-259017/23.  
 DR  
 XX  
 PT Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA  
 PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,  
 PT rheumatoid arthritis, etc., in a human patient.  
 XX  
 PS Claim 4; Page 109; 218pp; English.  
 XX  
 CC The present invention describes nucleic acid molecules which modulate the  
 CC synthesis, expression and/or stability of a mRNA encoding 1 or more  
 CC receptors of vascular endothelial growth factor (VEGF). A patient  
 CC (preferably human) having a condition associated with the level of the  
 CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing  
 CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour  
 CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be  
 CC treated by administering the nucleic acid molecule or the expression  
 CC vector to the patient. AAX67275 to AAX75752 represent specific examples  
 CC of nucleic acid molecules from the present invention  
 XX  
 SQ Sequence 17 BP; 4 A; 6 C; 4 G; 0 T; 3 U; 0 Other;  
 Query Match 1.4%; Score 14.4; DB 1; Length 17;  
 Best Local Similarity 75.0%; Pred. No. 2.3e+02;  
 Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
 OY 1749 TGCTCTTAACAGCCA 1764  
 Db :|||:|||||  
 2 UGCCUGUACCAAGCCA 17  
 RESULT 294  
 AAT47175  
 ID AAT47175 standard; DNA; 17 BP.  
 AC  
 AC AAT47175;  
 XX  
 DT 27-MAR-1997 (first entry)  
 XX  
 XX Primer RG286 used in pJCA080 construction.  
 XX  
 DE Feline herpes virus type 1; FHV-1; vaccine; poxvirus; ALVAC; vCP243;  
 KW canarypox virus; antigen; vector; primer; PCR; polymerase chain reaction;  
 KW pJCA109; pJCA080; ss.  
 KW  
 XX Synthetic.  
 OS  
 XX WO9640241-A1.  
 FN  
 XX  
 PD 19-DEC-1996.  
 XX  
 PF 03-JUN-1996; 96WO-IB000715.  
 XX  
 XX 07-JUN-1995; 95US-00486969.  
 PR

XX (VIRO-) VIROGENETICS CORP.  
 PA  
 XX Paoletti E, Maki J;  
 PI  
 XX WPI; 1997-051904/05.  
 DR  
 XX  
 PT Compen. for inducing immunological response, esp. in dogs - comprises  
 PT recombinant virus or expression prod., and additional antigen.  
 XX  
 XX Example 18; Page 168; 243pp; English.  
 PS  
 CC PCR primers (AAT47153-78) were used in the construction of plasmid  
 CC intermediates used in the generation of donor plasmid pJCA109. This  
 CC plasmid is required for the insertion of genes encoding the feline herpes  
 CC virus (FHV-1) homologues of gB, gC and gD under control of the I3L, H6  
 CC and 42K promoters, respectively, into the C6 site of an ALVAC vector.  
 CC Recombinant vCP243 is generated. Primers RG286 (AAT47175) and M13F  
 CC (AAT47176) were used to synthesise by PCR a 130 bp EcoRI-blunt fragment  
 CC contg. the 42K promoter using pJCA038 as template. The amplified fragment  
 CC was used in the construction of intermediate plasmid pJCA080  
 XX  
 SQ Sequence 17 BP; 6 A; 0 C; 1 G; 10 T; 0 U; 0 Other;  
 Query Match 1.4%; Score 14.4; DB 1; Length 17;  
 Best Local Similarity 93.8%; Pred. No. 2.3e+02;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 OY 1777 TTTATATTCTAAATAT 1792  
 Db |||||  
 1 TTTATATTCTAAATAT 16  
 RESULT 295  
 AAV91398  
 ID AAV91398 standard; RNA; 17 BP.  
 XX  
 AC AAV91398;  
 XX  
 DT 18-FEB-1999 (first entry)  
 XX  
 XX Human C-raf target site nucleotide position 2898.  
 DE  
 XX Human: c-raf; A-raf; B-raf; hammerhead ribozyme; hairpin ribozyme;  
 KW target; substrate; catalyst; modulation; expression; Raf gene; delivery;  
 KW screening; identification; synthesis; deprotection; purification; cancer;  
 KW inflammation; psoriasis; non-hepatic ascites; infection; genetic drift;  
 KW restenosis; rheumatoid arthritis; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO9850530-A2.  
 PN  
 XX 12-NOV-1998.  
 PD  
 XX  
 PF 05-MAY-1998; 98WO-US009249.  
 XX  
 XX 09-MAY-1997; 97US-0046059P.  
 PR  
 PR 09-JUN-1997; 97US-0049002P.  
 PR 03-JUL-1997; 97US-0051718P.  
 PR 22-AUG-1997; 97US-0056808P.  
 PR 02-OCT-1997; 97US-0061321P.  
 PR 02-OCT-1997; 97US-0061324P.  
 PR 05-NOV-1997; 97US-0064866P.  
 PR 19-DEC-1997; 97US-0068212P.  
 XX  
 XX (RIBO-) RIBOZYME PHARM INC.  
 PA  
 XX Jarvis T, Matulic-Adamic J, Reynolds M, Kisich K, Bellon L;  
 PI Parry T, Beigelman L, Mcswiggen JA, Karpeisky A, Burgin A;  
 PI Thompson J, Workman CT, Beaudry A, Sweedler D;  
 XX WPI; 1999-009494/01.  
 DR

XX Identifying new catalytic nucleic acid that modulates selected processes  
 PT - especially ribozymes that cleave Raf RNA for treating cancer,  
 PT restenosis, and also new ribozymes and modified nucleoside triphosphates  
 PT used as antiviral agents and synthons.  
 XX  
 XX Claim 177; Page 154; 259pp; English.  
 XX  
 CC A method has been developed for the identification of a nucleic acid  
 CC capable of modulating a process in a biological system. The method  
 CC comprises: (a) introducing into the system a random library of nucleic  
 CC acid catalysts (NAC) having a substrate binding domain (SBD), comprising  
 CC a random sequence, and a catalytic domain (CD); and (b) identifying NAC  
 CC in systems where modulation has occurred and/or determining the sequence  
 CC of at least part of the SBDs in such systems. Nucleic acid molecules with  
 CC endonuclease activity and catalytic activity, from the present invention,  
 CC are used to modulate gene expression in plant and mammalian cells and to  
 CC cleave target nucleic acid, particularly for treating systemic diseases  
 CC caused by specific RNA, e.g. cancer, inflammation, psoriasis, non-hepatic  
 CC ascites and infection. They may also be used to detect genetic drift and  
 CC mutations in diseased cells and to determine c-raf RNA. Specifically NACs  
 CC with RNA-cleaving activity that modulate expression of the Raf gene, are  
 CC used to treat cancer, restenosis, psoriasis or rheumatoid arthritis, or  
 CC generally any condition associated with the level of c-raf. Introduction  
 CC of sugar/phosphate modifications increases stability against nuclease and  
 CC activity. AAV90922 to AAV93877 represent NACs that can be used in the  
 CC method, specifically for modulating the expression of a Raf gene  
 XX  
 SQ Sequence 17 BP; 2 A; 0 C; 2 G; 0 T; 13 U; 0 Other;  
 Query Match 1.4%; Score 14.4; DB 1; Length 17;  
 Best Local Similarity 12.8%; Pred. No. 2.3e+02;  
 Matches 2; Conservative 13; Mismatches 1; Indels 0; Gaps 0;  
 QY 1866 TTTTATTTTCTTTT 1881  
 Db 2 UUUUAAUUUUUUUUUU 17  
 RESULT 296  
 AAV91400  
 ID AAV91400 standard; RNA; 17 BP.  
 AC AAV91400;  
 XX  
 XX 18-FEB-1999 (first entry)  
 XX Human C-raf target site nucleotide position 2900.  
 DE  
 DE Human; c-raf; A-raf; B-raf; hammerhead ribozyme; hairpin ribozyme;  
 KW target; substrate; catalyst; modulation; expression; Raf gene; delivery;  
 KW screening; identification; synthesis; deprotection; purification; cancer;  
 KW inflammation; psoriasis; non-hepatic ascites; infection; genetic drift;  
 KW restenosis; rheumatoid arthritis; ss.  
 XX  
 OS Homo sapiens.  
 PN WO9850530-A2.  
 XX  
 PD 12-NOV-1998.  
 XX  
 XX 05-MAY-1998; 98WO-US009249.  
 PF  
 XX 09-MAY-1997; 97US-0046039P.  
 PR 09-JUN-1997; 97US-0049002P.  
 PR 03-JUL-1997; 97US-0051718P.  
 PR 22-AUG-1997; 97US-0086808P.  
 PR 02-OCT-1997; 97US-0061321P.  
 PR 02-OCT-1997; 97US-0061321P.  
 PR 05-NOV-1997; 97US-0064866P.  
 PR 19-DEC-1997; 97US-0068212P.  
 XX (RIBO-) RIBOZYME PHARM INC.

XX Jarvis T, Matulic-Adamic J, Reynolds M, Kisich K, Bellon L;  
 PI Parry T, Baigelman L, Mcswiggen JA, Karpelsky A, Burgin A;  
 PI Thompson J, Workman CT, Beaudry A, Sweedler D;  
 XX WPI; 1999-009494/01.  
 XX  
 XX Identifying new catalytic nucleic acid that modulates selected processes  
 PT - especially ribozymes that cleave Raf RNA for treating cancer,  
 PT restenosis, and also new ribozymes and modified nucleoside triphosphates  
 PT used as antiviral agents and synthons.  
 XX  
 XX Claim 177; Page 154; 259pp; English.  
 XX  
 CC A method has been developed for the identification of a nucleic acid  
 CC capable of modulating a process in a biological system. The method  
 CC comprises: (a) introducing into the system a random library of nucleic  
 CC acid catalysts (NAC) having a substrate binding domain (SBD), comprising  
 CC a random sequence, and a catalytic domain (CD); and (b) identifying NAC  
 CC in systems where modulation has occurred and/or determining the sequence  
 CC of at least part of the SBDs in such systems. Nucleic acid molecules with  
 CC endonuclease activity and catalytic activity, from the present invention,  
 CC are used to modulate gene expression in plant and mammalian cells and to  
 CC cleave target nucleic acid, particularly for treating systemic diseases  
 CC caused by specific RNA, e.g. cancer, inflammation, psoriasis, non-hepatic  
 CC ascites and infection. They may also be used to detect genetic drift and  
 CC mutations in diseased cells and to determine c-raf RNA. Specifically NACs  
 CC with RNA-cleaving activity that modulate expression of the Raf gene, are  
 CC used to treat cancer, restenosis, psoriasis or rheumatoid arthritis, or  
 CC generally any condition associated with the level of c-raf. Introduction  
 CC of sugar/phosphate modifications increases stability against nuclease and  
 CC activity. AAV90922 to AAV93877 represent NACs that can be used in the  
 CC method, specifically for modulating the expression of a Raf gene  
 XX  
 SQ Sequence 17 BP; 3 A; 0 C; 1 G; 0 T; 13 U; 0 Other;  
 Query Match 1.4%; Score 14.4; DB 1; Length 17;  
 Best Local Similarity 18.8%; Pred. No. 2.3e+02;  
 Matches 3; Conservative 12; Mismatches 1; Indels 0; Gaps 0;  
 QY 1867 TTTTATTTTCTTTT 1882  
 Db 1 UUUUAAUUUUUUUUUU 16  
 RESULT 297  
 AAZ43714/C  
 ID AAZ43714 standard; DNA; 17 BP.  
 AC AAZ43714;  
 XX  
 XX 23-FEB-2000 (first entry)  
 XX Mass spectrometric mutation analysis primer 24.  
 DE  
 DE Mass spectrometric mutation analysis primer 24.  
 KW  
 KW Primer; mass-spectrometry; genetic mutation; amplification; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN DE19824280-A1.  
 XX  
 PD 02-DEC-1999.  
 XX  
 XX 29-MAY-1998; 98DE-01024280.  
 XX  
 XX 29-MAY-1998; 98DE-01024280.  
 XX (BRUK-) BRUKER DALTONIK GMBH.  
 XX WPI; 2000-073581/07.  
 XX Mass-spectrometric analysis of known gene mutations.  
 PT

PS Example; Page 9; 16pp; German.  
 XX This invention describes a method for mass-spectrometric analysis of  
 CC known genetic mutations, using modified nucleoside triphosphates to  
 CC improve the performance. The method comprises: (1) amplifying a DNA  
 CC sequence by polymerase chain reaction (PCR) using primers selected to  
 CC amplify a sequence containing the mutation; (2) adding a particular set  
 CC of modified nucleoside triphosphates (NTPs) to effect limited extension  
 CC of already present or newly added primers, where: (a) the extension  
 CC reaction stops at the next occurrence of a particular base in the DNA  
 CC strand being copied; (b) the extension reaction proceeds up to or past  
 CC the mutation site, so that wild-type amplification products will have a  
 CC different molecular weight from mutant amplification products; and (c)  
 CC the modification of the NTPs results in stabilization of the DNA chains  
 CC during ionization, a reduction in ion adduct formation, an increase in  
 CC ionization yields and/or a change in the mass of the DNA chains; (3)  
 CC performing the limited primer extension using an enzyme that generates  
 CC the complement of the DNA strand being copied; (4) performing at least  
 CC partial primer degradation and optionally further modification of the  
 CC amplification products; and (5) determining the mass of the modified  
 CC amplification products by mass spectrometry and assigning the masses to  
 CC wild type or mutant. AA243691-243717 represent primers used in the method  
 CC of the invention  
 XX  
 SQ Sequence 17 BP; 6 A; 2 C; 4 G; 5 T; 0 U; 0 Other;  
 Query Match 1.4%; Score 14.4; DB 1; Length 17;  
 Best Local Similarity 93.8%; Pred. No. 2.3e+02;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1991 ATATTTCAAGTGTAGC 1906  
 DB 16 ATATTTCAAGTGTAGC 1  
 RESULT 298  
 AA247021  
 ID AA247021 standard; DNA; 17 BP.  
 AC  
 XX AA247021;  
 XX  
 DT 29-FEB-2000 (first entry)  
 XX  
 DE Primer RG286 for PCR of promoter entomopoxvirus AmEPV 42K.  
 XX  
 KW Antibacterial; antiviral; primer; RT-PCR; amplification; haemagglutinin;  
 KW recombinant; vaccine; viral vector; pathogen; adjuvant; methacrylic acid;  
 KW maleic anhydride; alkenyl derivative; animal; herpes virus; tetanus;  
 KW influenza virus; feline leukemia; canine distemper; promoter; ss.  
 XX  
 OS Synthetic.  
 XX  
 XX WO9944633-A1.  
 XX  
 XX 10-SEP-1999.  
 XX  
 XX 01-MAR-1999; 99WO-FR000453.  
 XX  
 XX 03-MAR-1998; 98FR-00002800.  
 XX  
 XX (MERI-) MERIAL.  
 XX  
 XX Audonnet JF, Minke JM;  
 XX  
 XX WPI; 2000-022918/02.  
 XX  
 XX Live recombinant vaccine comprising viral vector and polymeric adjuvant,  
 XX particularly directed against animal herpes and influenza viruses.  
 PT  
 XX Example 7; Page 14; 41pp; French.  
 PS  
 XX Primers AA247021-247022 were used to PCR amplify the entomopoxvirus AmEPV  
 CC 42K promoter for generating a plasmid construct in which the feline

CC herpes virus glycoprotein D (gD) gene is expressed under control of the  
 CC 42K promoter. The gD gene is used to generate a live recombinant vaccine  
 CC which comprises: (1) a viral vector including, and expressing in vivo, a  
 CC heterologous nucleotide sequence particularly a gene from a pathogen; and  
 CC (2) at least one adjuvant, i.e. a (meth)acrylic acid polymer or a  
 CC copolymer of maleic anhydride and alkenyl derivatives. The vaccines are  
 CC used particularly to protect against animal herpes or influenza viruses,  
 CC but also feline leukemia, tetanus and canine distemper  
 XX  
 SQ Sequence 17 BP; 6 A; 0 C; 1 G; 10 T; 0 U; 0 Other;  
 Query Match 1.4%; Score 14.4; DB 1; Length 17;  
 Best Local Similarity 93.8%; Pred. No. 2.3e+02;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1777 TTTATATTGTAATAT 1792  
 DB 1 TTTATATTGTAATAT 16  
 RESULT 299  
 AA25184  
 ID AA25184 standard; DNA; 17 BP.  
 XX  
 AC AA25184;  
 XX  
 XX 19-JUL-2000 (first entry)  
 DT  
 XX  
 DE Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1692.  
 XX  
 KW Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;  
 KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;  
 KW gene expression modification; cancer; phosphorothioate; endonuclease;  
 KW anticancer; breast cancer; endometrium cancer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO9954459-A2.  
 XX  
 XX 28-OCT-1999.  
 XX  
 XX 19-APR-1999; 99WO-US008547.  
 XX  
 XX 20-APR-1998; 98US-0082404P.  
 XX  
 XX 23-JUN-1998; 98US-00103636.  
 XX  
 XX (RIBO-) RIBOZYME PHARM INC.  
 XX  
 XX Thompson JD, Beigelman L, McSwiggen JA, Karpeisky A, Bellon L;  
 XX Reynolds M, Zwick M, Jarvis T, Woolf T, Haeblerli P;  
 XX Matulic-Adamic J;  
 XX  
 XX WPI; 2000-013248/01.  
 XX  
 XX New nucleic acids that interact, and optionally cleave, target sequences,  
 XX used to treat cancer.  
 PT  
 XX  
 XX Claim 77; Page 71; 148pp; English.  
 XX  
 XX The present invention describes nucleic acids (A) that interact stably  
 XX with a target sequence and contain at least one phosphoro(di)thioate  
 XX link, having endonuclease activity. (A), and more generally any catalytic  
 XX nucleic acid (A') that modulates expression of the oestrogen receptor  
 XX gene, are used to treat cancer (particularly of breast or endometrium), or  
 XX in vivo or by transforming cells ex vivo and implanting treated cells, or  
 XX for other conditions associated with levels of oestrogen receptor.  
 XX Because of the high selectivity for targeted RNA, (A) can also be used to  
 XX correlate inhibition of gene expression with alterations in phenotype,  
 XX particularly for identification of therapeutic targets, and as research  
 XX reagents (for RNA, in the same way that restriction endonucleases are  
 XX used with DNA). The combination of modifications in (A) improves  
 XX resistance to nucleases, binding affinity and/or activity. AA23503 to  
 XX AA24747 represent oestrogen receptor hammerhead ribozyme sequences, and

CC AAA24748 to AAA25992 represent their corresponding target sequences.  
 CC AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme  
 CC sequences, and AAA26219 to AAA26271 represent their corresponding target  
 CC sequences. AAA26219 to AAA26271 represent other ribozyme sequences and  
 CC antisense oligonucleotides used in the exemplification of the present  
 CC invention

XX Sequence 17 BP; 1 A; 0 C; 3 G; 13 T; 0 U; 0 Other;  
 SQ

Query Match 1.4%; Score 14.4; DB 1; Length 17;  
 Best Local Similarity 93.8%; Pred. No. 2.3e+02;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1865 TTTTATTTTGTGTT 1880  
 |||||  
 Db 2 TTTTATTTTGTGTT 17

RESULT 300  
 AAA25185  
 ID AAA25185 standard; DNA; 17 BP.  
 XX  
 AC AAA25185;  
 XX  
 DT 19-JUL-2000 (first entry)  
 XX  
 DE Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1683.  
 XX  
 KW Oestrogen receptor; c-ras; bcl-2; ribozyme; cleavage;  
 KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;  
 KW gene expression modification; cancer; phosphorothioate; endonuclease;  
 KW anticancer; breast cancer; endometrium cancer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO954459-A2.  
 XX  
 PD 28-OCT-1999.  
 XX  
 PF 19-APR-1999; 99WO-US008547.  
 XX  
 PR 20-APR-1998; 98US-0082404P.  
 PR 23-JUN-1998; 98US-00103636.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 XX  
 PI Thompson JD, Beigelman L, Mcswiggen JA, Karpelsky A, Bellon L;  
 PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haeberli P;  
 PI Matulic-Adamic J;  
 XX  
 DR WPI; 2000-013248/01.  
 XX  
 PT New nucleic acids that interact, and optionally cleave, target sequences,  
 PT used to treat cancer.  
 XX  
 PS Claim 77; Page 71; 148pp; English.  
 XX

The present invention describes nucleic acids (A) that interact stably  
 with a target sequence and contain at least one phosphorodithioate  
 link, having endonuclease activity. (A), and more generally any catalytic  
 nucleic acid (A') that modulates expression of the oestrogen receptor  
 gene, are used to treat cancer (particularly of breast or endometrium),  
 in vivo or by transforming cells ex vivo and implanting treated cells, or  
 for other conditions associated with levels of oestrogen receptor.  
 CC Because of the high selectivity for targeted RNA, (A) can also be used to  
 CC correlate inhibition of gene expression with alterations in phenotype,  
 CC particularly for identification of therapeutic targets, and as research  
 CC reagents (for RNA, in the same way that restriction endonucleases are  
 CC used with DNA). The combination of modifications in (A) improves  
 CC resistance to nucleases, binding affinity and/or activity. AAA23503 to  
 CC AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and  
 CC AAA24748 to AAA25992 represent their corresponding target sequences.  
 CC AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme

CC sequences, and AAA26219 to AAA26271 represent their corresponding target  
 CC sequences. AAA26219 to AAA26271 represent other ribozyme sequences and  
 CC antisense oligonucleotides used in the exemplification of the present  
 CC invention

XX Sequence 17 BP; 2 A; 0 C; 2 G; 13 T; 0 U; 0 Other;  
 SQ

Query Match 1.4%; Score 14.4; DB 1; Length 17;  
 Best Local Similarity 93.8%; Pred. No. 2.3e+02;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1865 TTTTATTTTGTGTT 1880  
 |||||  
 Db 1 TTTTATTTTGTGTT 16

RESULT 301  
 ABV82842  
 ID ABV82842 standard; DNA; 17 BP.  
 XX  
 AC ABV82842;  
 XX  
 DT 03-JAN-2003 (first entry)  
 XX  
 DE Human HTPc scanning oligonucleotide SEQ ID 4088.  
 XX  
 KW Human; gene therapy; tumour suppressor; HTPc; chromosome 10p12.1;  
 KW human testis expressed Patched like protein; testis; adrenal; liver;  
 KW male germ cell development; bone marrow; brain; kidney; lung; placenta;  
 KW prostate; skeletal muscle; colon; male infertility; cancer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EP1229046-A2.  
 XX  
 PD 07-AUG-2002.  
 XX  
 PF 28-JAN-2002; 2002EP-00001167.  
 XX  
 PR 30-JAN-2001; 2001WO-US000663.  
 PR 30-JAN-2001; 2001WO-US000664.  
 PR 30-JAN-2001; 2001WO-US000665.  
 PR 30-JAN-2001; 2001WO-US000667.  
 PR 30-JAN-2001; 2001WO-US000668.  
 PR 30-JAN-2001; 2001WO-US000669.  
 PR 23-MAY-2001; 2001US-00864761.  
 PR 09-OCT-2001; 2001US-0327898P.  
 XX  
 PA (AEOM-) AEOMICA INC.  
 XX  
 PI Zhan J;  
 XX  
 DR WPI; 2002-676582/73.  
 XX  
 PT Novel isolated human testis expressed Patched like protein (HTPL), useful  
 PT for identifying agonist and antagonist and specific binding partners, and  
 PT for treating subjects having defects in HTPL.  
 XX  
 PS Example 2; Page 599; 718pp; English.  
 XX

The present invention relates to human testis expressed Patched like  
 protein (HTPL, see ABV8759 to ABV8762 and ABV88519 to ABV88520). HTPL  
 has two isoforms, with a few single base pair differences between the  
 two. One of the single base pair changes introduces a premature stop  
 codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL  
 shares an overall structure organisation with the Patched protein. The  
 shared structural features strongly imply that HTPL plays a role similar  
 to that of Patched, and is a potential tumour suppressor. HTPL is  
 CC important in regulating male germ cell development, and the HTPL gene was  
 CC mapped to human chromosome 10p12.1. HTPL and its coding sequence are  
 CC useful for diagnosing a disorder caused by mutation in HTPL, and in  
 CC therapy and manufacture of a medicament for treatment or prevention of  
 CC such disorder associated with decreased expression or activity of human



CC HTPL. Such disorders include disorders of testis, or adrenal, adult and  
 CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,  
 CC skeletal muscle or colon function. HTPL proteins and nucleic acids are  
 CC clinically useful diagnostic markers and potential therapeutic agents for  
 CC male infertility and cancer. The present oligonucleotide was used in an  
 CC example from the invention

XX Sequence 17 BP; 2 A; 3 C; 3 G; 10 T; 0 U; 0 Other;  
 SQ

Query Match 1.4%; Score 14.4; DB 1; Length 17;  
 Best Local Similarity 93.8%; Pred. No. 2.3e-02;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2162 GCATTGGTTCTACTT 2177  
 |||||  
 DB 2 GCATTGGTTCTAGTT 17

RESULT 302  
 ABV82843  
 ID ABV82843 standard; DNA; 17 BP.  
 XX  
 AC ABV82843;  
 XX  
 DT 03-JAN-2003 (first entry)  
 XX  
 DE Human HTPL scanning oligonucleotide SEQ ID 4089.  
 XX  
 KW Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;  
 KW human testis expressed patched like protein; testis; adrenal; liver;  
 KW male germ cell development; bone marrow; brain; kidney; lung; placenta;  
 KW prostate; skeletal muscle; colon; male infertility; cancer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 EP1229046-A2.  
 PN  
 XD 07-AUG-2002.  
 XX  
 XX 28-JAN-2002; 2002EP-00001167.  
 XX  
 PR 30-JAN-2001; 2001WO-US0000663.  
 PR 30-JAN-2001; 2001WO-US0000664.  
 PR 30-JAN-2001; 2001WO-US0000665.  
 PR 30-JAN-2001; 2001WO-US0000667.  
 PR 30-JAN-2001; 2001WO-US0000668.  
 PR 30-JAN-2001; 2001WO-US0000669.  
 PR 23-MAY-2001; 2001US-00864761.  
 PR 03-OCT-2001; 2001US-0327698P.  
 XX  
 PA (AEOM-) ABOMICA INC.  
 XX  
 PI Zhan J;  
 XX  
 WI; 2002-676582/73.  
 XX  
 PT Novel isolated human testis expressed patched like protein (HTPL), useful  
 PT for identifying agonist and antagonist and specific binding partners, and  
 PT for treating subjects having defects in HTPL.  
 XX  
 PS Example 2; Page 600; 718pp; English.  
 XX  
 CC The present invention relates to human testis expressed Patched like  
 CC protein (HTPL, see ABV78759 to ABV78762 and ABV98519 to ABV98520). HTPL  
 CC has two isoforms, with a few single base pair differences between the  
 CC two. One of the single base pair changes introduces a premature stop  
 CC codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL  
 CC shares an overall structure organisation with the Patched protein. The  
 CC shared structural features strongly imply that HTPL plays a role similar  
 CC to that of Patched, and is a potential tumour suppressor. HTPL is  
 CC important in regulating male germ cell development, and the HTPL gene was  
 CC mapped to human chromosome 10p12.1. HTPL and its coding sequence are  
 CC useful for diagnosing a disorder caused by mutation in HTPL, and in

CC therapy and manufacture of a medicament for treatment or prevention of  
 CC such disorder associated with decreased expression or activity of human  
 CC HTPL. Such disorders include disorders of testis, or adrenal, adult and  
 CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,  
 CC skeletal muscle or colon function. HTPL proteins and nucleic acids are  
 CC clinically useful diagnostic markers and potential therapeutic agents for  
 CC male infertility and cancer. The present oligonucleotide was used in an  
 CC example from the invention

XX Sequence 17 BP; 2 A; 3 C; 3 G; 9 T; 0 U; 0 Other;  
 SQ

Query Match 1.4%; Score 14.4; DB 1; Length 17;  
 Best Local Similarity 93.8%; Pred. No. 2.3e-02;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2162 GCATTGGTTCTACTT 2177  
 |||||  
 DB 1 GCATTGGTTCTAGTT 16

RESULT 303  
 ABK18059/C  
 ID ABK18059 standard; RNA; 17 BP.  
 XX  
 AC ABK18059;  
 XX  
 DT 09-APR-2002 (first entry)  
 XX  
 DE Human ERG hammerhead ribozyme target sequence, Seq ID No 706.  
 XX  
 KW Human; hammerhead ribozyme; cytostatic; antitumour; antidiabetic;  
 KW ophthalmological; antiarthritic; antipsoriatic; virucide; osteopathic;  
 KW vulvar; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis;  
 KW tumour angiogenesis; diabetic retinopathy; macular degeneration;  
 KW neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris;  
 KW angiofibroma of tuberous sclerosis; port-wine stain; wound healing;  
 KW Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss;  
 KW Osler-Weber-rendu syndrome; leukaemia; osteoporosis; DNAzyme; inozyme;  
 KW amberzyme.  
 XX  
 OS Homo sapiens.  
 XX  
 WO200188124-A2.  
 PN  
 PD 22-NOV-2001.  
 XX  
 PF 16-MAY-2001; 2001WO-US015866.  
 XX  
 PR 16-MAY-2000; 2000US-00572021.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 PA (GLAX) GLAXO GROUP LTD.  
 XX  
 PI Jarvis T, Von Carlwitz I, Mcswiggen JA, McLaughlin P, Randi AM;  
 XX  
 WI; 2002-082995/11.  
 XX  
 PT Novel polynucleotide which down regulates expression of Ets-related gene,  
 PT useful for treating cancer, diabetic retinopathy, macular degeneration,  
 PT arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome.  
 XX  
 PS Claim 4; Page 71; 149pp; English.  
 XX  
 CC The invention relates to a nucleic acid molecule (I) which down regulates  
 CC expression of an Ets-related gene (ERG). (I) is useful for treating  
 CC conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma,  
 CC tumour angiogenesis, diabetic retinopathy, macular degeneration,  
 CC neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca  
 CC vulgaris, angiofibroma of tuberous sclerosis, port-wine stains, Sturge  
 CC Weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-rendu  
 CC syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for  
 CC treating a patient having a condition associated with the level of ERG,  
 CC by contacting cells of the patient with (I) under conditions suitable for

CC the treatment. The method comprises the use of one or more therapies  
CC under conditions suitable for the treatment. Leukemia or tumour  
CC angiogenesis is treated by administering (I) to the patient in  
CC conjunction with one or more of other therapies such as radiation or  
CC chemotherapy treatment. (I) is useful for reducing ERG activity in a  
CC cell, by contacting the cell with (I). (I) is useful for cleaving RNA of  
CC ERG gene, by contacting (I) with RNA, in the presence of a divalent  
CC cation such as Mg<sup>2+</sup>. (I) is useful for diagnosis of conditions and  
CC diseases related to the expression of ERG, and as diagnostic tool to  
CC examine genetic drift and mutations within diseased cells or to detect  
CC the presence of ERG RNA in a cell. (I) is useful for specifically  
CC targeting genes that share homology with ERG gene or ERG fusion genes.  
CC ABK17354-ABK22719 represent nucleic acids, including antisense and  
CC enzymatic nucleic acid molecules which regulate expression of ERG, and  
CC related PCR primers of the invention  
XX  
SQ Sequence 17 BP; 8 A; 3 C; 2 G; 0 T; 4 U; 0 Other;

Query Match 1.4%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 2.3e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1289 TAAATCTGTTTCTA 1304  
Db 17 TAAATCTGTTTCTA 2

RESULT 304  
ACCS1306/c  
ID ACCS1306 standard; DNA; 17 BP.  
XX  
AC ACCS1306;  
XX  
DT 27-JUN-2003 (first entry)  
DE Human tumour suppressor sequence #73.  
XX  
KW ss; tumour suppressor; antitumour; cytostatic; tumour suppression;  
KW tumour regression; apoptosis; virus resistance; diagnosis;  
KW cellular degeneration.  
OS Homo sapiens.  
XX  
PN FR2826373-A1.  
XX  
PD 27-DEC-2002.  
XX  
PF 20-JUN-2001; 2001FR-00008139.  
XX  
PR 20-JUN-2001; 2001FR-00008139.  
XX  
PA (MOLE-) MOLECULAR ENGINES LAB SA.  
XX  
PI Tuijnder M, Telerman A, Amson R;  
XX  
DR WPI; 2003-250498/25.  
XX  
PT New nucleic acid sequences associated with tumor suppression, regression,  
PT apoptosis or virus resistance are useful to diagnose and treat viral  
PT disease, development of tumor cells and cell degeneration.  
XX  
PS Claim 1; Page 57; 798pp; French.  
XX  
CC This sequence represents an isolated nucleic acid sequence associated  
CC with tumour suppression or regression, apoptosis or virus resistance. The  
CC invention relates to these sequences or sequences having at least 80%  
CC identity to them, and polypeptides encoded by the sequences or  
CC polypeptides having 80% identity to the polypeptide sequences. The  
CC invention is used to diagnose or treat viral disease or disease  
CC characterized by development of tumour cells or cellular degeneration  
XX  
SQ Sequence 17 BP; 10 A; 2 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 1.4%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 2.3e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2166 TTGTTTCTCTTGTAT 2181  
Db 17 TTGTTTCTCTTGTAT 2

RESULT 305  
ABT38195/c  
ID ABT38195 standard; DNA; 17 BP.  
XX  
AC ABT38195;  
XX  
DT 12-JUN-2003 (first entry)  
DE Tumour suppression related human fukutin oligo SEQ ID No 3832.  
XX  
KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;  
KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;  
KW schizophrenia; protein chip; gene therapy; tumour suppression;  
KW human fukutin; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200303025175-A2.  
XX  
PD 27-MAR-2003.  
XX  
PF 17-SEP-2002; 2002WO-IB004208.  
XX  
PR 17-SEP-2001; 2001FR-00011978.  
XX  
PA (MOLE-) MOLECULAR ENGINES LAB.  
XX  
PI Telerman A, Amson R, Tuijnder M;  
XX  
DR WPI; 2003-313353/30.  
XX  
PT New isolated nucleic acid, useful for treating viral diseases associated  
PT with tumors and cell degeneration, also related polypeptides, antibodies  
PT and transfected cells.  
XX  
PS Disclosure; Page 482; 720pp; French.  
XX  
CC The invention relates to a novel isolated 17 mer nucleic acid sequence,  
CC given in the specification, a sequence containing at least 15 consecutive  
CC nucleotides from the 17 mer sequence, a sequence with, after optimal  
CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that  
CC hybridizes to them under highly stringent conditions, or the complement  
CC of any of them, or the corresponding RNA. The novel isolated nucleic  
CC acids of the invention are useful as probes and primers for detecting,  
CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one  
CC component of a gene chip, in vitro as (anti)sense reagents, and for  
CC production of recombinant polypeptides. Any of the nucleic acids,  
CC polypeptides, vectors containing the nucleic acids, cells containing the  
CC vector or antibodies directed against the polypeptides are useful for  
CC preparation of pharmaceuticals for prevention and/or treatment of viral  
CC diseases that are characterised by development of tumors or cell  
CC degeneration, specifically cancer but also Alzheimer's disease and  
CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in  
CC patient samples is useful for diagnosis and/or prognosis of these  
CC diseases. The polypeptides can also be used to generate antibodies, and  
CC both the polypeptide and antibodies are useful as components of protein  
CC chips. The nucleic acid sequences of the invention can be used in gene  
CC therapy. This polynucleotide sequence represents a tumour suppression  
CC related human fukutin oligonucleotide of the invention  
XX  
SQ Sequence 17 BP; 8 A; 2 C; 2 G; 5 T; 0 U; 0 Other;

Query Match 1.4%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 2.3e+02;

```
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1888 TTGATATTTCAATGTT 1903
    |||||
Db 17 TTGATATTTCAATGAT 2

RESULT 306
ACC64096
ID ACC64096 standard; DNA; 17 BP.
XX
AC ACC64096;
XX
DT 01-JUL-2003 (first entry)
DE Murine oligonucleotide associated with tumour suppression, SEQ ID 1343.
XX
KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine;
KW tumour suppression; tumour reversion; apoptosis; virus resistance;
KW viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;
KW schizophrenia; ss.
XX
OS Mus musculus.
XX
PN WO2003025176-A2.
XX
PD 27-MAR-2003.
XX
PF 17-SEP-2002; 2002WO-IB004210.
XX
PR 17-SEP-2001; 2001FR-00011979.
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
PI Telerman A, Amson R, Tuijnder M;
XX
DR WPI; 2003-333167/31.
XX
PT New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
XX
PS Disclosure; Page 188; 738pp; French.
XX
CC The present invention relates to murine oligonucleotides (ACC62754-
CC ACC6806), which are associated with tumour suppression, tumour
CC reversion, apoptosis and virus resistance. The oligonucleotides are
CC useful as (1) as probes and primers for detecting, identifying,
CC quantifying and/or amplifying nucleic acid, e.g. as one component of a
CC gene chip; in vitro as (anti)sense reagents; and (2) for production of
CC recombinant polypeptides. The oligonucleotides are useful for preparation
CC of pharmaceuticals for prevention and/or treatment of viral diseases that
CC are characterised by development of tumours or cell degeneration,
CC specifically cancer but also Alzheimer's disease and schizophrenia.
XX
SQ Sequence 17 BP; 2 A; 4 C; 2 G; 9 T; 0 U; 0 Other;

Query Match 1.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1292 ATCTGTTTTCTAACT 1307
    |||||
Db 2 ATCTGTTTTCTACT 17

RESULT 307
ADB43929/c
ID ADB43929 standard; DNA; 17 BP.
XX
AC ADB43929;
XX
DT 18-DEC-2003 (revised)
XX
```

```
DT 04-DEC-2003 (first entry)
XX Tumour suppression/reversion associated nucleotide #4252.
DE
XX Cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
KW Primer; probe; tumour suppression; tumour reversion; apoptosis;
KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
KW diagnosis.
XX
OS Homo sapiens.
XX
PN WO2003040369-A2.
XX
PD 15-MAY-2003.
XX
PF 17-SEP-2002; 2002WO-IB004219.
XX
PR 17-SEP-2001; 2001FR-00011981.
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
PI Telerman A, Amson R, Tuijnder M;
XX
DR WPI; 2003-441574/41.
XX
PT New nucleic acid encoding human prostate membrane-specific antigen,
PT useful e.g. for treatment of tumors and viral infection, also related
PT polypeptide and antibodies.
XX
PS Disclosure; Page 529; 771pp; French.
XX
CC The invention relates to the isolation of 6327 nucleotide sequences,
CC fragments of at least 15 consecutive nucleotides of these nucleotides, a
CC sequence having at least 80% identity, after optimal alignment, with the
CC nucleotides, a sequence that hybridizes under stringent conditions with
CC the nucleotides, or the complement, or corresponding RNA, of the
CC nucleotides. The nucleotides are used as probes or primers for detecting,
CC identifying, quantifying and/or amplifying nucleic acids, as in vitro
CC sense and antisense sequences, of nucleotides involved in tumour
CC suppression or reversion, apoptosis and or viral resistance, to produce
CC recombinant polypeptides, and to prepare transgenic animals, as
CC experimental models. The nucleotides (also vectors containing them and
CC cells containing the vectors), the encoded polypeptides and antibodies
CC (Ab) against the polypeptide are useful for prevention and/or treatment
CC of viral infections or diseases characterized by development of tumours
CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
CC Analysis of the expression of the nucleotides can be used for diagnosis
CC and/or prognosis of these diseases. The nucleotides and polypeptides can
CC also be used to screen for their specific interactive molecules,
CC potentially useful for treating diseases associated with abnormal
CC expression of the nucleotides.
XX
SQ Sequence 17 BP; 8 A; 2 C; 2 G; 5 T; 0 U; 0 Other;

Query Match 1.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1888 TTGATATTTCAATGTT 1903
    |||||
Db 17 TTGATATTTCAATGAT 2

RESULT 308
ADB44998/c
ID ADB44998 standard; DNA; 17 BP.
XX
AC ADB44998;
XX
DT 18-DEC-2003 (first entry)
XX
DE Tumour suppression/reversion associated nucleotide #5321.
XX
```

KW cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;  
KW primer; probe; tumour suppression; tumour reversion; apoptosis;  
KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;  
XX diagnosis.  
XX Homo sapiens.  
XX OS  
XX W02003040369-A2.  
XX PD 15-MAY-2003.  
XX PF 17-SEP-2002; 2002WC-IB004219.  
XX XX  
XX PR 17-SEP-2001; 2001FR-00011981.  
XX XX  
XX PA (MOLE-) MOLECULAR ENGINES LAB.  
XX XX  
XX PI Teleman A, Anson R, Tuijnder M;  
XX XX  
XX DR WPI; 2003-441574/41.  
XX XX  
XX PT New nucleic acid encoding human prostate membrane-specific antigen,  
XX useful e.g. for treatment of tumors and viral infection, also related  
XX polypeptide and antibodies.  
XX XX  
XX PS Disclosure; Page 654; 771pp; French.  
XX XX  
XX CC The invention relates to the isolation of 6327 nucleotide sequences,  
XX fragments of at least 15 consecutive nucleotides of these nucleotides, a  
XX sequence having at least 80% identity, after optimal alignment, with the  
XX nucleotides, a sequence that hybridizes under stringent conditions with  
XX the nucleotides, or the complement, or corresponding RNA, of the  
XX nucleotides. The nucleotides are used as probes or primers for detecting,  
XX identifying, quantifying and/or amplifying nucleic acids, as in vitro  
XX sense and antisense sequences, of nucleotides involved in tumour  
XX suppression or reversion, apoptosis and or viral resistance, to produce  
XX recombinant polypeptides, and to prepare transgenic animals, as  
XX experimental models. The nucleotides (also vectors containing them and  
XX cells containing the vectors), the encoded polypeptides and antibodies  
XX (Ab) against the polypeptide are useful for prevention and/or treatment  
XX of viral infections or diseases characterized by development of tumours  
XX or cell degeneration (e.g. Alzheimer's disease or schizophrenia).  
XX Analysis of the expression of the nucleotides can be used for diagnosis  
XX and/or prognosis of these diseases. The nucleotides and polypeptides can  
XX also be used to screen for their specific interactive molecules,  
XX potentially useful for treating diseases associated with abnormal  
XX expression of the nucleotides.  
XX SQ  
XX Sequence 17 BP; 10 A; 2 C; 4 G; 1 T; 0 U; 0 Other;  
Query Match 1.4%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. NO. 2.3e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2166 TTGTTCTACCTTGAT 2181  
DB 17 TTGTTCTCCCTTGAT 2  
RESULT 309  
AAQ20109  
ID AAQ20109 standard; DNA; 18 BP.  
XX AC  
XX AAQ20109;  
XX XX  
XX DT 01-APR-1992 (first entry)  
XX DE Cross-linking oligomer 943 to target human TNF Receptor mRNA.  
XX XX  
XX KW deoxyribonucleic acid; major groove; ethanocino group;  
XX tumour necrosis factor; receptor; messenger RNA; aziridinylcytosine;  
XX cross-linking group; ss.  
XX XX

OS Synthetic.  
XX Key Location/Qualifiers  
XX modified\_base 5  
XX /\*tag= a  
XX /mod\_base= OTHER  
XX /note= "N-methyl-8-oxo-2'-deoxyadenine"  
XX modified\_base 18  
XX /\*tag= b  
XX /mod\_base= OTHER  
XX /note= "N4N4-ethanocytosine"  
XX PN W09118997-A.  
XX PD 12-DEC-1991.  
XX XX  
XX PF 25-MAY-1990; 90US-00529346.  
XX XX  
XX PR 25-MAY-1990; 90US-00529346.  
XX 14-JAN-1991; 91US-00640654.  
XX XX  
XX PA (GILE-) GILEAD SCIE INC.  
XX XX  
XX PI Matteucci MD, Krawczyk S;  
XX XX  
XX DR WPI; 1992-007480/01.  
XX XX  
XX PT New sequence-specific non-photo-activated crosslinking agents - bind to  
XX the major groove of duplex DNA and are esp. useful for treating latent  
XX PT infections e.g. HIV.  
XX XX  
XX PS Example 4; Page 27; 42pp; English.  
XX CC  
XX CC The oligomer was designed to target human TNF receptor mRNA beginning at  
XX CC nucleotide 2354 and to covalently cross-link to the target via the N4N4-  
XX CC ethanocytosine group. See also AAQ20108  
XX XX  
XX SQ Sequence 18 BP; 1 A; 1 C; 0 G; 16 T; 0 U; 0 Other;  
Query Match 1.4%; Score 14.4; DB 1; Length 18;  
Best Local Similarity 93.8%; Pred. NO. 2.4e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1866 TTTTATTTTGTGTTT 1881  
DB 1 TTTTATTTTGTGTTT 16  
RESULT 310  
AAQ30448  
ID AAQ30448 standard; DNA; 18 BP.  
XX AC  
XX AAQ30448;  
XX XX  
XX DT 25-MAR-2003 (revised)  
XX DT 07-DEC-1992 (first entry)  
XX XX  
XX DE Oligomer TNFR943 for forming triplex with HUMNFR target duplex.  
XX XX  
XX KW Human tumour necrosis factor receptor mRNA; AIDS; modified; HIV; RSV;  
XX HPV; malignancy; hepatitis; inflammation; ss.  
XX XX  
XX OS Synthetic.  
XX Key Location/Qualifiers  
XX modified\_base 5  
XX /\*tag= a  
XX /mod\_base= OTHER  
XX /note= "N6 methyl-8-oxo-2' deoxyadenine"  
XX modified\_base 18  
XX /\*tag= b  
XX /mod\_base= OTHER  
XX /note= "OTHER= N4 N4 ethanocytosine"  
XX FT

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XX WO9209705-A1.
PN
XX
XX
PD 11-JUN-1992.
XX
XX 25-NOV-1991; 91WO-US008811.
XX
XX 23-NOV-1990; 90US-00617907.
PR 18-JAN-1991; 91US-00643382.
PR 08-APR-1991; 91US-00683420.
PR 17-APR-1991; 91US-00685544.
PR 17-APR-1991; 91US-00686546.
PR 17-APR-1991; 91US-00686547.
PR 27-SEP-1991; 91US-00766733.
XX
XX (GILE-) GILEAD SCI INC.
XX
XX Froehler B, Krawczyk S, Matteucci MD, Milligan J;
PI
XX WPI; 1992-217083/26.
XX
XX New oligomers contg. modified bases - which form a triplex with G-C
PT doublet in a DNA duplex, for treating and diagnosing HIV, hepatitis,
PT herpes malignancy and inflammation.
XX
XX Claim 12; Page 72; 77pp; English.
XX
XX The synthetic oligomer is capable of forming a triplex at physiological
CC pH with a purine rich target sequence by coupling into the major groove
CC of the duplex. The specific target sequence of this oligomer is the human
CC tumour necrosis factor receptor mRNA beginning at nucleotide 2354 contg.
CC a purine rich sequence concd. on one strand of the duplex. The oligomer,
CC and others like it are useful in diagnosis and therapy of diseases
CC characterised by specific DNA duplex targets, e.g. HPV, HBV, HIV,
CC hepatitis B, herpes, malignant tumours and inflammation. The triple
CC helices form under mild conditions thus assays may be carried out without
CC subjecting the test specimen to harsh conditions. See also AAQ25452-25501
CC and AAQ30226-447. (Updated on 25-MAR-2003 to correct PN field.) (Updated
CC on 25-MAR-2003 to correct PD field.)
XX
XX Sequence 18 BP; 1 A; 1 C; 1 G; 16 T; 0 U; 0 Other;
SQ
Query Match 1.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1866 TTTTATTTTGTGTTTT 1881
Db 1 TTTTATTTTGTGTTTT 16
RESULT 311
ABL56770
ID ABL56770 standard; DNA; 18 BP.
XX
XX ABL56770;
AC
XX
XX 20-AUG-2002 (first entry)
DT
XX
DE Sequence of an oligonucleotide used for triple helix construction.
XX
XX Nucleic acid detection; nucleic acid labelling; gene therapy;
KW nucleic acid purification; triple helix; ss.
XX
XX Synthetic.
OS
XX
XX WO200077250-A2.
PN
XX
XX 21-DEC-2000.
PD
XX
XX 14-JUN-2000; 2000WO-FR001655.
PF
XX
XX 14-JUN-1999; 99FR-00007503.
PR

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XX (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
PA (CNRS ) CNRS CENT NAT RECH SCI.
XX
XX Escude C, Garestier T, Helene C, Roulon T;
PI
XX WPI; 2001-080698/09.
XX
XX Circularizing oligonucleotide around double-stranded nucleic acid, useful
PT e.g. for detecting mutations, using target-binding oligonucleotide with
PT complementary end sequences.
XX
XX Example 10; Page 41; 91pp; French.
XX
XX The specification describes a process for circularizing an
CC oligonucleotide around a double-stranded nucleic acid that contains a
CC target sequence. The method is used to detect or label nucleic acids,
CC particularly plasmids, to detect target sequences in the nucleic acid,
CC and to distinguish between two sequences that differ in only 1 or 2
CC mutations. It can be used to select, e.g. from degenerate single-stranded
CC nucleic acids, sequences that can bind to the nucleic acid, particularly
CC sequences that promote entry of the nucleic acid into cells or can target
CC the nucleic acid to specific cellular compartments. The method can also
CC be used to purify nucleic acids, particularly plasmids, and in gene
CC therapy for specific inhibition of a gene contained in the nucleic acid.
CC The present sequence represents an oligonucleotide used in the course of
CC the invention, during construction of a triple helix
XX
XX Sequence 18 BP; 0 A; 0 C; 10 G; 8 T; 0 U; 0 Other;
SQ
Query Match 1.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1792 TTGCTGCTGCTGCTGCT 1807
Db 3 TTGCTGCTGCTGCTGCT 18
RESULT 312
ABL31526
ID ABL31526 standard; DNA; 18 BP.
XX
XX ABL31526;
AC
XX
XX 21-MAR-2002 (first entry)
DT
XX
DE Human HLA genotyping oligonucleotide SEQ ID NO 1015.
XX
XX Human; human leukocyte antigen; HLA; genotype; polymorphism;
KW immunogenetic; transplantation; genetic disease; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200192572-A1.
PN
XX
XX 06-DEC-2001.
PD
XX
XX 01-JUN-2001; 2001WO-JP004662.
PF
XX
XX 01-JUN-2000; 2000JP-00164798.
PR
XX
XX (NISN ) NISSHINBO IND INC.
PA (SYST-) SYSTEM RES INC.
PA
XX
XX Inoko H, Kagiya T, Ichihara T, Matsumura Y, Moriya S, Nishida M;
PI
XX WPI; 2002-122074/16.
XX
XX Human leukocyte antigen (HLA) typing, useful for judging HLA genotypes of
PT individuals e.g. by determining immunogenetic differences when
PT transplanting between them.
XX
XX

```

The invention relates to antisense oligonucleotides targeted to a nucleic acid molecule encoding human Survivin, where the antisense oligonucleotide inhibits the expression of human Survivin. These antisense oligonucleotides are used in the treatment of an animal suffering from a disease or condition associated with Survivin, e.g. a hyperproliferative condition such as cancer, and comprises administering a therapeutically or prophylactically effective amount of the antisense oligonucleotide so that expression of Survivin is inhibited. The oligonucleotides can also be used to treat a human suffering from a disease or condition characterised by a reduction in apoptosis comprising administering the antisense oligonucleotide to a human. In addition, the antisense oligonucleotide and a cytotoxic chemotherapeutic agent e.g.

```

QY 1794 GTGTGTGTGTGT 1807
DB 14 GTGTGTGTGTGT 1

RESULT 315
AAZ98486/c
ID AAZ98486 standard; DNA; 14 BP.
AC AAZ98486;
XX
DT 19-JUN-2000 (first entry)
DE H. discuss derived sequence #4.
XX
KW Satellite sequence; DNA fragmentation; microsatellite DNA; DNA marker;
KW Haliotis discus; ss.
XX
OS Haliotis discus.
XX
PN WO200011156-A1.
XX
PD 02-MAR-2000.
XX
PF 01-JUL-1999; 99WO-JP003551.
XX
PR 18-AUG-1998; 98JP-00232153.
XX
XX (NORQ) JAPAN MIN AGRIC FORESTRY & FISHERIES.
PA Takahashi H, Sekino M;
XX
XX WPI; 2000-224692/19.
XX
PT Isolation of satellite sequences from genomic DNA for use as DNA markers
PT comprises isolating a library with high homogeneity by DNA fragmentation.
XX
PS Example 5; Page 14; 35pp; Japanese.
XX
XX The invention provides a novel method for isolation of satellite
CC sequences from genomic DNA that comprises fragmentation of the DNA by a
CC method which is not dependent on base sequences, then selection of the
CC satellite sequences from the obtained genomic library of high
CC homogeneity. The method is useful for the isolation of microsatellite DNA
CC sequences which can be used as DNA markers. The new method markedly
CC improves the efficiency of isolation of satellite sequences in comparison
CC to prior art methods which are reliant on base sequences. Sequences
CC AAZ98483-514 represent sequences from Haliotis discus, used in the method
CC of the invention
XX
SQ Sequence 14 BP; 7 A; 7 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGT 1806
DB 14 TGTGTGTGTGTGT 1

RESULT 316
AAZ13716/c
ID AAZ13716 standard; DNA; 14 BP.
XX
AC AAZ13716;
XX
DT 08-MAY-2002 (first entry)
XX
DE Simple sequence repeat, SSR, #13.
XX
KW Simple sequence repeat; plant; ds; SSR; ryegrass; fescue; tandem repeat;
KW cereal profiling; grass profiling; seed batch purity testing.

```

```

XX Poae.
OS
XX
PN NZ509193-A.
XX
PD 25-MAY-2001.
XX
XX 03-JAN-2001; 2001NZ-00509193.
XX
PR 24-DEC-1999; 99AU-00004906.
XX
PR 04-MAY-2000; 2000AU-00007310.
XX
XX (SAUS-) STATE SOUTH AUSTRALIA SOUTH AUSTRALIAN R.
XX (UYSC-) UNIV SOUTHERN CROSS.
XX (VICT-) STATE VICTORIA DEPT NATURAL RES & ENVIRO.
XX (UVAD-) UNIV ADELAIDE.
XX (ITMA-) INT MAIZE & WHEAT IMPROVEMENT CENT.
XX
PI Forster JW, Jones ES;
XX
XX WPI; 2001-512563/56.
XX
XX New simple sequence repeats having 2 or more tandemly repeated nucleotide
XX core elements isolated from ryegrass and fescue, useful for selecting of
XX genes in grass or cereal breeding or profiling grass or cereal species
XX varieties.
XX
XX Claim 6; Page 51; 72pp; English.
XX
XX The invention relates to a substantially purified or isolated nucleic
XX acid (I) from ryegrass or fescue species including a simple sequence
XX repeat (SSR), having 2 or more tandemly repeated nucleotide core elements
XX 2-6 nucleotides in length. Also included are a nucleic acid primer
XX suitable for amplifying an SSR, identifying (M1) an SSR by preparing a
XX library of ryegrass or fescue genomic DNA enriched for SSRs and
XX identifying clones in the library containing SSRs, a library of ryegrass
XX or fescue genomic DNA enriched for SSRs prepared by the M1, selecting for
XX a gene in grass or cereal breeding by identifying an SSR that is closely
XX associated with the gene such that the SSR and the gene are
XX preferentially co-inherited, and selecting for the SSR in the breeding, a
XX method for DNA profiling grass or cereal species varieties by assessing
XX variation between SSR varieties and testing the purity of grass or cereal
XX seed batches by assessing variation within seed batch of an SSR. The SSRs
XX may be used in the selection of genes in grass or cereal breeding, for
XX profiling grass or cereal species varieties, for testing the purity of
XX grass or cereal seed batches, and for DNA profiling to establish the
XX distinct identity, uniformity and/or stability of a cultivar. The present
XX sequence is a ryegrass or fescue SSR
XX
SQ Sequence 14 BP; 7 A; 7 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGT 1806
DB 14 TGTGTGTGTGTGT 1

RESULT 317
AAH46009
ID AAH46009 standard; DNA; 14 BP.
XX
AC AAH46009;
XX
DT 12-SEP-2001 (first entry)
XX
DE Synthetic oligonucleotide 9.
XX
XX Synthetic oligonucleotide; dinucleotide repeat; cytostatic; apoptosis;
XX cell cycle arrest; cell proliferation; caspase; cytokine; interleukin;
XX tumour necrosis factor; TNF; cancer; carcinoma; sarcoma; leukemia;

```





XX PS Claim 7; Col 17; 13pp; English.

XX CC The invention relates to detecting (M1) polymorphisms in a uridine

XX CC diphosphate glucuronosyltransferase (UGT) gene promoter by determining

CC CC the presence of five thymidine-adenine (TA) repeats in the promoter,

CC CC where the presence of the five TA repeats correlates with increased

CC CC expression of the gene. The method is used for detecting polymorphisms in

CC CC a UGT gene promoter, preferably a UGT I (UGT1A1) gene promoter. (M1) is

CC CC useful for screening individuals for variation in glucuronidation

CC CC (e.g. irinotecan or TAS-103) are glucuronidated by UGT (preferably

CC CC UGT1A1) and the activity of the drug is effected by its level of

CC CC glucuronidation. The method preferably involves obtaining DNA from an

CC CC individual, amplifying all or part of a UGT gene promoter (UGT1A1 gene

CC CC promoter) contained in the DNA and determining the number of TA repeats

CC CC in the promoter. Thus the DNA being amplified comprises all or part of

CC CC UGT1A1 promoter. The DNA is amplified by a polymerase chain reaction and

CC CC the number of TA repeats is determined by gel electrophoresis or by

CC CC sequencing the amplified DNA. The polymorphism comprises an allele

CC CC consisting of five TA repeats (TA)5, six TA repeats (TA)6, or seven TA

CC CC repeats (TA)7. The promoter has any one of the genotypes (TA)5/(TA)5,

CC CC (TA)5/(TA)6, (TA)5/(TA)7, (TA)5/(TA)8, (TA)6/(TA)8, (TA)7/(TA)8 or

CC CC (TA)8/(TA)8. (M1) is also useful for predicting an individual's

CC CC sensitivity to xenobiotics that are glucuronidated by a UGT (preferably

CC CC UGT1A1) gene product, the method comprising determining the number of TA

CC CC repeats in a UGT gene promoter, where the number of TA repeats correlates

CC CC with expression of the UGT gene, and the individual's sensitivity to

CC CC xenobiotics is effected by glucuronidation activity. The methods

CC CC preferably involve determining the presence of five, six or seven TA

CC CC repeats in the promoter. Defects in glucuronidation is associated with

CC CC Gilbert's syndrome (hyperbilirubinaemia) and Crigler-Najjar syndrome. The

CC CC present sequence is the UGT1A1 promoter (TA)7 repeat

XX SQ Sequence 14 BP; 7 A; 0 C; 0 G; 7 T; 0 U; 0 Other;

Query Match 1.3%; Score 14; DB 1; Length 14;

Best Local Similarity 100.0%; Pred. No. 2.2e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1813 TATATATATATA 1826

DB 1 TATATATATATA 14

RESULT 320

ABK90418/c

ID ABK90418 standard; DNA; 14 BP.

XX AC ABK90418;

XX DT 05-NOV-2002 (first entry)

XX DE Human UGT1A1 promoter polymorphism (TA)7 repeat.

XX KW Human; ds; UGT1A1; promoter; Gilbert's syndrome; hyperbilirubinaemia;

XX KW uridine diphosphate glucuronosyltransferase; Crigler-Najjar syndrome;

XX KW UGT; polymorphism detection; TA repeat; glucuronidation; irinotecan;

XX KW TAS-103; xenobiotic.

XX OS Homo sapiens.

XX PN US6395481-B1.

XX PD 28-MAY-2002.

XX PF 16-FEB-1999; 99US-00251274.

XX PR 16-FEB-1999; 99US-00251274.

XX FA (ARCH-) ARCH DEV CORP.

XX PI Di Rienzo A, Iyer L, Ratain MJ;

XX WPI; 2002-588597/63.

XX PT Detecting polymorphisms in uridine diphosphate glucuronosyltransferase

PT gene promoter, useful for optimizing drug dosages for a patient,

PT comprises determining the presence of five thymidine-adenine repeats in

PT the promoter.

XX PS Claim 7; Col 17; 13pp; English.

XX CC The invention relates to detecting (M1) polymorphisms in a uridine

CC CC diphosphate glucuronosyltransferase (UGT) gene promoter by determining

CC CC the presence of five thymidine-adenine (TA) repeats in the promoter,

CC CC where the presence of the five TA repeats correlates with increased

CC CC expression of the gene. The method is used for detecting polymorphisms in

CC CC a UGT gene promoter, preferably a UGT I (UGT1A1) gene promoter. (M1) is

CC CC useful for screening individuals for variation in glucuronidation

CC CC (e.g. irinotecan or TAS-103) are glucuronidated by UGT (preferably

CC CC UGT1A1) and the activity of the drug is effected by its level of

CC CC glucuronidation. The method preferably involves obtaining DNA from an

CC CC individual, amplifying all or part of a UGT gene promoter (UGT1A1 gene

CC CC promoter) contained in the DNA and determining the number of TA repeats

CC CC in the promoter. Thus the DNA being amplified comprises all or part of

CC CC UGT1A1 promoter. The DNA is amplified by a polymerase chain reaction and

CC CC the number of TA repeats is determined by gel electrophoresis or by

CC CC sequencing the amplified DNA. The polymorphism comprises an allele

CC CC consisting of five TA repeats (TA)5, six TA repeats (TA)6, or seven TA

CC CC repeats (TA)7. The promoter has any one of the genotypes (TA)5/(TA)5,

CC CC (TA)5/(TA)6, (TA)5/(TA)7, (TA)5/(TA)8, (TA)6/(TA)8, (TA)7/(TA)8 or

CC CC (TA)8/(TA)8. (M1) is also useful for predicting an individual's

CC CC sensitivity to xenobiotics that are glucuronidated by a UGT (preferably

CC CC UGT1A1) gene product, the method comprising determining the number of TA

CC CC repeats in a UGT gene promoter, where the number of TA repeats correlates

CC CC with expression of the UGT gene, and the individual's sensitivity to

CC CC xenobiotics is effected by glucuronidation activity. The methods

CC CC preferably involve determining the presence of five, six or seven TA

CC CC repeats in the promoter. Defects in glucuronidation is associated with

CC CC Gilbert's syndrome (hyperbilirubinaemia) and Crigler-Najjar syndrome. The

CC CC present sequence is the UGT1A1 promoter (TA)7 repeat

XX SQ Sequence 14 BP; 7 A; 0 C; 0 G; 7 T; 0 U; 0 Other;

Query Match 1.3%; Score 14; DB 1; Length 14;

Best Local Similarity 100.0%; Pred. No. 2.2e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1813 TATATATATATA 1826

DB 14 TATATATATATA 1

RESULT 321

AAL50676

ID AAL50676 standard; DNA; 14 BP.

XX AC AAL50676;

XX DT 16-JAN-2003 (first entry)

XX DE Human uridine diphosphate glucuronosyltransferase gene polymorphism #10.

XX KW Human; polymorphism; TA repeat; ds; UGT; thymidine-adenine repeat;

XX KW uridine diphosphate glucuronosyltransferase gene promoter; UGT1A1;

XX KW drug dosage optimisation; xenobiotic sensitivity.

XX OS Homo sapiens.

XX PN US2002115097-A1.

XX PD 22-AUG-2002.

XX PF 01-FEB-2002; 2002US-00061693.



CC in the promoter. Thus the DNA being amplified comprises all or part of  
 CC UGT1A1 promoter. The DNA is amplified by a polymerase chain reaction and  
 CC sequencing the amplified DNA. The polymorphism comprises an allele  
 CC consisting of five TA repeats (TA)5, six TA repeats (TA)6, or seven TA  
 CC repeats (TA)7. The promoter has any one of the genotypes (TA)5/(TA)5,  
 CC (TA)5/(TA)6, (TA)5/(TA)7, (TA)5/(TA)8, (TA)6/(TA)8, (TA)7/(TA)8 or  
 CC (TA)8/(TA)8. (M1) is also useful for predicting an individual's  
 CC sensitivity to xenobiotics that are glucuronidated by a UGT (preferably  
 CC UGT1A1) gene product, the method comprising determining the number of TA  
 CC repeats in a UGT gene promoter, where the number of TA repeats correlates  
 CC with expression of the UGT gene, and the individuals sensitivity to  
 CC xenobiotics is effected by glucuronidation activity. The methods  
 CC preferably involve determining the presence of five, six or seven TA  
 CC repeats in the promoter. Defects in glucuronidation is associated with  
 CC Gilbert's syndrome (hyperbilirubinaemia) and Crigler-Najjar syndrome. The  
 CC present sequence is the UGT1A1 promoter (TA)6 repeat region  
 CC  
 CC Sequence 15 BP; 8 A; 0 C; 0 G; 7 T; 0 U; 0 Other;

Query Match 1.3%; Score 14; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1813 TATATATATATATA 1826  
 DB 1 TATATATATATATA 14

RESULT 324  
 ABK90421/C  
 ID ABK90421 standard; DNA; 15 BP.

AC ABK90421;  
 DT 05-NOV-2002 (first entry)

DE Human UGT1A1 promoter polymorphism (TA)6 repeat region.

Human; ds; UGT1A1; promoter; Gilbert's syndrome; hyperbilirubinaemia;  
 uridine diphosphate glucuronosyltransferase; Crigler-Najjar syndrome;  
 UGT; polymorphism detection; TA repeat; glucuronidation; Irinotecan;  
 TAS-103; xenobiotic.

Homo sapiens.  
 US6395481-B1.  
 28-MAY-2002.  
 16-FEB-1999; 99US-00251274.  
 16-FEB-1999; 99US-00251274.

(ARCH-) ARCH DEV CORP.

Di Rienzo A, Iyer L, Ratain MJ;

WPI; 2002-588597/63.

Detecting polymorphisms in uridine diphosphate glucuronosyltransferase  
 gene promoter, useful for optimizing drug dosages for a patient,  
 comprises determining the presence of five thymidine-adenine repeats in  
 the promoter.

Example 6; Col 11; 13pp; English.

The invention relates to detecting (M1) polymorphisms in a uridine  
 diphosphate glucuronosyltransferase (UGT) gene promoter by determining  
 the presence of five thymidine-adenine (TA) repeats in the promoter,  
 where the presence of the five TA repeats correlates with increased  
 expression of the gene. The method is used for detecting polymorphisms in  
 a UGT gene promoter, preferably a UGT 1 (UGT1A1) gene promoter. (M1) is

CC useful for screening individuals for variation in glucuronidation  
 CC activity, for optimizing drug dosages for a patient, where the drugs  
 CC (e.g. Irinotecan or TAS-103) are glucuronidated by UGT (preferably  
 CC UGT1A1) and the activity of the drug is effected by its level of  
 CC glucuronidation. The method preferably involves obtaining DNA from an  
 CC individual, amplifying all or part of a UGT gene promoter (UGT1A1 gene  
 CC promoter) contained in the DNA and determining the number of TA repeats  
 CC in the promoter. Thus the DNA being amplified comprises all or part of  
 CC UGT1A1 promoter. The DNA is amplified by a polymerase chain reaction and  
 CC the number of TA repeats is determined by gel electrophoresis or by  
 CC sequencing the amplified DNA. The polymorphism comprises an allele  
 CC consisting of five TA repeats (TA)5, six TA repeats (TA)6, or seven TA  
 CC repeats (TA)7. The promoter has any one of the genotypes (TA)5/(TA)5,  
 CC (TA)5/(TA)6, (TA)5/(TA)7, (TA)5/(TA)8, (TA)6/(TA)8, (TA)7/(TA)8 or  
 CC (TA)8/(TA)8. (M1) is also useful for predicting an individual's  
 CC sensitivity to xenobiotics that are glucuronidated by a UGT (preferably  
 CC UGT1A1) gene product, the method comprising determining the number of TA  
 CC repeats in a UGT gene promoter, where the number of TA repeats correlates  
 CC with expression of the UGT gene, and the individuals sensitivity to  
 CC xenobiotics is effected by glucuronidation activity. The methods  
 CC preferably involve determining the presence of five, six or seven TA  
 CC repeats in the promoter. Defects in glucuronidation is associated with  
 CC Gilbert's syndrome (hyperbilirubinaemia) and Crigler-Najjar syndrome. The  
 CC present sequence is the UGT1A1 promoter (TA)6 repeat region  
 CC

SQ Sequence 15 BP; 8 A; 0 C; 0 G; 7 T; 0 U; 0 Other;

Query Match 1.3%; Score 14; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1813 TATATATATATATA 1826  
 DB 14 TATATATATATATA 1

RESULT 325

AAL50678

ID AAL50678 standard; DNA; 15 BP.

AC AAL50678;

16-JAN-2003 (first entry)

Human uridine diphosphate glucuronosyltransferase gene polymorphism #12.

Human; polymorphism; TA repeat; ds; UGT; thymidine-adenine repeat;  
 uridine diphosphate glucuronosyltransferase gene promoter; UGT1A1;  
 drug dosage optimisation; xenobiotic sensitivity.

Homo sapiens.

US2002115097-A1.

22-AUG-2002.

01-FEB-2002; 2002US-00061693.

16-FEB-1999; 99US-00251274.

(ARCH-) ARCH DEV CORP.

Rienzo AD, Iyer L, Ratain MJ;

WPI; 2002-740095/80.

Detecting polymorphisms in uridine diphosphate glucuronosyltransferase  
 gene promoter, useful for optimizing drug dosages for a patient, involves  
 determining number of thymidine-adenine repeats in the promoter.

Example 6; Page 2; 13pp; English.

The invention comprises a method for detecting polymorphisms in a uridine

CC diphosphate glucuronosyltransferase (UGT) gene promoter (preferably  
 CC UGT1A1). The method involves determining the number of thymidine-adenine  
 CC (TA) repeats in the promoter - as the number of TA repeats correlates  
 CC with expression of the UGT gene. The method of the invention is useful  
 CC for detecting polymorphisms in a UGT gene promoter. The method of the  
 CC invention is also useful in optimising drug dosages and predicting an  
 CC individual's sensitivity to xenobiotics for drugs and xenobiotics that  
 CC are glucuronidated by UGT. The present DNA sequence represents a UGT gene  
 CC TA repeat polymorphism

XX  
 SQ Sequence 15 BP; 8 A; 0 C; 0 G; 7 T; 0 U; 0 Other;

Query Match 1.3%; Score 14; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. NO. 2.3e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1813 TATATATATATATA 1826  
 Db 1 TATATATATATATA 14

RESULT 326  
 AAL50678/c  
 ID AAL50678 standard; DNA; 15 BP.  
 XX  
 AC AAL50678;  
 XX  
 DT 16-JAN-2003 (first entry)  
 XX  
 DE Human uridine diphosphate glucuronosyltransferase gene polymorphism #12.  
 XX  
 KW Human; polymorphism; TA repeat; ds; UGT; thymidine-adenine repeat;  
 KW uridine diphosphate glucuronosyltransferase gene promoter; UGT1A1;  
 KW drug dosage optimisation; xenobiotic sensitivity.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2002115097-A1.  
 XX  
 PD 22-AUG-2002.  
 XX  
 PF 01-FEB-2002; 2002US-00061693.  
 XX  
 PR 16-FEB-1999; 99US-00251274.  
 XX  
 PA (ARCH-) ARCH DEV CORP.  
 XX  
 PI Rlenzo AD, Iyer L, Ratain MJ;  
 XX  
 DR WPI; 2002-740095/80.  
 XX  
 PT Detecting polymorphisms in uridine diphosphate glucuronosyltransferase  
 PT gene promoter, useful for optimizing drug dosages for a patient, involves  
 PT determining number of thymidine-adenine repeats in the promoter.  
 XX  
 PS Example 6; Page 2; 13pp; English.  
 XX

CC The invention comprises a method for detecting polymorphisms in a uridine  
 CC diphosphate glucuronosyltransferase (UGT) gene promoter (preferably  
 CC UGT1A1). The method involves determining the number of thymidine-adenine  
 CC (TA) repeats in the promoter - as the number of TA repeats correlates  
 CC with expression of the UGT gene. The method of the invention is useful  
 CC for detecting polymorphisms in a UGT gene promoter. The method of the  
 CC invention is also useful in optimising drug dosages and predicting an  
 CC individual's sensitivity to xenobiotics for drugs and xenobiotics that  
 CC are glucuronidated by UGT. The present DNA sequence represents a UGT gene  
 CC TA repeat polymorphism

XX  
 SQ Sequence 15 BP; 8 A; 0 C; 0 G; 7 T; 0 U; 0 Other;

Query Match 1.3%; Score 14; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. NO. 2.3e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1813 TATATATATATATA 1826  
 Db 14 TATATATATATATA 1

RESULT 327  
 AAT81559/c  
 ID AAT81559 standard; RNA; 17 BP.  
 XX  
 AC AAT81559;  
 XX  
 DT 14-DEC-1997 (first entry)  
 XX  
 DE Human c-myb hammerhead ribozyme target sequence (nt. position 2898).  
 XX  
 KW Enzymatic nucleic acid; hammerhead; ribozyme; cleavage; human;  
 KW smooth muscle cell; hyperproliferation; restenosis; cancer; c-myb;  
 KW coronary angioplasty; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W09531541-A2.  
 XX  
 PD 23-NOV-1995.  
 XX  
 PF 18-MAY-1995; 95WO-US006368.  
 XX  
 PR 18-MAY-1994; 94US-00245466.  
 PR 13-JAN-1995; 95US-00373124.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 XX  
 PI Stinchcomb DT, Draper K, Mcswiggen J, Jarvis T;  
 XX  
 DR WPI; 1996-010927/01.  
 XX  
 PT New enzymatic nucleic acid molecules - cleave RNA produced by e.g. c-myb,  
 PT for treating restenosis or cancer.  
 XX  
 PS Claim 1; Page 78; 128pp; English.  
 XX

CC The present sequence represents the preferred target sequence for an  
 CC enzymatic nucleic acid, especially a hammerhead ribozyme, which cleaves  
 CC the human c-myb sequence at the base position indicated in the descriptor  
 CC line. The c-myb sequence was screened for optimal ribozyme target sites  
 CC using a computer folding algorithm, and regions of the mRNA which did not  
 CC form secondary folding structures and contained potential ribozyme  
 CC cleavage sites were identified. Ribozymes were synthesised and their  
 CC activities optimised by either varying the length of the binding arms or  
 CC by modification to prevent degradation by nucleases. The ribozymes cleave  
 CC the c-myb sequence and can be used to prevent smooth muscle cell  
 CC hyperproliferation in restenosis, especially after coronary angioplasty,  
 CC and in cancers

XX  
 SQ Sequence 17 BP; 7 A; 1 C; 0 G; 0 T; 9 U; 0 Other;

Query Match 1.3%; Score 14; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. NO. 2.5e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1811 TGTATATATATATA 1824  
 Db 15 TGTATATATATATA 2

RESULT 328  
 AAT27921/c  
 ID AAT27921 standard; DNA; 17 BP.  
 XX  
 AC AAT27921;  
 XX  
 DT 28-JAN-1997 (first entry)

XX DE 5'-anchored simple sequence repeat primer CGG(CA)6.5.  
 XX KW Detection; polymorphism; perfect compound simple sequence repeat;  
 KW adaptor directed primer; genome; genetic; fingerprinting;  
 KW amplified fragment length polymorphism assay; microsatellite region;  
 KW genetic trait marking; germplasm comparisons; 5'-anchored; ss.  
 XX OS Synthetic.  
 XX XX WO9617082-A2.  
 PN WO9617082-A2.  
 XX PD 06-JUN-1996.  
 XX PF 21-NOV-1995; 95WO-US015150.  
 XX PR 28-NOV-1994; 94US-00346456.  
 XX PA (DUPO) DU PONT DE NEMOURS & CO E I.  
 XX PI Morgante M, Vogel JM;  
 XX XX WPI; 1996-277795/28.  
 DR Modified amplified fragment length polymorphism assay - for detection of  
 PT polymorphism esp. in micro-satellite regions.  
 XX Example 1; Page 77; 173pp; English.  
 XX Detecting polymorphisms between 2 nucleic acid samples, esp. in  
 CC microsatellite regions, comprises digesting the nucleic acid to generate  
 CC fragments, ligating adaptor segments to their ends, amplifying them using  
 CC primer directed amplification and comparing the prods to detect  
 CC differences. The primers used in the amplification comprise a primer  
 CC consisting of a perfect cpd. simple sequence complementary to an adaptor  
 CC directed primer, comprising a sequence complementary to an adaptor  
 CC segment. The present sequence is an example of a SSR primer. The method  
 CC represents a modified amplified fragment length polymorphism assay, which  
 CC is partic. useful for genome fingerprinting, i.e. for genetic trait  
 CC marking and germplasm comparisons  
 XX XX Sequence 17 BP; 7 A; 8 C; 2 G; 0 T; 0 U; 0 Other;  
 SQ Query Match 1.3%; Score 14; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. NO. 2.5e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1793 TGTGTGTGTGTGTGTG 1806  
 Db 17 TGTGTGTGTGTGTG 4  
 RESULT 329  
 AAH74947  
 ID AAH74947 standard; DNA; 17 BP.  
 AC AAH74947;  
 XX 29-OCT-2001 (first entry)  
 DT Nucleotide sequence identified using ligation-based DNA sequencing.  
 DE Nucleotide sequence signature; nucleotide sequencing; ss.  
 XX Unidentified.  
 OS WO200161044-A1.  
 PN 23-AUG-2001.  
 XX 15-FEB-2001; 2001WO-US005032.  
 PF 15-FEB-2000; 2000US-0182454P.  
 XX PR

PR 01-SEP-2000; 2000US-0654187P.  
 XX (LYNX-) LYNX THERAPEUTICS INC.  
 PA Corcoran KC, Eletr S;  
 XX WPI; 2001-522608/57.  
 DR Determining nucleotide sequence signature, by obtaining optical values  
 PT for each nucleotide position in a group, adjusting them to get ratio of  
 PT final highest values near predetermined factor, generating base call.  
 XX Disclosure; Fig 120; 73pp; English.  
 PS The specification describes a method for determining a nucleotide  
 CC sequence signature. The method comprises obtaining optical measurements  
 CC with values indicating each nucleotide in a group of nucleotide  
 CC positions, adjusting the values until the ratio of highest value in the  
 CC set to next highest values in the set is at least a predetermined factor,  
 CC and generating a base call for a position in the group based on results  
 CC after the adjustment of values. The method is used for determining a  
 CC signature of a nucleotide sequence, and for determining a nucleotide  
 CC sequence of a polynucleotide from a series of optical measurements.  
 CC AAH74933-50 represent yeast sequences, identified using the method of the  
 CC invention  
 XX Sequence 17 BP; 7 A; 1 C; 4 G; 5 T; 0 U; 0 Other;  
 SQ Query Match 1.3%; Score 14; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. NO. 2.5e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 2245 TCTAGTTGAAATA 2258  
 Db 3 TCTAGTTGAAATA 16  
 RESULT 330  
 ADB45500  
 ID ADB45500 standard; DNA; 17 BP.  
 XX ADB45500;  
 AC 18-DEC-2003 (first entry)  
 DT Tumour suppression/reversion associated nucleotide #5823.  
 DE cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;  
 KW primer; probe; tumour suppression; tumour reversion; apoptosis;  
 KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;  
 KW diagnosis.  
 XX Homo sapiens.  
 OS WO2003040369-A2.  
 PN 15-MAY-2003.  
 PD 17-SEP-2002; 2002WO-IB004219.  
 PF 17-SEP-2001; 2001FR-00011981.  
 XX (MOLE-) MOLECULAR ENGINES LAB.  
 PA Telerman A, Amson R, Tuijnder M;  
 PI WPI; 2003-441574/41.  
 XX New nucleic acid encoding human prostate membrane-specific antigen,  
 XX useful e.g. for treatment of tumors and viral infection, also related  
 PT polypeptide and antibodies.  
 XX Disclosure; Page 712; 771pp; French.  
 PS

XX The invention relates to the isolation of 6327 nucleotide sequences,  
CC fragments of at least 15 consecutive nucleotides of these nucleotides, a  
CC sequence having at least 80% identity, after optimal alignment, with the  
CC nucleotides, a sequence that hybridizes under stringent conditions with  
CC the nucleotides, or the complement, or corresponding RNA, of the  
CC nucleotides. The nucleotides are used as probes or primers for detecting,  
CC identifying, quantifying and/or amplifying nucleic acids, as in vitro  
CC sense and antisense sequences, of nucleotides involved in tumour  
CC suppression or reversion, apoptosis and or viral resistance, to produce  
CC recombinant polypeptides, and to prepare transgenic animals, as  
CC cell lines containing the vectors), the encoded polypeptides and antibodies  
CC (Ab) against the polypeptide are useful for prevention and/or treatment  
CC of viral infections or diseases characterized by development of tumours  
CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).  
CC Analysis of the expression of the nucleotides can be used for diagnosis  
CC and/or prognosis of these diseases. The nucleotides and polypeptides can  
CC also be used to screen for their specific interactive molecules,  
CC potentially useful for treating diseases associated with abnormal  
CC expression of the nucleotides.

XX Sequence 17 BP; 4 A; 2 C; 2 G; 9 T; 0 U; 0 Other;  
SQ Query Match 1.3%; Score 14; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1292 ATCTGTTTCTTAA 1305  
DB 2 ATCTGTTTCTTAA 15

RESULT 331  
AAT53762/C  
ID AAT53762 standard; RNA; 17 BP.  
XX AC AAT53762;  
XX AC  
XX 25-MAR-2003 (revised)  
DT 03-APR-1997 (first entry)  
XX DE Rat ICAM hammerhead ribozyme target sequence (nt. position 2911).  
XX Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;  
KW gene expression; downregulation; interleukin-5; IL-5; ICAM-1;  
KW intercellular adhesion molecule; rel A; tumour necrosis factor;  
KW TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;  
KW translocation; chronic myelogenous leukaemia; CML; cancer;  
KW Philadelphia chromosome; inflammation; autoimmune disease;  
KW atherosclerosis; myocardial infarction; stroke; restenosis;  
KW transplant rejection; rheumatoid arthritis; psoriasis; HIV;  
KW myocardial ischaemia; Kawasaki disease; septic shock; HIV;  
KW human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;  
SS.

XX Rattus rattus.  
XX OS  
XX WO9523225-A2.  
XX PD  
XX 31-AUG-1995.  
XX PF 23-FEB-1995; 95WO-IB000156.  
XX 23-FEB-1994; 94US-00201109.  
XX 29-MAR-1994; 94US-00218934.  
XX 04-APR-1994; 94US-00222795.  
XX 07-APR-1994; 94US-00224483.  
XX 15-APR-1994; 94US-00227958.  
XX 15-APR-1994; 94US-00228041.  
XX 18-MAY-1994; 94US-00245736.  
XX 06-JUL-1994; 94US-00271280.  
XX 15-AUG-1994; 94US-00291932.

PR 16-AUG-1994; 94US-00291433.  
PR 17-AUG-1994; 94US-00292620.  
PR 18-AUG-1994; 94US-00293520.  
PR 02-SEP-1994; 94US-00300000.  
PR 08-SEP-1994; 94US-00303039.  
PR 23-SEP-1994; 94US-00311486.  
PR 23-SEP-1994; 94US-00311749.  
PR 28-SEP-1994; 94US-00314397.  
PR 03-OCT-1994; 94US-00316771.  
PR 07-OCT-1994; 94US-00319492.  
PR 11-OCT-1994; 94US-00321893.  
PR 14-OCT-1994; 94US-00334847.  
PR 10-NOV-1994; 94US-00337608.  
PR 28-NOV-1994; 94US-00345516.  
PR 16-DEC-1994; 94US-00357577.  
PR 23-DEC-1994; 94US-00363233.  
PR 30-JAN-1995; 95US-00380734.  
XX (RIBO-) RIBOZYME PHARM INC.  
XX Stinchcomb DT, Chowrira B, Drenzo A, Draper KG, Dudycz LW;  
PI Grimm S, Karpeisky A, Kisich K, Matulic-Adamic J, Mcswiggen JA;  
PI Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;  
PI Tracz D, Usman N, Wincott FE, Woolf T;  
XX WPI; 1995-351090/45.  
XX Ribozymes having modified bases and methods for producing them - for use  
PT in inhibiting disease related genes.  
XX Claim 2; Page 204; 407pp; English.  
XX The present sequence represents a preferred target sequence for an  
CC enzymatic nucleic acid (i.e. a ribozyme) which cleaves ICAM-1 mRNA at the  
CC nucleotide base position indicated in the DE line. Regions of the mRNA  
CC that do not form secondary folding structures and that contain potential  
CC hammerhead and hairpin ribozyme cleavage sites were identified by  
CC computer analysis. Ribozymes directed against these mRNA sequences were  
CC designed and synthesised with modifications that improve their nuclease  
CC resistance. The ribozymes cleave the ICAM-1 target sequences and thereby  
CC inhibit ICAM-1 expression, making them useful for reducing transplant  
CC rejection and alleviating symptoms in patients with rheumatoid arthritis,  
CC asthma and other inflammatory disorders. (Updated on 25-MAR-2003 to  
CC correct PI field.)  
XX Sequence 17 BP; 2 A; 7 C; 0 G; 0 T; 8 U; 0 Other;  
SQ Query Match 1.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.7e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1537 GTGTAATTGAGAGGAA 1553  
DB 17 GCGTATATAGAGAGGAA 1

RESULT 332  
AAT81448/C  
ID AAT81448 standard; RNA; 17 BP.  
XX AC AAT81448;  
XX 07-DEC-1997 (first entry)  
XX Human c-myc hammerhead ribozyme target sequence (nt. position 2527).  
XX Enzymatic nucleic acid; hammerhead; ribozyme; cleavage; human;  
KW smooth muscle cell; hyperproliferation; restenosis; cancer; c-myc;  
KW coronary angioplasty; ss.  
XX Homo sapiens.  
XX OS  
XX WO9531541-A2.

XX PD 23-NOV-1995.  
 XX PF 18-MAY-1995; 95WO-US006368.  
 XX PR 18-MAY-1994; 94US-00245466.  
 XX PR 13-JAN-1995; 95US-00373124.  
 XX PA (RIBO-) RIBOZYME PHARM INC.  
 XX STinchcomb DT, Draper K, Mcswiggen J, Jarvis T;  
 XX WPI; 1996-010927/01.  
 XX New enzymatic nucleic acid molecules - cleave RNA produced by e.g. c-myc,  
 XX for treating restenosis or cancer.  
 XX Claim 1; Page 75; 128pp; English.  
 XX The present sequence represents the preferred target sequence for an  
 CC enzymatic nucleic acid, especially a hammerhead ribozyme, which cleaves  
 CC the human c-myc sequence at the base position indicated in the descriptor  
 CC line. The c-myc sequence was screened for optimal ribozyme target sites  
 CC using a computer folding algorithm, and regions of the mRNA which did not  
 CC form secondary folding structures and contained potential ribozyme  
 CC cleavage sites were identified. Ribozymes were synthesised and their  
 CC activities optimised by either varying the length of the binding arms or  
 CC by modification to prevent degradation by nucleases. The ribozymes cleave  
 CC the c-myc sequence and can be used to prevent smooth muscle cell  
 CC hyperproliferation in restenosis, especially after coronary angioplasty,  
 CC and in cancers  
 XX Sequence 17 BP; 8 A; 1 C; 0 G; 0 T; 8 U; 0 Other;  
 SQ Query Match 1.3%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 2.7e+02;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1765 GATTTTAAATTTAT 1781  
 DB 17 GATTTTAAATATAT 1  
 RESULT 333  
 AAT27920  
 ID AAT27920 standard; DNA; 17 BP.  
 AC AAT27920;  
 XX 28-JAN-1997 (first entry)  
 DE 5'-anchored simple sequence repeat primer VHVF(TG)6.5.  
 XX Detection; polymorphism; perfect compound simple sequence repeat;  
 KW adaptor directed primer; Genome; genetic; fingerprinting;  
 KW amplified fragment length polymorphism assay; microsatellite region;  
 KW genetic trait marking; germplasm comparisons; 5'-anchored; ss.  
 XX Synthetic.  
 OS WO9617082-A2.  
 XX 06-JUN-1996.  
 XX 21-NOV-1995; 95WO-US015150.  
 XX 28-NOV-1994; 94US-00346456.  
 XX (DUPO) DU PONT DE NEMOURS & CO E. I.  
 XX Morgante M, Vogel JM;  
 XX WPI; 1996-277795/28.

XX Modified amplified fragment length polymorphism assay - for detection of  
 PT polymorphism esp. in micro:satellite regions.  
 XX Example 1; Page 77; 173pp; English.  
 XX Detecting polymorphisms between 2 nucleic acid samples, esp. in  
 CC microsatellite regions, comprises digesting the nucleic acid to generate  
 CC fragments, ligating adaptor segments to their ends, amplifying them using  
 CC primer directed amplification and comparing the prods. to detect  
 CC differences. The primers used in the amplification comprise a primer  
 CC consisting of a perfect cpd. simple sequence repeat (SSR), and an adaptor  
 CC directed primer, comprising a sequence complementary to an adaptor  
 CC segment. The present sequence is an example of a SSR primer, which is  
 CC flanked at its 5'-end by degenerate nucleotides. The method represents a  
 CC modified amplified fragment length polymorphism assay, which is partic.  
 CC useful for genome fingerprinting, i.e. for genetic trait marking and  
 CC germplasm comparisons  
 XX Sequence 17 BP; 0 A; 0 C; 6 G; 7 T; 0 U; 4 Other;  
 SQ Query Match 1.3%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 76.8%; Pred. No. 2.7e+02;  
 Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
 QY 1789 ATATTGTGTGTGTGT 1805  
 DB 1 VHVHTGTGTGTGTGT 17  
 RESULT 334  
 AAX69800  
 ID AAX69800 standard; RNA; 17 BP.  
 XX AAX69800;  
 AC AAX69800;  
 XX 28-JUL-1999 (first entry)  
 DE Human flt1 VEGF receptor hammerhead ribozyme substrate #1095.  
 XX Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;  
 KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;  
 KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;  
 KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;  
 KW foetal liver kinase 1; ss.  
 XX Homo sapiens.  
 OS WO9715662-A2.  
 XX 01-MAY-1997.  
 XX 25-OCT-1996; 96WO-US017480.  
 XX 26-OCT-1995; 95US-0005974P.  
 PR 11-JAN-1996; 96US-00584040.  
 XX (RIBO-) RIBOZYME PHARM INC.  
 PA (CHIR) CHIRON CORP.  
 XX Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;  
 PI WPI; 1997-259017/23.  
 XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA  
 PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,  
 PT rheumatoid arthritis, etc., in a human patient.  
 XX Claim 4; Page 79; 218pp; English.  
 XX The present invention describes nucleic acid molecules which modulate the  
 CC synthesis, expression and/or stability of a mRNA encoding 1 or more  
 CC receptors of vascular endothelial growth factor (VEGF). A patient

CC (preferably human) having a condition associated with the level of the  
 CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing  
 CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour  
 CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be  
 CC treated by administering the nucleic acid molecule or the expression  
 CC vector to the patient. AAX67275 to AAX75752 represent specific examples  
 CC of nucleic acid molecules from the present invention  
 XX  
 SQ Sequence 17 BP; 0 A; 1 C; 0 G; 0 T; 16 U; 0 Other;  
 Query Match 1.3%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 5.9%; Pred. No. 2.7e+02;  
 Matches 1; Conservative 14; Mismatches 2; Indels 0; Gaps 0;  
 QY 1864 CTTTATTATTTCTGTTT 1880  
 DB 1 CUUUUUUUUUUUUUUUU 17  
 RESULT 335  
 AAX73299  
 ID AAX73299 standard; RNA; 17 BP.  
 XX  
 AC AAX73299;  
 XX  
 XX  
 DT 28-JUL-1999 (first entry)  
 DE Mouse flk-1 VEGF receptor hammerhead ribozyme substrate #732.  
 XX  
 KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;  
 KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;  
 KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;  
 KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;  
 KW foetal liver kinase 1; ss.  
 XX  
 OS Mus sp.  
 XX  
 PN WO9715662-A2.  
 XX  
 PD 01-MAY-1997.  
 XX  
 PF 25-OCT-1996; 96WO-US017480.  
 XX  
 PR 26-OCT-1995; 95US-0005974P.  
 PR 11-JAN-1996; 96US-00584040.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 PA (CHIR) CHIRON CORP.  
 XX  
 PI Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;  
 XX  
 XX WPI; 1997-259017/23.  
 XX  
 PF Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA  
 PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,  
 PT rheumatoid arthritis, etc., in a human patient.  
 XX  
 PS Claim 4; Page 146; 218pp; English.  
 XX  
 CC The present invention describes nucleic acid molecules which modulate the  
 CC synthesis, expression and/or stability of a mRNA encoding 1 or more  
 CC receptors of vascular endothelial growth factor (VEGF). A patient  
 CC (preferably human) having a condition associated with the level of the  
 CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing  
 CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour  
 CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be  
 CC treated by administering the nucleic acid molecule or the expression  
 CC vector to the patient. AAX67275 to AAX75752 represent specific examples  
 CC of nucleic acid molecules from the present invention  
 XX  
 SQ Sequence 17 BP; 6 A; 6 C; 1 G; 0 T; 4 U; 0 Other;  
 Query Match 1.3%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 5.9%; Pred. No. 2.7e+02;  
 Matches 1; Conservative 14; Mismatches 2; Indels 0; Gaps 0;  
 QY 1864 CTTTATTATTTCTGTTT 1880  
 DB 1 CUUUUUUUUUUUUUUUU 17  
 RESULT 335  
 AAX73299  
 ID AAX73299 standard; RNA; 17 BP.  
 XX  
 AC AAX73299;  
 XX  
 XX  
 DT 28-JUL-1999 (first entry)  
 DE Mouse flk-1 VEGF receptor hammerhead ribozyme substrate #732.  
 XX  
 KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;  
 KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;  
 KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;  
 KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;  
 KW foetal liver kinase 1; ss.  
 XX  
 OS Mus sp.  
 XX  
 PN WO9715662-A2.  
 XX  
 PD 01-MAY-1997.  
 XX  
 PF 25-OCT-1996; 96WO-US017480.  
 XX  
 PR 26-OCT-1995; 95US-0005974P.  
 PR 11-JAN-1996; 96US-00584040.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 PA (CHIR) CHIRON CORP.  
 XX  
 PI Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;  
 XX  
 XX WPI; 1997-259017/23.  
 XX  
 PF Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA  
 PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,  
 PT rheumatoid arthritis, etc., in a human patient.  
 XX  
 PS Claim 4; Page 146; 218pp; English.  
 XX  
 CC The present invention describes nucleic acid molecules which modulate the  
 CC synthesis, expression and/or stability of a mRNA encoding 1 or more  
 CC receptors of vascular endothelial growth factor (VEGF). A patient  
 CC (preferably human) having a condition associated with the level of the  
 CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing  
 CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour  
 CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be  
 CC treated by administering the nucleic acid molecule or the expression  
 CC vector to the patient. AAX67275 to AAX75752 represent specific examples  
 CC of nucleic acid molecules from the present invention  
 XX  
 SQ Sequence 17 BP; 6 A; 6 C; 1 G; 0 T; 4 U; 0 Other;  
 Query Match 1.3%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 5.9%; Pred. No. 2.7e+02;  
 Matches 1; Conservative 14; Mismatches 2; Indels 0; Gaps 0;

Best Local Similarity 70.6%; Pred. No. 2.7e+02;  
 Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
 QY 1643 CCCTAAGTCTCAGAACACG 1659  
 DB 1 CCUUAUUCUAGAACACC 17  
 RESULT 336  
 AAX73297  
 ID AAX73297 standard; RNA; 17 BP.  
 XX  
 AC AAX73297;  
 XX  
 DT 28-JUL-1999 (first entry)  
 DE Mouse flk-1 VEGF receptor hammerhead ribozyme substrate #730.  
 XX  
 KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;  
 KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;  
 KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;  
 KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;  
 KW foetal liver kinase 1; ss.  
 XX  
 OS Mus sp.  
 XX  
 PN WO9715662-A2.  
 XX  
 PD 01-MAY-1997.  
 XX  
 PF 25-OCT-1996; 96WO-US017480.  
 XX  
 PR 26-OCT-1995; 95US-0005974P.  
 PR 11-JAN-1996; 96US-00584040.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 PA (CHIR) CHIRON CORP.  
 XX  
 PI Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;  
 XX  
 XX WPI; 1997-259017/23.  
 XX  
 PF Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA  
 PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,  
 PT rheumatoid arthritis, etc., in a human patient.  
 XX  
 PS Claim 4; Page 146; 218pp; English.  
 XX  
 CC The present invention describes nucleic acid molecules which modulate the  
 CC synthesis, expression and/or stability of a mRNA encoding 1 or more  
 CC receptors of vascular endothelial growth factor (VEGF). A patient  
 CC (preferably human) having a condition associated with the level of the  
 CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing  
 CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour  
 CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be  
 CC treated by administering the nucleic acid molecule or the expression  
 CC vector to the patient. AAX67275 to AAX75752 represent specific examples  
 CC of nucleic acid molecules from the present invention  
 XX  
 SQ Sequence 17 BP; 5 A; 3 C; 3 G; 0 T; 6 U; 0 Other;  
 Query Match 1.3%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 58.8%; Pred. No. 2.7e+02;  
 Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;  
 QY 1639 TGTCTCTAAGTCAGAA 1655  
 DB 1 UGUGCUUUAUUCAGAA 17  
 RESULT 337  
 AAV91401  
 ID AAV91401 standard; RNA; 17 BP.







CC method comprises preparing a reduced complexity genome (RCG) from the  
 CC genomic sample and analysing the RCG for the presence or absence of a SNP  
 CC allele. The method can be used to characterise a tumour, to generate a  
 CC genomic pattern for an individual genome or to generate a genomic  
 CC classification code for a genome. The method can be used to assess  
 CC whether a subject is at risk for developing a disease or to identify a  
 CC set of SNP alleles associated with a disease. The method can also be used  
 CC to perform linkage analysis. AAA35944 to AAA35947 represent sequences  
 CC used in the exemplification of the present invention. AAA35948 to  
 CC AAA36632 represent nucleotide sequences containing SNPs  
 XX  
 SQ Sequence 17 BP; 6 A; 4 C; 2 G; 5 T; 0 U; 0 Other;

Query Match 1.3%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 2.7e+02;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1379 TGGTTTGAAGAATGTTA 1395  
 DB 17 TGGCTTCAAGAATGTTA 1

RESULT 342  
 AAA35972/c  
 ID AAA35972 standard; DNA; 17 BP.  
 AC AAA35972;  
 XX  
 XX 26-JUL-2000 (first entry)  
 DT  
 DE Human genomic SNP allele specific oligonucleotide SEQ ID NO:29.

Human; single nucleotide polymorphism; SNP; genotyping; DNA analysis;  
 allele specific oligonucleotide; ASO; reduced complexity genome; RCG;  
 genomic classification; identification; DNA fingerprinting;  
 tumour characterisation; hybridisation; ss.

OS Homo sapiens.  
 XX  
 XX WO200018960-A2.  
 XX  
 XX 06-APR-2000.  
 XX  
 XX 24-SEP-1999; 99WO-US022283.  
 XX  
 XX 25-SEP-1998; 98US-0101757P.  
 XX  
 XX (MASI ) MASSACHUSETTS INST TECHNOLOGY.  
 XX  
 XX Landers JE, Jordan B, Houseman DE, Charest A;  
 PI  
 XX WPI; 2000-293181/25.

Detection of single nucleotide polymorphisms in genomes by preparation  
 PT and analysis of reduced complexity genomes, useful for genotyping,  
 PT fingerprinting and determining allele frequency of SNPs.

XX Disclosure; Page 54; 11pp; English.  
 XX  
 XX A method has been developed for detecting the presence or absence of a  
 CC single nucleotide polymorphism (SNP) allele in a genomic sample. The  
 CC method comprises preparing a reduced complexity genome (RCG) from the  
 CC genomic sample and analysing the RCG for the presence or absence of a SNP  
 CC allele. The method can be used to characterise a tumour, to generate a  
 CC genomic pattern for an individual genome or to generate a genomic  
 CC classification code for a genome. The method can be used to assess  
 CC whether a subject is at risk for developing a disease or to identify a  
 CC set of SNP alleles associated with a disease. The method can also be used  
 CC to perform linkage analysis. AAA35944 to AAA35947 represent sequences  
 CC used in the exemplification of the present invention. AAA35948 to  
 CC AAA36632 represent nucleotide sequences containing SNPs

XX Sequence 17 BP; 6 A; 4 C; 2 G; 5 T; 0 U; 0 Other;

Query Match 1.3%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 2.7e+02;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1379 TGGTTTGAAGAATGTTA 1395  
 DB 17 TGGCTTCAAGAATGTTA 1

RESULT 343  
 AAA25450  
 ID AAA25450 standard; DNA; 17 BP.  
 XX  
 AC AAA25450;  
 XX  
 XX 19-JUL-2000 (first entry)  
 DT  
 DE Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1948.

Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;  
 hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;  
 gene expression modification; cancer; phosphorothioate; endonuclease;  
 anticancer; breast cancer; endometrium cancer; ss.

OS Homo sapiens.  
 XX  
 XX WO9954459-A2.  
 XX  
 XX 28-OCT-1999.  
 XX  
 XX 19-APR-1999; 99WO-US008547.  
 XX  
 XX 20-APR-1998; 98US-0082404P.  
 PR  
 XX 23-JUN-1998; 98US-00103636.  
 XX  
 XX (RIBO-) RIBOZYME PHARM INC.

XX Thompson JD, Beigelman L, Mcswiggen JA, Karpeisky A, Bellon L;  
 PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haerberli P;  
 PI Matulic-Adamic J;  
 XX  
 XX WPI; 2000-013248/01.

New nucleic acids that interact, and optionally cleave, target sequences,  
 PT used to treat cancer.

XX Claim 77; Page 79; 148pp; English.  
 XX  
 XX The present invention describes nucleic acids (A) that interact stably  
 CC with a target sequence and contain at least one phosphoro(di)thioate  
 CC link, having endonuclease activity. (A), and more generally any catalytic  
 CC nucleic acid (A') that modulates expression of the oestrogen receptor  
 CC gene, are used to treat cancer (particularly of breast or endometrium),  
 CC in vivo or by transforming cells ex vivo and implanting treated cells, or  
 CC for other conditions associated with levels of oestrogen receptor.  
 CC Because of the high selectivity for targeted RNA, (A) can also be used to  
 CC correlate inhibition of gene expression with alterations in phenotype,  
 CC particularly for identification of therapeutic targets, and as research  
 CC reagents for RNA, in the same way that restriction endonucleases are  
 CC used with DNA. The combination of modifications in (A) improves  
 CC resistance to nucleases, binding affinity and/or activity. AAA23503 to  
 CC AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and  
 CC AAA24748 to AAA25992 represent their corresponding target sequences.  
 CC AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme  
 CC sequences, and AAA26107 to AAA26218 represent their corresponding target  
 CC sequences. AAA26219 to AAA26271 represent other ribozyme sequences and  
 CC antisense oligonucleotides used in the exemplification of the present  
 CC invention

XX Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;

Query Match 1.3%; Score 13.8; DB 1; Length 17;



QY 1865 TTTTATTTTGTGTTT 1881  
| | | | | | | | | |  
Db 1 TTTTATTTTGTGTTT 17

RESULT 346  
AAA50197  
ID ID AAA50197 standard; DNA; 17 BP.  
XX  
AC AAA50197;  
XX  
DT 07-NOV-2000 (first entry)  
XX  
DE 2'-Methoxyethoxy-modified phosphorothioate oligonucleotide.  
XX  
KW Phosphorothioate oligonucleotide; H-phosphonate chemistry; ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 1..19  
FT /\*tag= a  
FT /note= "2'-methoxyethoxy modified thymidine"  
FT modified\_base 1..17  
FT /\*tag= b  
FT /note= "phosphorothioate internucleoside linkages"  
XX  
PN WO200047593-A1.  
XX  
PD 17-AUG-2000.  
XX  
PF 11-FEB-2000; 2000WO-US003543.  
XX  
PR 12-FEB-1999; 99US-00250075.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Manoharan M, Maier MA;  
XX  
DR WPI; 2000-558188/51.  
XX  
PT Preparation of mixed backbone oligomeric compounds useful as e.g. primers  
PT for diagnostic tests, involves oxidation of H-phosphonate internucleoside  
PT linkages to phosphodiester internucleoside linkages.  
XX  
PS Example 12; Page 34; 49pp; English.  
XX  
CC The present sequence is that of a phosphorothioate oligonucleotide  
CC containing 20 T nucleobases, each having a 2'-methoxyethoxy group on its  
CC 5' ribosyl sugar moiety. It is an example of an oligomeric compound  
CC produced according to the methods of the invention. The invention  
CC provides compounds and methods for the preparation of mixed backbone  
CC oligomeric, or chimeric, compounds having phosphodiester internucleoside  
CC linkages in addition to phosphorothioate and/or phosphoramidate  
CC internucleoside linkages. The methods also include incorporation of  
CC boranophosphate internucleoside linkages. The methods utilize H-  
CC phosphonate intermediates that are coupled together forming contiguous  
CC regions of 1 or more H-phosphonate internucleoside linkages. Each  
CC phosphorothioate, phosphoramidate or boranophosphate internucleoside  
CC contiguous region is subsequently oxidized to phosphodiester,  
CC linkages prior to further elongation. Mixed backbone oligomeric compounds  
CC are prepared in this manner by oxidizing adjacent regions with different  
CC reagents. Oligomeric compounds of the invention are prepared using novel  
CC oxidation steps that oxidize a region of 1 or more H-phosphonate  
CC internucleoside linkages without degrading existing linkages that have  
CC been previously oxidized. The oligonucleotides obtained are useful as  
CC primers in PCR, probes, linkers, gene fragments and for other diagnostic  
CC tests on e.g. biological tissue, fluid, cells etc., as research reagents,  
CC and as antiviral agents  
XX  
SQ Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;  
Query Match 1.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.7e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTT 1881  
| | | | | | | | | |  
Db 1 TTTTATTTTGTGTTT 17

RESULT 347  
AAF02995  
ID ID AAF02995 standard; DNA; 17 BP.  
XX  
AC AAF02995;  
XX  
DT 16-FEB-2001 (first entry)  
XX  
DE Hammerhead ribozyme substrate #1290.  
XX  
KW Ribozyme; erythropoietin; granulocyte colony stimulating factor;  
KW interferon alpha; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO2000061729-A2.  
XX  
PD 19-OCT-2000.  
XX  
PF 11-APR-2000; 2000WO-US009721.  
XX  
PR 12-APR-1999; 99US-0129390P.  
XX  
PA (RIBO-) RIBOZYME PHARM INC.  
XX  
PI Blatt L, Zwick M, Pavco P, Meswigen J;  
XX  
DR WPI; 2000-647423/62.  
XX  
PT Enzymatic and antisense nucleic acid inhibition of repressor genes,  
PT useful for producing e.g. granulocyte colony stimulating factor protein,  
PT interferon alpha and erythropoietin.  
XX  
PS Claim 37; Page 85; 164pp; English.  
XX  
CC The present invention relates to enzymatic and antisense nucleic acid  
CC molecules that act as inhibitors of the expression of repressor genes  
CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription  
CC factor gene, IRP-2 and/or the CAAT Displacement Protein (CDP).  
CC Inhibition of the repressors removes prevents inhibition (and  
CC consequently increases expression of) genes involved in the production of  
CC erythropoietin, granulocyte colony stimulating factor protein and  
CC interferon alpha  
XX  
SQ Sequence 17 BP; 8 A; 0 C; 3 G; 6 T; 0 U; 0 Other;  
Query Match 1.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.7e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1760 ACCGAGATTTTAAAA 1776  
| | | | | | | | | |  
Db 1 ACAGAGATTTTAAAA 17

RESULT 348  
AAF02349  
ID ID AAF02349 standard; DNA; 17 BP.  
XX  
AC AAF02349;  
XX  
DT 16-FEB-2001 (first entry)  
XX  
DE Hammerhead ribozyme substrate #644.  
XX

KW Ribozyme; erythropoietin; granulocyte colony stimulating factor;  
KW interferon alpha; ss.  
XX  
OS Homo sapiens.  
XX WO200061729-A2.  
XX  
XX 19-OCT-2000.  
XX  
XX 11-APR-2000; 2000WO-US009721.  
XX  
XX 12-APR-1999; 99US-0129390P.  
XX  
XX (RIBO-) RIBOZYME PHARM INC.  
XX  
XX Blatt L, Zwick M, Pavco P, Mcswiggen J;  
XX WPI; 2000-647423/62.  
XX  
XX Enzymatic and antisense nucleic acid inhibition of repressor genes,  
PT useful for producing e.g. granulocyte colony stimulating factor protein,  
PT interferon alpha and erythropoietin.  
XX  
XX Claim 37; Page 70; 164pp; English.  
XX  
XX The present invention relates to enzymatic and antisense nucleic acid  
CC molecules that act as inhibitors of the expression of repressor genes  
CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription  
CC factor gene, IRF-2 and/or the C/EBP Displacement Protein (CDP).  
CC Inhibition of the repressors removes prevents inhibition (and  
CC consequently increases expression of) genes involved in the production of  
CC erythropoietin, granulocyte colony stimulating factor protein and  
CC interferon alpha  
XX  
XX Sequence 17 BP; 7 A; 1 C; 1 G; 8 T; 0 U; 0 Other;  
SQ  
  
Query Match 1.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.7e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1772 TAAATTTATATTGTAA 1788  
DB 1 TATAACTTATATTGTAA 17  
  
RESULT 349  
ABV82841  
ID ABV82841 standard; DNA; 17 BP.  
AC ABV82841;  
XX  
XX 03-JAN-2003 (first entry)  
XX  
XX Human HTPL scanning oligonucleotide SEQ ID 4087.  
XX  
XX Human; Gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;  
KW human testis expressed Patched like protein; testis; adrenal; liver;  
KW male germ cell development; bone marrow; brain; kidney; lung; placenta;  
KW prostate; skeletal muscle; colon; male infertility; cancer; ss.  
XX  
XX Homo sapiens.  
OS  
XX  
XX EP1229046-A2.  
XX  
XX 07-AUG-2002.  
XX  
XX 28-JAN-2002; 2002EP-00001167.  
XX  
XX 30-JAN-2001; 2001WO-US000663.  
PR 30-JAN-2001; 2001WO-US000664.  
PR 30-JAN-2001; 2001WO-US000665.  
PR 30-JAN-2001; 2001WO-US000667.  
PR 30-JAN-2001; 2001WO-US000668.

PR 30-JAN-2001; 2001WO-US000669.  
PR 23-MAY-2001; 2001US-00864761.  
PR 09-OCT-2001; 2001US-0327898P.  
XX  
XX (ABOM-) ABOMICA INC.  
XX  
XX Zhan J;  
XX  
XX WPI; 2002-676582/73.  
XX  
XX Novel isolated human testis expressed Patched like protein (HTPL), useful  
PT for identifying agonist and antagonist and specific binding partners, and  
PT for treating subjects having defects in HTPL.  
XX  
XX Example 2; Page 599; 718pp; English.  
XX  
XX The present invention relates to human testis expressed Patched like  
CC protein (HTPL, see ABV78759 to ABV78762 and ABV8519 to ABV8520). HTPL  
CC has two isoforms, with a few single base pair differences between the  
CC two. One of the single base pair changes introduces a premature stop  
CC codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL  
CC shares an overall structure organisation with the Patched protein. The  
CC shared structural features strongly imply that HTPL plays a role similar  
CC to that of Patched, and is a potential tumour suppressor. HTPL is  
CC important in regulating male germ cell development, and the HTPL gene was  
CC mapped to human chromosome 10p12.1. HTPL and its coding sequence are  
CC useful for diagnosing a disorder caused by mutation in HTPL, and in  
CC therapy and manufacture of a medicament for treatment or prevention of  
CC such disorder associated with decreased expression or activity of human  
CC HTPL. Such disorders include disorders of testis, or adrenal, adult and  
CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,  
CC skeletal muscle or colon function. HTPL proteins and nucleic acids are  
CC clinically useful diagnostic markers and potential therapeutic agents for  
CC male infertility and cancer. The present oligonucleotide was used in an  
CC example from the invention  
XX  
XX Sequence 17 BP; 3 A; 2 C; 3 G; 9 T; 0 U; 0 Other;  
SQ  
  
Query Match 1.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.7e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 2160 AAGCATTGTTTCTACT 2176  
DB 1 ATGCATTGTTTCTAGT 17  
  
RESULT 350  
ABS74863  
ID ABS74863 standard; DNA; 17 BP.  
XX  
XX ABS74863;  
XX  
XX 24-DEC-2002 (first entry)  
XX  
XX Human PAPP-Ea associated 17-mer SEQ ID 389.  
XX  
XX PAPP-E; human; pregnancy associated plasma protein E; abortive;  
KW contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis;  
KW dysgenetic pregnancy; primer; ss.  
XX  
XX Homo sapiens.  
OS  
XX  
XX US2002102252-A1.  
XX  
XX 01-AUG-2002.  
XX  
XX 06-APR-2001; 2001US-00827998.  
XX  
XX 26-MAY-2000; 2000US-0207456P.  
XX  
XX (GUY/) GU Y.  
XX (SHAN/) SHANNON M E.  
PA

XX Gu Y, Shannon ME;  
PI WPI; 2002-697817/75.  
XX  
DR New isolated nucleic acid encoding an isoform of human pregnancy  
PT associated plasma protein E, for preventing or aborting pregnancy.  
XX  
PS Example 2; Page 126; 353pp; English.  
XX  
CC This invention describes a novel isolated nucleic acid that encodes one  
CC of three new isoforms of human pregnancy associated plasma protein E,  
CC hPAPP-E. The products of the invention have abortive and contraceptive  
CC activity and can be used for gene therapy or in a vaccine. The nucleic  
CC acid, polypeptide encoded by it, or antibody to the polypeptide can be  
CC used in pharmaceutical compositions or vaccines for preventing or  
CC aborting pregnancy. PAPP-E is used in the antenatal diagnosis of  
CC the level of PAPP-E isoform mRNA in chorionic villus samples, and the  
CC dysgenetic pregnancies. The nucleic acids are used as probes to assess  
CC antibodies can be used to assess the expression levels of PAPP-E isoform  
CC proteins in chorionic villus samples, to diagnose dysgenetic pregnancies  
CC antenatally. This sequence represents an oligomer used in scanning the  
CC human PAPP-E genes described in the disclosure of the invention  
XX  
SQ Sequence 17 BP; 2 A; 0 C; 6 G; 9 T; 0 U; 0 Other;  
  
Query Match 1.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.7e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1799 TGTGTGTGTGTGTGTAT 1815  
Db 1 TGTGTGTGTGTGTAT 17  
|||||  
RESULT 351  
ABS74859  
ID ABS74859 standard; DNA; 17 BP.  
XX  
AC ABS74859;  
XX  
XX 24-DEC-2002 (first entry)  
XX  
DE Human PAPP-Ea associated 17-mer SEQ ID 385.  
XX  
XX PAPP-E; human; pregnancy associated plasma protein E; abortive;  
XX contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis;  
XX dysgenetic pregnancy; primer; ss.  
XX  
XX Homo sapiens.  
XX  
XX US2002102252-A1.  
XX  
XX 01-AUG-2002.  
XX  
XX 06-APR-2001; 2001US-00827998.  
XX  
XX 26-MAY-2000; 2000US-0207456P.  
XX  
XX (GUY/) GU Y.  
XX (SHAN/) SHANNON M E.  
XX  
XX Gu Y, Shannon ME;  
XX  
XX WPI; 2002-697817/75.  
XX  
XX New isolated nucleic acid encoding an isoform of human pregnancy  
PT associated plasma protein E, for preventing or aborting pregnancy.  
XX  
PS Example 2; Page 125; 353pp; English.  
XX  
CC This invention describes a novel isolated nucleic acid that encodes one  
CC of three new isoforms of human pregnancy associated plasma protein E,

CC hPAPP-E. The products of the invention have abortive and contraceptive  
CC activity and can be used for gene therapy or in a vaccine. The nucleic  
CC acid, polypeptide encoded by it, or antibody to the polypeptide can be  
CC used in pharmaceutical compositions or vaccines for preventing or  
CC aborting pregnancy. PAPP-E is used in the antenatal diagnosis of  
CC the level of PAPP-E isoform mRNA in chorionic villus samples, and the  
CC dysgenetic pregnancies. The nucleic acids are used as probes to assess  
CC antibodies can be used to assess the expression levels of PAPP-E isoform  
CC proteins in chorionic villus samples, to diagnose dysgenetic pregnancies  
CC antenatally. This sequence represents an oligomer used in scanning the  
CC human PAPP-E genes described in the disclosure of the invention  
XX  
SQ Sequence 17 BP; 1 A; 0 C; 7 G; 9 T; 0 U; 0 Other;  
  
Query Match 1.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.7e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1793 TGTGTGTGTGTGTGT 1809  
Db 1 TGTGTGTGTGTGTGT 17  
|||||  
RESULT 352  
ABS74862  
ID ABS74862 standard; DNA; 17 BP.  
XX  
AC ABS74862;  
XX  
XX 24-DEC-2002 (first entry)  
XX  
XX Human PAPP-Ea associated 17-mer SEQ ID 388.  
XX  
XX PAPP-E; human; pregnancy associated plasma protein E; abortive;  
XX contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis;  
XX dysgenetic pregnancy; primer; ss.  
XX  
XX Homo sapiens.  
XX  
XX US2002102252-A1.  
XX  
XX 01-AUG-2002.  
XX  
XX 06-APR-2001; 2001US-00827998.  
XX  
XX 26-MAY-2000; 2000US-0207456P.  
XX  
XX (GUY/) GU Y.  
XX (SHAN/) SHANNON M E.  
XX  
XX Gu Y, Shannon ME;  
XX  
XX WPI; 2002-697817/75.  
XX  
XX New isolated nucleic acid encoding an isoform of human pregnancy  
PT associated plasma protein E, for preventing or aborting pregnancy.  
XX  
PS Example 2; Page 126; 353pp; English.  
XX  
XX This invention describes a novel isolated nucleic acid that encodes one  
XX of three new isoforms of human pregnancy associated plasma protein E,  
XX hPAPP-E. The products of the invention have abortive and contraceptive  
XX activity and can be used for gene therapy or in a vaccine. The nucleic  
XX acid, polypeptide encoded by it, or antibody to the polypeptide can be  
XX used in pharmaceutical compositions or vaccines for preventing or  
XX aborting pregnancy. PAPP-E is used in the antenatal diagnosis of  
XX the level of PAPP-E isoform mRNA in chorionic villus samples, and the  
XX dysgenetic pregnancies. The nucleic acids are used as probes to assess  
XX antibodies can be used to assess the expression levels of PAPP-E isoform  
XX proteins in chorionic villus samples, to diagnose dysgenetic pregnancies  
XX antenatally. This sequence represents an oligomer used in scanning the  
XX human PAPP-E genes described in the disclosure of the invention  
XX

SQ Sequence 17 BP; 2 A; 0 C; 7 G; 8 T; 0 U; 0 Other;  
Query Match 1.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.7e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1798 GTGTGTGTGTGTGTGTA 1814  
DB 1 GTGTGTGTGTGTGTGTA 17  
RESULT 353  
ABS74861  
ID ABS74861 standard; DNA; 17 BP.  
XX  
AC ABS74861;  
XX  
XX  
XX  
XX 24-DEC-2002 (first entry)  
XX Human PAPP-Ea associated 17-mer SEQ ID 387.  
XX PAPP-E; human; pregnancy associated plasma protein E; abortive;  
KW contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis;  
KW dysgenetic pregnancy; primer; ss.  
XX  
XX Homo sapiens.  
XX  
XX US2002102252-A1.  
XX  
XX 01-AUG-2002.  
XX  
XX 06-APR-2001; 2001US-00827998.  
XX  
XX 26-MAY-2000; 2000US-0207456P.  
XX (GUY/) GU Y.  
XX (SHAN/) SHANNON M E.  
XX  
XX Gu Y, Shannon ME;  
XX WPI; 2002-697817/75.  
XX  
XX New isolated nucleic acid encoding an isoform of human pregnancy  
XX associated plasma protein E, for preventing or aborting pregnancy.  
XX  
XX Example 2; Page 126; 353pp; English.  
XX This invention describes a novel isolated nucleic acid that encodes one  
XX of three new isoforms of human pregnancy associated plasma protein E,  
XX hPAPP-E. The products of the invention have abortive and contraceptive  
XX activity and can be used for gene therapy or in a vaccine. The nucleic  
XX acid, polypeptide encoded by it, or antibody to the polypeptide can be  
XX used in pharmaceutical compositions or vaccines for preventing or  
XX aborting pregnancy. PAPP-E is used in the antenatal diagnosis of  
XX the level of PAPP-E isoform mRNA in chorionic villus samples, and the  
XX antibodies can be used to assess the expression levels of PAPP-E isoform  
XX proteins in chorionic villus samples, to diagnose dysgenetic pregnancies  
XX antenatally. This sequence represents an oligomer used in scanning the  
XX human PAPP-E genes described in the disclosure of the invention  
XX  
SQ Sequence 17 BP; 1 A; 0 C; 7 G; 9 T; 0 U; 0 Other;  
Query Match 1.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.7e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1793 TGTGTGTGTGTGTGTGT 1809  
DB 1 TGTGTGTGTGTGTGTGT 17  
RESULT 354

ABS74858  
ID ABS74858 standard; DNA; 17 BP.  
XX  
XX ABS74858;  
AC  
XX  
XX 24-DEC-2002 (first entry)  
DT  
XX  
XX Human PAPP-Ea associated 17-mer SEQ ID 384.  
DE  
XX PAPP-E; human; pregnancy associated plasma protein E; abortive;  
KW contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis;  
KW dysgenetic pregnancy; primer; ss.  
XX  
XX Homo sapiens.  
OS  
XX US2002102252-A1.  
XX  
XX 01-AUG-2002.  
PD  
XX  
XX 06-APR-2001; 2001US-00827998.  
PF  
XX  
XX 26-MAY-2000; 2000US-0207456P.  
PR  
XX (GUY/) GU Y.  
XX (SHAN/) SHANNON M E.  
PA  
XX  
XX Gu Y, Shannon ME;  
PI  
XX WPI; 2002-697817/75.  
DR  
XX  
XX New isolated nucleic acid encoding an isoform of human pregnancy  
XX associated plasma protein E, for preventing or aborting pregnancy.  
PT  
XX  
XX Example 2; Page 125; 353pp; English.  
XX This invention describes a novel isolated nucleic acid that encodes one  
XX of three new isoforms of human pregnancy associated plasma protein E,  
XX hPAPP-E. The products of the invention have abortive and contraceptive  
XX activity and can be used for gene therapy or in a vaccine. The nucleic  
XX acid, polypeptide encoded by it, or antibody to the polypeptide can be  
XX used in pharmaceutical compositions or vaccines for preventing or  
XX aborting pregnancy. PAPP-E is used in the antenatal diagnosis of  
XX the level of PAPP-E isoform mRNA in chorionic villus samples, and the  
XX antibodies can be used to assess the expression levels of PAPP-E isoform  
XX proteins in chorionic villus samples, to diagnose dysgenetic pregnancies  
XX antenatally. This sequence represents an oligomer used in scanning the  
XX human PAPP-E genes described in the disclosure of the invention  
XX  
SQ Sequence 17 BP; 1 A; 0 C; 8 G; 8 T; 0 U; 0 Other;  
Query Match 1.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.7e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1794 GTGTGTGTGTGTGTGTG 1810  
DB 1 GTGTGTGTGTGTGTGTG 17  
RESULT 355  
ABS74860  
ID ABS74860 standard; DNA; 17 BP.  
XX  
XX ABS74860;  
AC  
XX  
XX 24-DEC-2002 (first entry)  
DT  
XX  
XX Human PAPP-Ea associated 17-mer SEQ ID 386.  
DE  
XX PAPP-E; human; pregnancy associated plasma protein E; abortive;  
KW contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis;  
KW dysgenetic pregnancy; primer; ss.



XX OS Homo sapiens.  
 XX PN US2002102252-A1.  
 XX PD 01-AUG-2002.  
 XX PF 06-APR-2001; 2001US-00827998.  
 XX PR 26-MAY-2000; 2000US-0207456P.  
 XX PA (GUY/) GU Y.  
 XX PA (SHAN/) SHANNON M E.  
 XX PI Gu Y, Shannon ME;  
 XX WPI; 2002-697817/75.  
 XX New isolated nucleic acid encoding an isoform of human pregnancy  
 PT associated plasma protein E, for preventing or aborting pregnancy.  
 XX Example 2; Page 126; 353pp; English.  
 XX This invention describes a novel isolated nucleic acid that encodes one  
 CC of three new isoforms of human pregnancy associated plasma protein E,  
 CC hPAPP-E. The products of the invention have abortive and contraceptive  
 CC activity and can be used for gene therapy or in a vaccine. The nucleic  
 CC acid, polypeptide encoded by it, or antibody to the polypeptide can be  
 CC used in pharmaceutical compositions or vaccines for preventing or  
 CC aborting pregnancy. PAPP-E is used in the antenatal diagnosis of  
 CC dysgenetic pregnancies. The nucleic acids are used as probes to assess  
 CC the level of PAPP-E isoform mRNA in chorionic villus samples, and the  
 CC antibodies can be used to assess the expression levels of PAPP-E isoform  
 CC proteins in chorionic villus samples, to diagnose dysgenetic pregnancies  
 CC antenatally. This sequence represents an oligomer used in scanning the  
 CC human PAPP-E genes described in the disclosure of the invention  
 XX SQ Sequence 17 BP; 1 A; 0 C; 8 G; 8 T; 0 U; 0 Other;  
 Query Match 1.3%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 2.7e+02;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1794 GTGTGTGTGTGTGTGTGTG 1810  
 DB 1 GTGTGTGTGTGTGTGTGTG 17  
 RESULT 356  
 ABK55689/c  
 ID ABK55689 standard; RNA; 17 BP.  
 XX AC ABK55689;  
 XX DT 02-JUL-2002 (first entry)  
 XX Human CLCA1 gene enzymatic nucleic acid #60.  
 XX Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic;  
 KW antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;  
 KW chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;  
 KW oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;  
 KW acetylcysteine.  
 XX OS Homo sapiens.  
 XX PN WO200211674-A2.  
 XX 14-FEB-2002.  
 XX PD 09-AUG-2001; 2001WO-US024970.  
 XX PF 09-AUG-2000; 2000US-0224383P.  
 XX PR

XX (RIBO-) RIBOZYME PHARM INC.  
 PA (SYNT ) SYNTX USA LLC.  
 PA (THOM/) THOMPSON J.  
 XX Thompson J, Mcswiggen J, McKenzie T, Ayers D, Szymkowski DE;  
 PI Grupe A;  
 XX WPI; 2002-217145/27.  
 XX Enzymatic polynucleotide that down regulates expression of chloride  
 PT channel calcium activated gene, useful for treating Chronic obstructive  
 PT pulmonary disease (COPD), chronic bronchitis and asthma.  
 XX Claim 4; Page 54; 152pp; English.  
 XX The invention relates to enzymatic nucleic acid molecules that down  
 CC regulate expression of chloride channel calcium activated 1 (CLCA1) genes  
 CC by cleaving RNA derived from the genes. The nucleic acid sequences are  
 CC useful as pharmaceutical agents for treating conditions such as chronic  
 CC obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic  
 CC fibrosis, obstructive bowel syndrome and any other diseases or conditions  
 CC that are related to or will respond to the levels of CLCA1 in a cell or  
 CC tissue. The sequences are useful for reducing CLCA1 activity in a cell,  
 CC hence, are useful for treatment of a patient having a condition  
 CC associated with the level of CLCA1, where the invention further comprises  
 CC the use of one or more therapies under conditions suitable for the  
 CC treatment, for example, oxygen therapy, bronchodilators, corticosteroids,  
 CC antibiotics, vaccinations, acetylcysteine and mucokinetic agents. The  
 CC nucleic acids of the invention are also used as diagnostic tools to  
 CC examine genetic drift and mutations within diseased cells or to detect  
 CC the presence of CLCA1 RNA in a cell. This sequence represents an  
 CC enzymatic nucleic acid molecule of the invention  
 XX SQ Sequence 17 BP; 7 A; 1 C; 1 G; 0 T; 8 U; 0 Other;  
 Query Match 1.3%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 2.7e+02;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1821 TATATATGTACAGTTAT 1837  
 DB 17 TATATATATACAGATAT 1  
 RESULT 357  
 ADB04271  
 ID ADB04271 standard; DNA; 17 BP.  
 XX AC ADB04271;  
 XX DT 20-NOV-2003 (first entry)  
 XX Human MDZ7 scanning oligonucleotide SEQ ID 5257.  
 XX Cytostatic; immunostimulant; gene therapy; vaccine; human;  
 KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;  
 KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q36.1; cancer;  
 KW developmental disorder; ss.  
 XX OS Homo sapiens.  
 XX PN EP1281758-A2.  
 XX 05-FEB-2003.  
 XX PD 30-JUL-2002; 2002EP-00016874.  
 XX PF 02-AUG-2001; 2001US-00922181.  
 XX PR (AEOM-) AEOMICA INC.  
 XX Shannon M, Gu Y, Nguyen C;  
 PI

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XX WPI; 2003-423107/40.
XX
XX New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MD23,
PT MD24, MD27 or MD212, e.g. cancer.
XX
XX Example 8; SEQ ID NO 5257; 103pp; English.
XX
XX The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
CC 15q26.1. The MD23, MD24, and MD212 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MD23,
CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
XX Sequence 17 BP; 0 A; 1 C; 0 G; 16 T; 0 U; 0 Other;
SQ
Query Match 1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.7e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1864 CTTTATTATTTGTTTT 1880
DB 1 CTTTTTTTTTTTTTTT 17

RESULT 358
AAD56441
ID AAD56441 standard; DNA; 17 BP.
XX
AC AAD56441;
XX
XX 07-AUG-2003 (first entry)
XX
XX Antisense oligo #2, to elicit RNase H degradation of target RNA.
XX
XX Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;
XX antisense; ss.
XX
XX Unidentified.
XX
XX Key Location/Qualifiers
XX misc_feature 9..10
XX /tag= a
XX /note= "Bases 9 and 10 are linked by a butanediol linker
XX which is represented as B in page 49 and X in page 59,
XX Fig 9 and 10 of the specification"
XX
XX WO2003037909-A1.
XX
XX 08-MAY-2003.
XX
XX 29-OCT-2002; 2002WO-CA001628.
XX
XX 29-OCT-2001; 2001US-0330719P.
XX (UYMC-) UNIV MCGILL.
XX
XX Damha MJ, Viarovkina E, Mangos MM, Parniak MA, Min K;
XX WPI; 2003-421516/39.
XX
XX Novel acyclic linker-containing oligonucleotide useful for preventing or
PT decreasing translation, reverse transcription and/or replication of a
PT

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PT Novel acyclic linker-containing oligonucleotide useful for preventing or
PT decreasing translation, reverse transcription and/or replication of a
PT target RNA in a system, comprises a modified deoxyribonucleotide.
XX
XX Example 2; Page 90; 104pp; English.
XX
XX The invention relates to an acyclic linker-containing oligonucleotide
CC comprising at least one modified deoxyribonucleotide. Oligonucleotides of
CC the invention are useful for preventing or decreasing translation,
CC reverse transcription and/or replication of a target RNA in a system.
CC They are useful for selectively preventing gene expression in a sequence-
CC specific manner, for hybridising to complementary RNA such as cellular
CC mRNA or viral RNA, to hybridise to and induce cleavage of complementary
CC RNA. They are also useful therapeutically in formulations or medicaments
CC to prevent or treat a disease characterised by the expression of a
CC particular target RNA. The invention is used in gene therapy. The present
CC sequence is an antisense oligo used to elicit human RNase (ribonuclease)
CC H degradation of target RNA. This sequence is used in the exemplification
CC of the invention
XX
XX Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;
SQ
Query Match 1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.7e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTATTTGTTTT 1881
DB 1 TTTTTTTTTTTTTTTT 17

RESULT 359
AAD56448
ID AAD56448 standard; DNA; 17 BP.
XX
AC AAD56448;
XX
XX 07-AUG-2003 (first entry)
XX
XX 2'-F-ANA antisense oligo #3, to elicit RNase H degradation of target RNA.
XX
XX Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;
XX antisense; ss.
XX
XX Unidentified.
XX
XX Key Location/Qualifiers
XX modified_base 1..17
XX /tag= a
XX /mod_base= OTHER
XX /note= "2'-deoxy-2'-fluoroarabinothymidine"
XX
XX misc_feature 9..10
XX /tag= b
XX /note= "Bases 9 and 10 are linked by a butanediol linker
XX which is represented as B in page 49 and Fig 5 and as X
XX in page 52, 55 and Fig 6 of the specification"
XX
XX WO2003037909-A1.
XX
XX 08-MAY-2003.
XX
XX 29-OCT-2002; 2002WO-CA001628.
XX
XX 29-OCT-2001; 2001US-0330719P.
XX (UYMC-) UNIV MCGILL.
XX
XX Damha MJ, Viarovkina E, Mangos MM, Parniak MA, Min K;
XX WPI; 2003-421516/39.
XX
XX Novel acyclic linker-containing oligonucleotide useful for preventing or
PT decreasing translation, reverse transcription and/or replication of a
PT

```

target RNA in a system, comprises a modified deoxyribonucleotide.

Example 2; Fig 5; 104pp; English.

The invention relates to an acyclic linker-containing oligonucleotide comprising at least one modified deoxyribonucleotide. Oligonucleotides of the invention are useful for preventing or decreasing translation, reverse transcription and/or replication of a target RNA in a system. They are useful for selectively preventing gene expression in a sequence-specific manner, for hybridising to complementary RNA such as cellular mRNA or viral RNA, to hybridise to and induce cleavage of complementary RNA. They are also useful therapeutically in formulations or medicaments to prevent or treat a disease characterised by the expression of a particular target RNA. The invention is used in gene therapy. The present sequence is an antisense oligo used to elicit human RNase (ribonuclease) H degradation of target RNA. This sequence is used in the exemplification of the invention

Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;

Query Match 1.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.7e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTTT 1881  
DB 1 TTTTATTTTGTGTTTT 17

RESULT 360

AAD56449  
ID AAD56449 standard; DNA; 17 BP.

AC AAD56449;

DT 07-AUG-2003 (first entry)

DE 2'-F-ANA antisense oligo #4, to elicit RNase H degradation of target RNA.

XX Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;  
KW antisense; ss.

OS Unidentified.

PH Key Location/Qualifiers

FT modified\_base 1..17

FT /tag= a

FT /mod\_base= OTHER

FT /note= "2'-deoxy-2'-fluoroarabinothymidine"

FT misc\_feature 12..13

FT /tag= b

FT /note= "Bases 12 and 13 are linked by a butanediol linker

FT which is represented as B in page 49 and Fig 5 and as X

FT in page 55 and Fig 6 of the specification"

XX WO2003037909-A1.

PN 08-MAY-2003.

PD 29-OCT-2002; 2002WO-CA001628.

PF 29-OCT-2001; 2001US-0330719P.

PR (UYMC-) UNIV MCGILL.

PA Damha MJ, Viarovkina E, Mangos MM, Parniak MA, Min K;

PI WPI; 2003-421516/39.

XX Novel acyclic linker-containing oligonucleotide useful for preventing or

XX decreasing translation, reverse transcription and/or replication of a

XX target RNA in a system, comprises a modified deoxyribonucleotide.

XX

XX

XX

XX

XX

Example 2; Fig 5; 104pp; English.

The invention relates to an acyclic linker-containing oligonucleotide comprising at least one modified deoxyribonucleotide. Oligonucleotides of the invention are useful for preventing or decreasing translation, reverse transcription and/or replication of a target RNA in a system. They are useful for selectively preventing gene expression in a sequence-specific manner, for hybridising to complementary RNA such as cellular mRNA or viral RNA, to hybridise to and induce cleavage of complementary RNA. They are also useful therapeutically in formulations or medicaments to prevent or treat a disease characterised by the expression of a particular target RNA. The invention is used in gene therapy. The present sequence is an antisense oligo used to elicit human RNase (ribonuclease) H degradation of target RNA. This sequence is used in the exemplification of the invention

Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;

Query Match 1.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.7e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTTT 1881  
DB 1 TTTTATTTTGTGTTTT 17

RESULT 361

AAD56447  
ID AAD56447 standard; DNA; 17 BP.

AC AAD56447;

DT 07-AUG-2003 (first entry)

DE 2'-F-ANA antisense oligo #2, to elicit RNase H degradation of target RNA.

XX Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;  
KW antisense; ss.

OS Unidentified.

PH Key Location/Qualifiers

FT modified\_base 1..17

FT /tag= a

FT /mod\_base= OTHER

FT /note= "2'-deoxy-2'-fluoroarabinothymidine"

FT misc\_feature 4..5

FT /tag= b

FT /note= "Bases 4 and 5 are linked by a butanediol linker

FT which is represented as B in page 49 and Fig 5 and as X

FT in page 55 and Fig 6 of the specification"

XX WO2003037909-A1.

PN 08-MAY-2003.

PD 29-OCT-2002; 2002WO-CA001628.

PF 29-OCT-2001; 2001US-0330719P.

PR (UYMC-) UNIV MCGILL.

PA Damha MJ, Viarovkina E, Mangos MM, Parniak MA, Min K;

PI WPI; 2003-421516/39.

XX Novel acyclic linker-containing oligonucleotide useful for preventing or

XX decreasing translation, reverse transcription and/or replication of a

XX target RNA in a system, comprises a modified deoxyribonucleotide.

XX

XX

XX

XX

XX

XX

XX

CC The invention relates to an acyclic linker-containing oligonucleotide comprising at least one modified deoxyribonucleotide. Oligonucleotides of CC reverse transcription and/or replication of a target RNA in a system. CC They are useful for selectively preventing gene expression in a sequence-specific manner, for hybridising to complementary RNA such as cellular mRNA or viral RNA, to hybridise to and induce cleavage of complementary RNA. They are also useful therapeutically in formulations or medicaments CC to prevent or treat a disease characterised by the expression of a particular target RNA. The invention is used in gene therapy. The present CC sequence is an antisense oligo used to elicit human RNase (ribonuclease) CC H degradation of target RNA. This sequence is used in the exemplification CC of the invention

XX  
SQ Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;

Query Match 1.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.7e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTGTTT 1881  
|||||  
1 TTTTATTGTTT 17

Db  
RESULT 362  
AAD56450  
ID AAD56450 standard; DNA; 17 BP.  
XX  
AC AAD56450;  
XX  
DT 07-AUG-2003 (first entry)  
XX  
DE 2'-F-ANA antisense oligo #5, to elicit RNase H degradation of target RNA.  
XX  
KW Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;  
KW antisense; ss.  
XX  
OS Unidentified.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 1..17  
FT /tag= a  
FT /mod\_base= OTHER  
FT /note= "2'-deoxy-2'-fluoroarabinothymidine"  
FT 9..10  
FT /tag= b  
FT /note= "Bases 9 and 10 are linked by a secouridine linker  
FT which is represented as S in page 49 and X in page 57 and  
FT Fig 1, 2, 7 and 8 of the specification"  
XX  
PN WO2003037909-A1.  
XX  
PD 08-MAY-2003.  
XX  
PF 29-OCT-2002; 2002WO-CA001628.  
XX  
PR 29-OCT-2001; 2001US-0330719P.  
XX  
PS (UYMC-) UNTV MCGILL.  
XX  
PA Damha M, Viazovkina E, Mangos MM, Parniak MA, Min K;  
PI WPI; 2003-421516/39.  
XX  
DR Novel acyclic linker-containing oligonucleotide useful for preventing or  
PT decreasing translation, reverse transcription and/or replication of a  
PT target RNA in a system, comprises a modified deoxyribonucleotide.  
XX  
PS Example 2; Fig 7; 104pp; English.  
XX  
CC The invention relates to an acyclic linker-containing oligonucleotide  
CC comprising at least one modified deoxyribonucleotide. Oligonucleotides of

CC the invention are useful for preventing or decreasing translation, CC reverse transcription and/or replication of a target RNA in a system. CC They are useful for selectively preventing gene expression in a sequence-specific manner, for hybridising to complementary RNA such as cellular mRNA or viral RNA, to hybridise to and induce cleavage of complementary RNA. They are also useful therapeutically in formulations or medicaments CC to prevent or treat a disease characterised by the expression of a particular target RNA. The invention is used in gene therapy. The present CC sequence is an antisense oligo used to elicit human RNase (ribonuclease) CC H degradation of target RNA. This sequence is used in the exemplification CC of the invention

XX  
SQ Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;

Query Match 1.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.7e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTGTTT 1881  
|||||  
1 TTTTATTGTTT 17

Db  
RESULT 363  
ABL45668/c  
ID ABL45668 standard; DNA; 15 BP.  
XX  
AC ABL45668;  
XX  
DT 19-APR-2002 (first entry)  
XX  
DE Human UBE3A gene ASO PCR primer SEQ ID NO: 35.  
XX  
KW Human; ubiquitin protein ligase E3A; UBE3A; haplotype; SNP; gene therapy;  
KW Angelman syndrome; human papilloma virus E6-associated gene;  
KW single nucleotide polymorphism; PCR primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200192582-A1.  
XX  
PD 06-DEC-2001.  
XX  
PF 01-JUN-2001; 2001WO-US017994.  
XX  
PR 01-JUN-2000; 2000US-0208539P.  
XX  
PA (GENA-) GENA-SSANCE PHARM INC.  
XX  
PI Duda A, Klien SE, Koshy B, Sausker EA;  
XX  
DR WPI; 2002-130535/17.  
XX  
PT Novel genetic variants of ubiquitin protein ligase E3A gene useful in  
PT studying expression and function of the protein, and for screening drugs  
PT to treat diseases e.g. Angelman syndrome.  
XX  
PS Claim 17; Page 14; 95pp; English.  
XX  
CC The present invention provides the sequences of fragments of the human  
CC ubiquitin protein kinase E3A (human papilloma virus E6-associated  
CC protein) UBE3A coding sequence and protein. Also described are a number  
CC of single nucleotide polymorphisms (SNPs) identified within these  
CC fragments. The fragments can be used in the gene therapy of Angelman  
CC syndrome and to haplotype the UBE3A gene. The present sequence is an  
CC allele specific primer for a coding sequence fragment of the invention

XX  
SQ Sequence 15 BP; 7 A; 2 C; 3 G; 2 T; 0 U; 1 Other;

Query Match 1.3%; Score 13.6; DB 1; Length 15;  
Best Local Similarity 92.9%; Pred. No. 2.6e+02;  
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2167 TGTTCCTACTTTGA 2180  
 Db :|||||  
 14 YGTTCTACTTTGA 1

RESULT 364  
 ABK16961/C  
 ID ABK16961 standard; DNA; 15 BP.  
 XX  
 AC ABK16961;  
 XX

DT 26-MAR-2002 (first entry)  
 XX

DE Pyridoxal (Pyridoxine, vitamin B6) Kinase (PDXX) PCR primer #22.  
 XX

KW Pyridoxal kinase; pyridoxine; vitamin B6;  
 XX

KW PDXX autoimmune polyglandular disease type 1; transgenic animal;  
 XX

KW gene therapy; allele specific oligonucleotide; ASO; PCR primer; ss.  
 XX

OS Homo sapiens.  
 XX

PN WO200190125-A2.  
 XX

PD 29-NOV-2001.  
 XX

PF 24-MAY-2001; 2001WO-US016909.  
 XX

PR 24-MAY-2000; 2000US-0206664P.  
 XX

PA (GENA-) GENASSANCE PHARM INC.  
 XX

PI Chew A, Duda A, Koshy B;  
 XX

DR WPI; 2002-106169/14.  
 XX

PT Isolated human pyridoxal (pyridoxine, vitamin B6) kinase polyNTs, useful  
 for therapeutic purposes, for studying the expression and function of the  
 PT polyNT, and for expressing pyridoxal protein.  
 XX

PS Claim 17; Page 13; 135pp; English.  
 XX

CC The invention describes an isolated human pyridoxal (pyridoxine, vitamin  
 B6) kinase, (PDXX) polynucleotide. The polynucleotide is useful in  
 CC studying the expression and function of PDXX, and in expressing PDXX  
 CC protein for use in screening for candidate drugs to treat PDXX related  
 CC diseases and for therapeutic purposes. A transgenic animal is useful for  
 CC studying expression of the PDXX isogenes in vivo, for in vivo screening  
 CC and testing of drugs targeted against PDXX protein, and for testing the  
 CC efficacy of therapeutic agents and compounds for autoimmune polyglandular  
 CC disease type 1. The polypeptide is useful for studying the effect of the  
 CC variation on the biological activity of PDXX and the binding affinity of  
 CC candidate drugs targeting PDXX for the treatment of autoimmune  
 CC polyglandular disease type 1. Genotyping and haplotyping is useful for  
 CC improving the efficacy and reliability of several steps in the discovery  
 CC and development of drugs for treating diseases associated with PDXX  
 CC activity, e.g., autoimmune polyglandular disease type 1, to validate PDXX  
 CC as a candidate agent for treating a specific condition or disease  
 CC predicted to be associated with PDXX activity, and in the design of  
 CC clinical trials of candidate drugs. This sequence is one of 37 (see  
 CC ABK16941-ABK16977) allele specific oligonucleotide (ASO) PCR primers used  
 CC for detecting PDXX gene polymorphisms, described in the method of the  
 CC invention  
 XX

SQ Sequence 15 BP; 7 A; 5 C; 1 G; 1 T; 0 U; 1 Other;  
 XX

Query Match 1.3%; Score 13.6; DB 1; Length 15;  
 Best Local Similarity 92.9%; Pred. No. 2.6e+02;  
 Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1801 TGTGTGTGTGTGTA 1814  
 Db :|||||  
 15 TRTGTGTGTGTGTA 2

RESULT 365

AAT96304  
 ID AAT96304 standard; DNA; 15 BP.  
 XX

AC AAT96304;  
 XX

DT 25-MAR-2003 (revised)  
 XX

DT 08-APR-1998 (first entry)  
 XX

DE Fungal telomeric nucleic acid sequence.  
 XX

KW Detection; eukaryotic pathogen; telomeric nucleic acid sequence;  
 telomerase activity; diagnosis; fungal infection; fungus; fungi;  
 KW malarial infection; malaria; ss.  
 XX

OS Saccharomyces cerevisiae.  
 XX

PN US5695932-A.  
 XX

PD 09-DEC-1997.  
 XX

PF 13-MAY-1993; 93US-00060952.  
 XX

PR 13-MAY-1992; 92US-00882438.  
 XX

PR 24-MAR-1993; 93US-00038766.  
 XX

PA (UYCA-) UNIV CALIFORNIA SAN FRANCISCO.  
 XX

PA (TEXA) UNIV TEXAS SYSTEM;  
 XX

PI Blackburn EH, Shay J, Meeachern MJ, West MD, Wright W;  
 XX

DR WPI; 1998-041292/04.  
 XX

PT Detection of eukaryotic pathogens, especially fungal or Plasmodium spp. -  
 by detecting telomerase activity.  
 XX

PS Claim 5; Col 93-94; 82pp; English.  
 XX

CC The present sequence can be used in a novel method for detecting a  
 eukaryotic pathogen in a patient. The method comprises obtaining a sample  
 CC of somatic tissue or cells from the patient, determining if telomerase  
 CC activity is present and correlating this with the presence of the  
 CC pathogen. The method is useful for diagnosis of fungal infections,  
 CC especially a fungus of the genus Candida, Kluyveromyces, Saccharomyces,  
 CC Sporothrix, Coccidioides, Histoplasma, Blastomyces, Paracoccidioides,  
 CC Cryptococcus, Aspergillus, Mucor or Rhizopus, or malarial infections,  
 CC especially Plasmodium vivax, P. ovale, P. malariae or P. falciparum.  
 CC (Updated on 25-MAR-2003 to correct PA field.)  
 XX

SQ Sequence 15 BP; 0 A; 0 C; 8 G; 7 T; 0 U; 0 Other;  
 XX

Query Match 1.3%; Score 13.4; DB 1; Length 15;  
 Best Local Similarity 93.3%; Pred. No. 2.7e+02;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1792 TTGTGTGTGTGTGTG 1806  
 Db 1 TGGTGTGTGTGTGTG 15

RESULT 366

AAF47617/C  
 ID AAF47617 standard; DNA; 15 BP.  
 XX

AC AAF47617;  
 XX

DT 30-MAR-2001 (first entry)  
 XX

DE IGFBP3 oligonucleotide #1037.  
 XX

KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;  
 cytostatic; dermatological; cardiac; virucide; ophthalmological; keloid;

KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; ptyriasis;  
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;  
 KW growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;  
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;  
 KW hyperneovascular condition; hyperplasia; kidney disease;  
 KW neovascular condition of the retina; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200078341-A1.  
 XX  
 PD 28-DEC-2000.  
 XX  
 PF 21-JUN-2000; 2000WO-AU000693.  
 XX  
 PR 21-JUN-1999; 99US-0140345P.  
 XX  
 PA (MURD-) MURDOCH CHILDRENS RES INST.  
 XX  
 PI Wright CJ, Werther GA, Edmondson SR;  
 DR WPI; 2001-041421/05.  
 XX  
 PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering  
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that  
 PT inhibits or reduces growth factor mediated cell proliferation and/or  
 PT inflammation.  
 XX  
 PS Example 7; Page 50; 201pp; English.  
 XX

XX The present invention relates to a method for ameliorating the effects of  
 CC skin disorders. The method comprises contacting the skin with an  
 CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1  
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of  
 CC inhibiting or reducing growth factor mediated cell proliferation,  
 CC inflammation and/or other disorders. The present sequence is an  
 CC oligonucleotide which can be used to design the antisense  
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-  
 CC F45161). The method is useful for ameliorating the effects of psoriasis,  
 CC ichthyosis, ptyriasis, ruba, pilaris, serborrhoea, keloids, keratosis,  
 CC neoplasia, scleroderma, warts, benign growths, cancers of the skin, a  
 CC hyperneovascular condition such as a neovascular condition of the retina,  
 CC brain or skin, growth factor-mediated malignancies, other sclerotic  
 CC disease, kidney disease, hyperproliferation of the inside of blood  
 CC vessels or any other hyperplasia  
 XX  
 SQ Sequence 15 BP; 6 A; 4 C; 4 G; 1 T; 0 U; 0 Other;  
 Query Match 1.3%; Score 13.4; DB 1; Length 15;  
 Best Local Similarity 93.3%; Pred. No. 2.7e+02;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2045 TGTCCTGGCAGGCT 2059  
 DB 15 TGTCCTGGCAGTCT 1  
 RESULT 367  
 AAF80919  
 ID AAF80919 standard; DNA; 15 BP.  
 XX  
 AC AAF80919;  
 XX  
 DT 02-MAY-2001 (first entry)  
 XX  
 DE PTGS2 allele specific oligonucleotide probe SEQ ID 25.  
 XX  
 DE Human; prostaglandin-endoperoxide synthase 2; PTGS2; cyclooxygenase 2;  
 KW single nucleotide polymorphism; SNP; immune-related disorder; arthritis;  
 KW inflammation; probe; ss.  
 XX  
 OS Homo sapiens.  
 XX

PN WO200107662-A1.  
 XX  
 PD 01-FEB-2001.  
 XX  
 PF 24-JUL-2000; 2000WO-US020114.  
 XX  
 PR 22-JUL-1999; 99US-0145170P.  
 XX  
 PA (GENA-) GENAISSANCE PHARM INC.  
 XX  
 PI Denton RR, Nandabalan K, Sanchis A, Stephens JC, Tanguay DA;  
 DR WPI; 2001-182805/19.  
 XX  
 PT New nucleic acid containing polymorphisms in the cyclooxygenase-2 gene,  
 PT for gene therapy of inflammation and for establishing a genotype or  
 PT haplotype.  
 XX  
 PS Disclosure; Page 21; 118pp; English.  
 XX  
 CC This invention relates to a polynucleotide sequence that is a polymorphic  
 CC variant of the human prostaglandin-endoperoxide synthase 2 (PTGS2) gene  
 CC also referred to as cyclooxygenase 2. The human PTGS2 gene sequence  
 CC AAF80896 contains 27 single nucleotide polymorphisms (SNPs). AAF80896 and  
 CC AAF80897 represent human PTGS2 gene and coding sequence, and the PTGS2  
 CC protein is represented by AAF872199. The invention includes PCR and  
 CC sequencing primers, and probes represented in AAF80898 - AAF81151 which  
 CC are used to isolate and characterise the PTGS2 gene sequence, and to  
 CC locate the positions of the SNPs. PTGS2 proteins and polynucleotide  
 CC sequences are used to express variant PTGS2 proteins, for structural  
 CC analysis or drug-binding studies and also in gene therapy (either  
 CC expressing PTGS2 or inhibitory RNA). Antibodies raised against PTGS2 are  
 CC useful for diagnosis, prognosis and therapy and analysis of the new, and  
 CC known, polymorphisms and used to determine PTGS2 haplotype and genotype.  
 CC especially for determining association between a particular trait, e.g. a  
 CC clinical response to drugs that target PTGS2 but also disease  
 CC susceptibility, severity or stage. Anti-PTGS2 antibodies are particularly  
 CC used for developing diagnostic tests and treatments for immune-related  
 CC disorders such as arthritis and inflammation. The polymorphisms may also  
 CC be used to study expression and biological function of PTGS2. Transgenic  
 CC animals that express PTGS2 are used to study expression of PTGS2  
 CC isogenes, for in vivo drug screening and testing, and for assessing  
 CC effects of therapeutic agents  
 XX  
 SQ Sequence 15 BP; 1 A; 0 C; 0 G; 14 T; 0 U; 0 Other;  
 Query Match 1.3%; Score 13.4; DB 1; Length 15;  
 Best Local Similarity 93.3%; Pred. No. 2.7e+02;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1867 TTTATTTTGTGTTTT 1881  
 DB 1 TTTATTTTGTGTTTT 15  
 RESULT 368  
 ABX79758/c  
 ID ABX79758 standard; cDNA; 15 BP.  
 XX  
 AC ABX79758;  
 XX  
 DT 17-APR-2003 (first entry)  
 XX  
 DE EST polymorphic DNA repeat polynucleotide #83.  
 XX  
 DE EST; expressed sequence tag; ss; polymorphic repeat; tandem repeat;  
 KW polymorphic marker prediction of ubiquitous simple sequences; POMPOUS;  
 KW Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;  
 KW Haw River syndrome; Huntington's disease; fragile-X syndrome;  
 KW Friedrich's ataxia; myotonic dystrophy; hyperandrogenaemia;  
 KW spinal atrophy; bulbar atrophy; spinocerebellar ataxia.  
 XX  
 OS Homo sapiens.  
 XX

XX US6472154-B1.  
 PN 29-OCT-2002.  
 XX 31-DEC-1999; 99US-00475947.  
 XX 31-DEC-1999; 99US-00475947.  
 XX (TEXA) UNIV TEXAS SYSTEM.  
 XX Garner HR, Wren JD, Minna JD, Fondon JW;  
 PI WPI; 2003-208819/20.  
 XX Identifying a candidate polymorphic repeat within a coding sequence, for  
 PT understanding or treating genetic disease, comprises detecting tandem  
 PT repeats in a target coding sequence and scoring the repeats for  
 PT polymorphic probability.  
 XX Example; Col 309; 588pp; English.  
 XX The invention discloses a method for identifying a candidate polymorphic  
 CC repeat within a coding sequence (expressed sequence tag, EST), which  
 CC comprises detecting tandem repeats in a target coding sequence, scoring  
 CC the repeats for polymorphic probability and generating a dataset  
 CC correlating the repeats with polymorphic probability to identify a  
 CC candidate polymorphic repeat. The computational methods (polymorphic  
 CC marker prediction of ubiquitous simple sequences, POMPUS, and Rep-X) are  
 CC useful for identifying and detecting candidate polymorphic repeats in  
 CC human genes, which can be used to understand, treat or eliminate genetic  
 CC diseases, predispositions or adverse drug-treatment reactions. Examples  
 CC of diseases linked to nucleotide repeats are Machado-Joseph, Haw River  
 CC syndrome, Huntington's disease, fragile-X syndrome, Friedreich's ataxia,  
 CC myotonic dystrophy, hyperandrogenaemia, spinal and bulbar atrophy and  
 CC spinocerebellar ataxia. The sequences presented in ABX79676-ABX80022 are  
 CC the polymorphic repeats identified for a search of human ESTs  
 XX  
 XX Sequence 15 BP; 9 A; 0 C; 0 G; 6 T; 0 U; 0 Other;  
 SQ  
 Query Match 1.3%; Score 13.4; DB 1; Length 15;  
 Best Local Similarity 93.3%; Pred.No. 2.7e+02;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1811 TGTATATATATATAT 1825  
 Db 15 TTTATATATATATAT 1  
 RESULT 369  
 ABX94519  
 ID ABX94519 standard; DNA; 15 BP.  
 XX  
 AC ABX94519;  
 XX  
 DT 10-JUN-2003 (first entry)  
 XX  
 DE 23S rDNA helix 54 region probe SEQ ID 37.  
 XX  
 KW Diagnostic; Gram-positive bacterium; high G+C content; amplification;  
 KW mycobacterial infection; PCR; primer; probe; detection; ss.  
 XX  
 OS Corynebacterium pseudotuberculosis.  
 OS Corynebacterium ulcerans.  
 XX  
 FN WO200297126-A2.  
 XX  
 PD 05-DEC-2002.  
 XX  
 PF 09-APR-2002; 2002WO-EP003956.  
 XX  
 PR 03-MAY-2001; 2001DE-01021505.  
 XX

PA (HAIN-) HAIN LIFESCIENCE GMBH.  
 XX Weizenegger M;  
 XX WPI; 2003-140491/13.  
 XX Detecting and identifying Gram-positive bacteria of high G/C content,  
 PT useful particularly for diagnosis of mycobacterial infection, by specific  
 PT amplification and hybridization.  
 XX Claim 1b; Fig 2B; 34pp; German.  
 XX This invention describes a novel method for the diagnostic detection  
 CC and/or identification of Gram-positive bacteria that have a high G+C  
 CC content, especially Mycobacteria. The method comprises subjecting a  
 CC sample to nucleic acid amplification using the PCR primers represented in  
 CC ABX94483-ABX94492. The amplification mixture, or part of it, is then  
 CC tested for hybridisation to at least one of the probes represented in  
 CC ABX94493-ABX94524 which can be immobilised on a solid phase or used in  
 CC kit form. The specified primers/probes provide highly specific detection  
 CC of particular Gram positive bacteria, which are difficult to  
 CC differentiate by morphological or biochemical tests and/or those which  
 CC take a long time to test because of their slow growth  
 XX  
 XX Sequence 15 BP; 0 A; 0 C; 8 G; 7 T; 0 U; 0 Other;  
 SQ  
 Query Match 1.3%; Score 13.4; DB 1; Length 15;  
 Best Local Similarity 93.3%; Pred.No. 2.7e+02;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1793 TGTGTGTGTGTGTGT 1807  
 Db 1 TGTGTGTGTGTGTGT 15  
 RESULT 370  
 ABX50028  
 ID ABX50028 standard; DNA; 15 BP.  
 XX  
 AC ABX50028;  
 XX  
 DT 12-FEB-2003 (first entry)  
 XX  
 DE Telomere length and/or telomerase activity related polynucleotide #51.  
 XX  
 KW Cell proliferation; cell senescence; telomere length;  
 KW telomerase activity; cell replication; neoplasia; cancer;  
 KW age-related macular degeneration; Alzheimer's disease; atherosclerosis;  
 KW telomerase; telomerase inhibitor; immortalised cell; ss.  
 XX  
 OS Synthetic.  
 XX  
 FN US2002127634-A1.  
 XX  
 PD 12-SEP-2002.  
 XX  
 PF 05-JUN-1995; 95US-00463404.  
 XX  
 PR 13-MAY-1992; 92US-00882438.  
 PR 24-MAR-1993; 93US-00038765.  
 PR 13-MAY-1993; 93US-00060952.  
 XX  
 PA (WEST/) WEST M D.  
 PA (SHAY/) SHAY J.  
 PA (WRIG/) WRIG W.  
 PA (BLAC/) BLACKBURN E H.  
 XX  
 PI West MD, Shay J, Wright W, Blackburn EH;  
 XX  
 XX WPI; 2003-066896/06.  
 XX Treating condition associated with cell senescence or increased rate of  
 PT cell proliferation, by administering to cell an agent that derepresses

PT telomerase in the senescing cells or that reduces loss of telomere  
 XX length.  
 PS Disclosure; Page 50; 86pp; English.  
 XX The invention describes a method use for treating increased rate of  
 CC proliferation of a cell or extending the ability of a cell to replicate,  
 CC or treating a disease associated with cell senescence. The method  
 CC comprises administering an agent to reduce loss of telomere length within  
 CC the cell during proliferation or replication, or to derepress telomerase  
 CC in the senescing cells. The method is useful for treating a condition  
 CC associated with an increased rate of proliferation of a cell extending  
 CC the ability of a cell to replicate, or for treating a disease or  
 CC condition associated with cell senescence e.g. neoplasia. A second method  
 CC disclosed in the invention is useful for treating a condition associated  
 CC with an elevated level of telomerase activity within a cell e.g. cancer.  
 CC Also disclosed is a method useful for diagnosis of a condition associated  
 CC with an increased rate of proliferation in a cell in an individual e.g.  
 CC age-related macular degeneration, astrocytes associated with Alzheimer's  
 CC disease and endothelial cells associated with atherosclerosis. This  
 CC sequence represents a polynucleotide used in the study of telomere length  
 CC and telomerase activity described in the invention  
 XX  
 SQ Sequence 15 BP; 0 A; 0 C; 8 G; 7 T; 0 U; 0 Other;

Query Match 1.3%; Score 13.4; DB 1; Length 15;  
 Best Local Similarity 93.3%; Pred. No. 2.7e+02;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1722 TTGTTGTTGTTGTTG 1806  
 DB 1 TGGTGTGTTGTTGTTG 15

RESULT 371  
 AAT81559  
 ID AAT81559 standard; RNA; 17 BP.  
 XX  
 AC AAT81559;  
 XX  
 DT 14-DEC-1997 (first entry)  
 DE Human c-myb hammerhead ribozyme target sequence (nt. position 2898).  
 XX Enzymatic nucleic acid; hammerhead; ribozyme; cleavage; human;  
 KW smooth muscle cell; hyperproliferation; restenosis; cancer; c-myb;  
 XX coronary angioplasty; ss.  
 XX Homo sapiens.  
 OS  
 PN WO9531541-A2.  
 XX  
 PD 23-NOV-1995.  
 XX  
 PF 18-MAY-1995; 95WO-US006368.  
 XX  
 PR 18-MAY-1994; 94US-00245466.  
 PR 13-JAN-1995; 95US-00373124.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 PI Stinchcomb DT, Draper K, Mcswiggen J, Jarvis T;  
 XX WPI; 1996-010927/01.  
 DR  
 XX New enzymatic nucleic acid molecules - cleave RNA produced by e.g. c-myb,  
 PT for treating restenosis or cancer.  
 PS Claim 1; Page 78; 128pp; English.  
 XX

The present sequence represents the preferred target sequence for an  
 CC enzymatic nucleic acid, especially a hammerhead ribozyme, which cleaves  
 CC the human c-myb sequence at the base position indicated in the descriptor

CC line. The c-myb sequence was screened for optimal ribozyme target sites  
 CC using a computer folding algorithm, and regions of the mRNA which did not  
 CC form secondary folding structures and contained potential ribozyme  
 CC cleavage sites were identified. Ribozymes were synthesised and their  
 CC activities optimised by either varying the length of the binding arms or  
 CC by modification to prevent degradation by nucleases. The ribozymes cleave  
 CC the c-myb sequence and can be used to prevent smooth muscle cell  
 CC hyperproliferation in restenosis, especially after coronary angioplasty,  
 CC and in cancers  
 XX

SQ Sequence 17 BP; 7 A; 1 C; 0 G; 0 T; 9 U; 0 Other;

Query Match 1.3%; Score 13.4; DB 1; Length 17;  
 Best Local Similarity 46.7%; Pred. No. 2.9e+02;  
 Matches 7; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

QY 1813 TATATATATATATAT 1827  
 DB 2 UAUUAUAUAUAUACAU 16

RESULT 372  
 ABA10358  
 ID ABA10358 standard; DNA; 13 BP.  
 XX  
 AC ABA10358;  
 XX

DT 03-JUL-2000 (first entry)

XX DNA ligand binding assay competitor oligonucleotide, SEQ ID NO:41.

DE Nucleic acid ligand binding assay; duplex formation; stability;  
 KW detectable signal; competition assay; competitor oligonucleotide; ds.  
 XX

OS Synthetic.

XX WO200015848-A1.

XX 23-MAR-2000.

XX 10-SEP-1999; 99WO-US020719.

XX 11-SEP-1998; 98US-00151890.

XX (GENE-) GENELABS TECHNOLOGIES INC.

XX Schroth GP, Bruice TW, Suh YJ;

XX WPI; 2000-271478/23.

XX Determining binding affinity of a ligand to an oligonucleotide sequence  
 PT in double stranded form, comprises measuring the effect of adding  
 PT increasing amounts of a ligand on a signal generated by two indicator  
 PT oligonucleotides of the duplex.  
 XX

XX Example 3; Page 19; 78pp; English.

XX The invention relates to new methods of determining the binding affinity  
 CC of a ligand to an oligonucleotide sequence, particularly to a duplex. The  
 CC ligand is typically a metal ion, a small organic or inorganic molecule, a  
 CC protein or a multi-protein complex. The methods comprise measuring the  
 CC effect of adding increasing amounts of a ligand on a signal generated by  
 CC two indicator oligonucleotides of the duplex. In the absence of ligand,  
 CC conditions are such that the oligonucleotides exist primarily in single-  
 CC stranded form; binding of ligand to double-stranded nucleic acids  
 CC stabilises the duplexes, such that duplex formation is favoured. One of  
 CC the indicator oligonucleotides contains a first group capable of  
 CC producing a detectable signal, while the other indicator oligonucleotide  
 CC contains a second group that on hybridisation of the two indicator  
 CC molecules, will detectably alter the signal produced by the first group.  
 CC The signal may be increased or decreased on hybridisation. For example,  
 CC the pairs of signalling groups used could be a radioactive group and a  
 CC scintillant (where an increase in signal intensity indicates that





Db 1 TATATTGTAATA 13

RESULT 375  
ABC98272  
ID ABC98272 standard; DNA; 13 BP.

XX AC ABC98272;  
XX  
DT 21-FEB-2002 (first entry)

XX DE Oligonucleotide SEQ ID NO 98289 for detecting SNP TSC0024420.

XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX OS Homo sapiens.  
XX PN WO200177384-A2.  
XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.  
XX PR 07-APR-2000; 2000DE-01019173.  
XX PA (EPIG-) EPIGENOMICS AG.  
XX PI Olek A, Piepenbrock C, Berlin K;  
XX PI WPI; 2001-657177/75.  
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
XX designed to detect single-nucleotide polymorphisms and cytosine  
XX methylation status.  
XX PS Claim 1; SEQ ID NO 98289; 29pp + Sequence Listing; German.

XX CC This invention describes novel oligonucleotide primers or peptide nucleic  
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
XX and cytosine methylation status in chemically pretreated genomic DNA. The  
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
XX range of diseases including immune system, gastrointestinal, respiratory,  
XX central nervous system, cardiovascular and metabolic disorders. The  
XX oligomers are also used for detecting cell type differentiation. ABC00010  
XX -ABF99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
XX represent the oligomers described in the invention. NOTE: The sequence  
XX data for this patent did not form part of the printed specification, but  
XX was obtained in electronic format from WIPO at  
XX ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 13 BP; 5 A; 0 C; 1 G; 7 T; 0 U; 0 Other;  
Query Match 1.2%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1811 TGTATATATATAT 1823  
DB 1 TGTATATATATAT 13

RESULT 376  
ABC13481  
ID ABC13481 standard; DNA; 13 BP.  
XX AC ABC13481;  
XX  
DT 20-FEB-2002 (first entry)

XX DE Oligonucleotide SEQ ID NO 13488 for detecting SNP TSC0003116.

KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX OS Homo sapiens.  
XX PN WO200177384-A2.  
XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.  
XX PR 07-APR-2000; 2000DE-01019173.  
XX PA (EPIG-) EPIGENOMICS AG.  
XX PI Olek A, Piepenbrock C, Berlin K;  
XX PI WPI; 2001-657177/75.  
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
XX designed to detect single-nucleotide polymorphisms and cytosine  
XX methylation status.  
XX PS Claim 1; SEQ ID NO 13488; 29pp + Sequence Listing; German.

XX CC This invention describes novel oligonucleotide primers or peptide nucleic  
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
XX and cytosine methylation status in chemically pretreated genomic DNA. The  
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
XX range of diseases including immune system, gastrointestinal, respiratory,  
XX central nervous system, cardiovascular and metabolic disorders. The  
XX oligomers are also used for detecting cell type differentiation. ABC00010  
XX -ABF99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
XX represent the oligomers described in the invention. NOTE: The sequence  
XX data for this patent did not form part of the printed specification, but  
XX was obtained in electronic format from WIPO at  
XX ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 13 BP; 4 A; 0 C; 0 G; 9 T; 0 U; 0 Other;  
Query Match 1.2%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1767 TTTTATAAATT 1779  
DB 1 TTTTATAAATT 13

RESULT 377  
ABC91693/C  
ID ABC91693 standard; DNA; 13 BP.  
XX AC ABC91693;  
XX  
DT 21-FEB-2002 (first entry)

XX DE Oligonucleotide SEQ ID NO 91710 for detecting SNP TSC0022946.

XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX OS Homo sapiens.  
XX PN WO200177384-A2.  
XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.  
XX PR 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.  
 XX Olek A, Piepenbrock C, Berlin K;  
 PI WPI; 2001-657177/75.  
 DR  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX  
 XX Claim 1; SEQ ID NO 91710; 29pp + Sequence Listing; German.  
 PS  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP).  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and AB100010-AB182073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 13 BP; 7 A; 2 C; 0 G; 4 T; 0 U; 0 Other;  
 Query Match 1.2%; Score 13; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 2259 AAGTGTATATTT 2271  
 DB 13 AAGTGTATATTT 1  
 RESULT 378  
 ABF90382  
 ID ABF90382 standard; DNA; 13 BP.  
 XX  
 AC ABF90382;  
 XX  
 DT 22-FEB-2002 (first entry)  
 XX  
 DE Oligonucleotide SEQ ID NO 190379 for detecting SNP TSC0046825.  
 XX  
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200177384-A2.  
 XX  
 PD 18-OCT-2001.  
 XX  
 PF 06-APR-2001; 2001WO-IB000713.  
 XX  
 PR 07-APR-2000; 2000DE-01019173.  
 XX  
 PA (EPIG-) EPIGENOMICS AG.  
 XX  
 PI Olek A, Piepenbrock C, Berlin K;  
 XX  
 DR WPI; 2001-657177/75.  
 XX  
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX  
 XX Claim 1; SEQ ID NO 190379; 29pp + Sequence Listing; German.

CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and AB100010-AB182073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 13 BP; 1 A; 0 C; 1 G; 11 T; 0 U; 0 Other;  
 Query Match 1.2%; Score 13; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1867 TTTATTTTGTGTT 1879  
 DB 1 TTTATTTTGTGTT 13  
 RESULT 379  
 ABF06851/c  
 ID ABF06851 standard; DNA; 13 BP.  
 XX  
 AC ABF06851;  
 XX  
 DT 21-FEB-2002 (first entry)  
 XX  
 DE Oligonucleotide SEQ ID NO 106848 for detecting SNP TSC0026750.  
 XX  
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200177384-A2.  
 XX  
 PD 18-OCT-2001.  
 XX  
 PF 06-APR-2001; 2001WO-IB000713.  
 XX  
 PR 07-APR-2000; 2000DE-01019173.  
 XX  
 PA (EPIG-) EPIGENOMICS AG.  
 XX  
 PI Olek A, Piepenbrock C, Berlin K;  
 XX  
 DR WPI; 2001-657177/75.  
 XX  
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX  
 XX Claim 1; SEQ ID NO 106848; 29pp + Sequence Listing; German.  
 XX  
 CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and AB100010-AB182073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX

SQ Sequence 13 BP; 10 A; 1 C; 0 G; 2 T; 0 U; 0 Other;  
 Query Match 1.2%; Score 13; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1871 TTTTGGTTTAA 1883  
 Db 13 TTTTGGTTTAA 1

RESULT 380  
 ABC37111/C  
 ID ABC37111 standard; DNA; 13 BP.  
 XX  
 AC ABC37111;  
 XX  
 DT 20-FEB-2002 (first entry)  
 XX  
 DE Oligonucleotide SEQ ID NO 37128 for detecting SNP TSC0011593.  
 XX  
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200177384-A2.  
 XX  
 PD 18-OCT-2001.  
 XX  
 PF 06-APR-2001; 2001WO-IB000713.  
 XX  
 PR 07-APR-2000; 2000DE-01019173.  
 XX  
 PA (EPIC-) EPIGENOMICS AG.  
 XX  
 PI Olek A, Piepenbrock C, Berlin K;  
 XX  
 DR WPI; 2001-657177/75.  
 XX  
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX  
 PS Claim 1; SEQ ID NO 37128; 29pp + Sequence Listing; German.  
 XX  
 CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 13 BP; 6 A; 2 C; 0 G; 5 T; 0 U; 0 Other;  
 Query Match 1.2%; Score 13; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1810 GTGTATATATATA 1822  
 Db 13 GTGTATATATATA 1

RESULT 381  
 ABC12933/C  
 ID ABC12933 standard; DNA; 13 BP.  
 XX  
 AC ABC12933;  
 XX  
 DT 21-FEB-2002 (first entry)  
 XX  
 DE Oligonucleotide SEQ ID NO 8054 for detecting SNP TSC0022135.  
 XX  
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX  
 OS Homo sapiens.

ID ABC12933 standard; DNA; 13 BP.  
 XX  
 AC ABC12933;  
 XX  
 DT 20-FEB-2002 (first entry)  
 XX  
 DE Oligonucleotide SEQ ID NO 12940 for detecting SNP TSC0003018.  
 XX  
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200177384-A2.  
 XX  
 PD 18-OCT-2001.  
 XX  
 PF 06-APR-2001; 2001WO-IB000713.  
 XX  
 PR 07-APR-2000; 2000DE-01019173.  
 XX  
 PA (EPIC-) EPIGENOMICS AG.  
 XX  
 PI Olek A, Piepenbrock C, Berlin K;  
 XX  
 DR WPI; 2001-657177/75.  
 XX  
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX  
 PS Claim 1; SEQ ID NO 12940; 29pp + Sequence Listing; German.  
 XX  
 CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 13 BP; 6 A; 1 C; 0 G; 6 T; 0 U; 0 Other;  
 Query Match 1.2%; Score 13; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1812 GTATATATATATA 1824  
 Db 13 GTATATATATATA 1

RESULT 382  
 ABC8037  
 ID ABC8037 standard; DNA; 13 BP.  
 XX  
 AC ABC8037;  
 XX  
 DT 21-FEB-2002 (first entry)  
 XX  
 DE Oligonucleotide SEQ ID NO 8054 for detecting SNP TSC0022135.  
 XX  
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX  
 OS Homo sapiens.

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XX PN WO200177384-A2.
XX XX
XX PD 18-OCT-2001.
XX XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX XX
XX PR 07-APR-2000; 2000DE-01019173.
XX XX
XX PA (EPIG-) EPIGENOMICS AG.
XX XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX XX
XX DR WPI; 2001-657177/75.
XX XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX XX
XX PS Claim 1; SEQ ID NO 8054; 29pp + Sequence Listing; German.
XX XX
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX XX
XX SQ Sequence 13 BP; 4 A; 2 C; 1 G; 6 T; 0 U; 0 Other;
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XX Query Match 1.2%; Score 13; DB 1; Length 13;
XX Best Local Similarity 100.0%; Pred. No. 2.7e+02;
XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1252 TTTTTCCTGATAA 1264
XX DB 1 TTTTTCCTGATAA 13
XX
XX RESULT 383
XX ABF19131/C
XX ID ABF19131 standard; DNA; 13 BP.
XX AC ABF19131;
XX XX
XX DT 21-FEB-2002 (first entry)
XX XX
XX DE Oligonucleotide SEQ ID NO 119128 for detecting SNP TSC0023746.
XX XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX XX
XX OS Homo sapiens.
XX XX
XX PN WO200177384-A2.
XX XX
XX PD 18-OCT-2001.
XX XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX XX
XX PR 07-APR-2000; 2000DE-01019173.
XX XX
XX PA (EPIG-) EPIGENOMICS AG.
XX XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX XX
XX DR WPI; 2001-657177/75.
XX XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX XX
XX PS Claim 1; SEQ ID NO 119128; 29pp + Sequence Listing; German.
XX XX
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX XX
XX SQ Sequence 13 BP; 6 A; 1 C; 0 G; 6 T; 0 U; 0 Other;
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XX Query Match 1.2%; Score 13; DB 1; Length 13;
XX Best Local Similarity 100.0%; Pred. No. 2.7e+02;
XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1916 ATATATATATATG 1928
XX DB 13 ATATATATATATG 1
XX
XX RESULT 384
XX ABC17782
XX ID ABC17782 standard; DNA; 13 BP.
XX AC ABC17782;
XX XX
XX DT 20-FEB-2002 (first entry)
XX XX
XX DE Oligonucleotide SEQ ID NO 17789 for detecting SNP TSC0003802.
XX XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX XX
XX OS Homo sapiens.
XX XX
XX PN WO200177384-A2.
XX XX
XX PD 18-OCT-2001.
XX XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX XX
XX PR 07-APR-2000; 2000DE-01019173.
XX XX
XX PA (EPIG-) EPIGENOMICS AG.
XX XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX XX
XX DR WPI; 2001-657177/75.
XX XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX XX
XX PS Claim 1; SEQ ID NO 17789; 29pp + Sequence Listing; German.
XX XX
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC range of diseases including immune system, gastrointestinal, respiratory,

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CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC000010  
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
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 SQ Sequence 13 BP; 3 A; 0 C; 4 G; 6 T; 0 U; 0 Other;  
 Query Match 1.2%; Score 13; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+02; Indels 0; Gaps 0;  
 Matches 13; Conservative 0; Mismatches 0;  
 QY 1806 GTGTGTGTATATA 1818  
 Db 1 GTGTGTGTATATA 13  
 RESULT 385  
 ABC82324  
 ID ABC82324 standard; DNA; 13 BP.  
 XX  
 AC ABC82324;  
 DT 21-FEB-2002 (first entry)  
 XX  
 DE Oligonucleotide SEQ ID NO 82341 for detecting SNP TSC0020792.  
 XX  
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX  
 OS Homo sapiens.  
 XX  
 WO200177384-A2.  
 XX  
 PD 18-OCT-2001.  
 XX  
 PF 06-APR-2001; 2001WO-IB000713.  
 XX  
 PR 07-APR-2000; 2000DE-01019173.  
 XX  
 PA (EPIG-) EPIGENOMICS AG.  
 XX  
 PI Olek A, Piepenbrock C, Berlin K;  
 XX  
 WPI; 2001-657177/75.  
 XX  
 Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX  
 Claim 1; SEQ ID NO 82341; 29pp + Sequence Listing; German.  
 XX  
 This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 13 BP; 5 A; 0 C; 1 G; 7 T; 0 U; 0 Other;  
 Query Match 1.2%; Score 13; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1778 TTATATTGTAAT 1790  
 Db 1 TTATATTGTAAT 13  
 RESULT 386  
 ABF60103  
 ID ABF60103 standard; DNA; 13 BP.  
 XX  
 AC ABF60103;  
 DT 22-FEB-2002 (first entry)  
 XX  
 DE Oligonucleotide SEQ ID NO 160100 for detecting SNP TSC0040305.  
 XX  
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX  
 OS Homo sapiens.  
 XX  
 WO200177384-A2.  
 XX  
 PD 18-OCT-2001.  
 XX  
 PF 06-APR-2001; 2001WO-IB000713.  
 XX  
 PR 07-APR-2000; 2000DE-01019173.  
 XX  
 PA (EPIG-) EPIGENOMICS AG.  
 XX  
 PI Olek A, Piepenbrock C, Berlin K;  
 XX  
 WPI; 2001-657177/75.  
 XX  
 Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX  
 Claim 1; SEQ ID NO 160100; 29pp + Sequence Listing; German.  
 XX  
 This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 13 BP; 5 A; 2 C; 1 G; 5 T; 0 U; 0 Other;  
 Query Match 1.2%; Score 13; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1253 TTTTCCGTAAAAA 1265  
 Db 1 TTTTCCGTAAAAA 13  
 RESULT 387  
 ABF61495/c  
 ID ABF61495 standard; DNA; 13 BP.  
 XX  
 AC ABF61495;  
 DT 22-FEB-2002 (first entry)

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XX DE Oligonucleotide SEQ ID NO 161492 for detecting SNP TSC0040647.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 161492; 29pp + Sequence Listing; German.
XX XX
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABG9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 13 BP; 11 A; 1 C; 0 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 1.2%; Score 13; DB 1; Length 13;
XX Best Local Similarity 100.0%; Pred. No. 2.7e+02;
XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1865 TTTTATTTCCT 1877
XX DB 13 TTTTATTTCCT 1
XX
XX RESULT 388
XX ABC5255/C
XX ID ABC5255 standard; DNA; 13 BP.
XX AC ABC5255;
XX XX
XX DT 21-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 55272 for detecting SNP TSC0015107.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 55272; 29pp + Sequence Listing; German.
XX XX
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABG9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 13 BP; 11 A; 1 C; 0 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 1.2%; Score 13; DB 1; Length 13;
XX Best Local Similarity 100.0%; Pred. No. 2.7e+02;
XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1865 TTTTATTTCCT 1877
XX DB 13 TTTTATTTCCT 1
XX
XX RESULT 388
XX ABC5255/C
XX ID ABC5255 standard; DNA; 13 BP.
XX AC ABC5255;
XX XX
XX DT 21-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 55272 for detecting SNP TSC0015107.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 55272; 29pp + Sequence Listing; German.
XX XX
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABG9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 13 BP; 7 A; 0 C; 0 G; 6 T; 0 U; 0 Other;
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XX Query Match 1.2%; Score 13; DB 1; Length 13;
XX Best Local Similarity 100.0%; Pred. No. 2.7e+02;
XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1771 TTTAAATTTTAT 1783
XX DB 13 TTTAAATTTTAT 1
XX
XX RESULT 389
XX ABC5807/C
XX ID ABC5807 standard; DNA; 13 BP.
XX AC ABC5807;
XX XX
XX DT 21-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 58824 for detecting SNP TSC0015758.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.

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XX PS Claim 1; SEQ ID NO 58824; 29pp + Sequence Listing; German.  
 XX CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX SQ Sequence 13 BP; 7 A; 5 C; 0 G; 1 T; 0 U; 0 Other;  
 Query Match 1.2%; Score 13; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1803 TGTGTGTGTGTAT 1815  
 Db 13 TGTGTGTGTGTAT 1  
 RESULT 390  
 ABC37110  
 ID ABC37110 standard; DNA; 13 BP.  
 AC ABC37110;  
 XX 20-FEB-2002 (first entry)  
 DE Oligonucleotide SEQ ID NO 37127 for detecting SNP TSC0011593.  
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 OS Homo sapiens.  
 XX WO200177384-A2.  
 FN 18-OCT-2001.  
 PD 06-APR-2001; 2001WO-IB000713.  
 PF 07-APR-2000; 2000DE-01019173.  
 PR (EPIG-) EPIGENOMICS AG.  
 PA Olek A, Piepenbrock C, Berlin K;  
 PI WPI; 2001-657177/75.  
 DR Set of oligonucleotides, useful for diagnosis and cell typing, is  
 XX designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 PS Claim 1; SEQ ID NO 37127; 29pp + Sequence Listing; German.  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
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CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX SQ Sequence 13 BP; 5 A; 0 C; 2 G; 6 T; 0 U; 0 Other;  
 Query Match 1.2%; Score 13; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1810 GTGTATATATATA 1822  
 Db 1 GTGTATATATATA 13  
 RESULT 391  
 ABF60102/c  
 ID ABF60102 standard; DNA; 13 BP.  
 AC ABF60102;  
 XX 22-FEB-2002 (first entry)  
 DE Oligonucleotide SEQ ID NO 160099 for detecting SNP TSC0040305.  
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 OS Homo sapiens.  
 XX WO200177384-A2.  
 FN 18-OCT-2001.  
 PD 06-APR-2001; 2001WO-IB000713.  
 PF 07-APR-2000; 2000DE-01019173.  
 PR (EPIG-) EPIGENOMICS AG.  
 PA Olek A, Piepenbrock C, Berlin K;  
 PI WPI; 2001-657177/75.  
 DR Set of oligonucleotides, useful for diagnosis and cell typing, is  
 XX designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 PS Claim 1; SEQ ID NO 160099; 29pp + Sequence Listing; German.  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
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 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX SQ Sequence 13 BP; 5 A; 1 C; 2 G; 5 T; 0 U; 0 Other;  
 Query Match 1.2%; Score 13; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1253 TTTTCGTAATAA 1265  
 Db 13 TTTTCGTAATAA 1



RESULT 392  
 ID ABC17780 standard; DNA; 13 BP.  
 XX  
 AC ABC17780;  
 XX  
 DT 20-FEB-2002 (first entry)  
 XX  
 DE Oligonucleotide SEQ ID NO 17787 for detecting SNP TSC0003802.  
 XX  
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200177384-A2.  
 XX  
 PD 18-OCT-2001.  
 XX  
 PF 06-APR-2001; 2001WO-IB000713.  
 XX  
 PR 07-APR-2000; 2000DE-01019173.  
 XX  
 PA (EPIG-) EPIGENOMICS AG.  
 XX  
 PI Olek A, Piepenbrock C, Berlin K;  
 XX  
 DR WPI; 2001-657177/75.  
 XX  
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX  
 PS Claim 1; SEQ ID NO 17787; 29pp + Sequence Listing; German.  
 XX  
 CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 PS Sequence 13 BP; 4 A; 0 C; 3 G; 6 T; 0 U; 0 Other;  
 XX  
 CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
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 PS Sequence 13 BP; 4 A; 0 C; 3 G; 6 T; 0 U; 0 Other;  
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 Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1808 GTGTGTATATATA 1820  
 DB 1 GTGTGTATATATA 13  
 RESULT 393  
 ID ABC98273 standard; DNA; 13 BP.  
 XX  
 AC ABC98273;  
 XX  
 DT 21-FEB-2002 (first entry)  
 XX  
 DE Oligonucleotide SEQ ID NO 98290 for detecting SNP TSC0024420.  
 XX  
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX Homo sapiens.  
 OS  
 PN WO200177384-A2.  
 XX  
 PD 18-OCT-2001.  
 XX  
 PF 06-APR-2001; 2001WO-IB000713.  
 XX  
 PR 07-APR-2000; 2000DE-01019173.  
 XX  
 PA (EPIG-) EPIGENOMICS AG.  
 XX  
 PI Olek A, Piepenbrock C, Berlin K;  
 XX  
 DR WPI; 2001-657177/75.  
 XX  
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX  
 PS Claim 1; SEQ ID NO 98290; 29pp + Sequence Listing; German.  
 XX  
 CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 PS Sequence 13 BP; 7 A; 1 C; 0 G; 5 T; 0 U; 0 Other;  
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 Query Match 1.2%; Score 13; DB 1; Length 13;  
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 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1811 TGTATATATATAT 1823  
 DB 13 TGTATATATATAT 1  
 RESULT 394  
 ID ABC79591/c  
 XX  
 AC ABC79591;  
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 DT 21-FEB-2002 (first entry)  
 XX  
 DE Oligonucleotide SEQ ID NO 79608 for detecting SNP TSC0020218.  
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 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200177384-A2.  
 XX  
 PD 18-OCT-2001.  
 XX  
 PF 06-APR-2001; 2001WO-IB000713.  
 XX  
 PR 07-APR-2000; 2000DE-01019173.  
 XX  
 PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;  
 XX WPI; 2001-657177/75.  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX PS Claim 1; SEQ ID NO 79608; 29pp + Sequence Listing; German.  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073  
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 CC data for this patent did not form part of the printed specification, but  
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 Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1802 GTGTGTGTGTGTA 1814  
 DB 13 GTGTGTGTGTGTA 1  
 RESULT 395  
 ABC29729/C  
 ID ABC29729 standard; DNA; 13 BP.  
 XX AC ABC29729;  
 XX 20-FEB-2002 (first entry)  
 DE Oligonucleotide SEQ ID NO 29746 for detecting SNP TSC0008889.  
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX Homo sapiens.  
 XX WO200177384-A2.  
 XX 18-OCT-2001.  
 XX 06-APR-2001; 2001WO-IB000713.  
 XX 07-APR-2000; 2000DE-01019173.  
 XX (EPIG-) EPIGENOMICS AG.  
 XX Olek A, Piepenbrock C, Berlin K;  
 XX WPI; 2001-657177/75.  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX PS Claim 1; SEQ ID NO 29746; 29pp + Sequence Listing; German.  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX SQ Sequence 13 BP; 6 A; 7 C; 0 G; 0 T; 0 U; 0 Other;  
 Query Match 1.2%; Score 13; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1794 GTGTGTGTGTG 1806  
 DB 13 GTGTGTGTGTG 1  
 RESULT 396  
 ABC33895/C  
 ID ABC33895 standard; DNA; 13 BP.  
 XX AC ABC33895;  
 XX 20-FEB-2002 (first entry)  
 DE Oligonucleotide SEQ ID NO 33912 for detecting SNP TSC0010852.  
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX Homo sapiens.  
 XX WO200177384-A2.  
 XX 18-OCT-2001.  
 XX 06-APR-2001; 2001WO-IB000713.  
 XX 07-APR-2000; 2000DE-01019173.  
 XX (EPIG-) EPIGENOMICS AG.  
 XX Olek A, Piepenbrock C, Berlin K;  
 XX WPI; 2001-657177/75.  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX PS Claim 1; SEQ ID NO 33912; 29pp + Sequence Listing; German.  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX SQ Sequence 13 BP; 10 A; 1 C; 0 G; 2 T; 0 U; 0 Other;

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Query Match      1.2%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred.No. 2.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1870 ATTTTGTGTTTA 1882
DB 13 ATTTTGTGTTTA 1
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RESULT 397
ABF48194
ID ABF48194 standard; DNA; 13 BP.
XX AC ABF48194;
XX DT 21-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 148191 for detecting SNP TSC0037417.
XX SNF; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX FN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX Claim 1; SEQ ID NO 148191; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX ftp.wipo.int/pub/published_pct_sequences
XX Sequence 13 BP; 5 A; 0 C; 0 G; 8 T; 0 U; 0 Other;
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
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XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
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XX data for this patent did not form part of the printed specification, but
XX ftp.wipo.int/pub/published_pct_sequences
XX Sequence 13 BP; 5 A; 0 C; 0 G; 8 T; 0 U; 0 Other;

Query Match      1.2%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred.No. 2.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1766 ATTTTGTGTTTA 1778
DB 1 ATTTTGTGTTTA 13
|||||

RESULT 398
ABF52649/c
ID ABF52649 standard; DNA; 13 BP.
XX

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AC ABF52649;
XX DT 21-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 152646 for detecting SNP TSC0038583.
XX SNF; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX FN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX Claim 1; SEQ ID NO 152646; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
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XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
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XX ftp.wipo.int/pub/published_pct_sequences
XX Sequence 13 BP; 6 A; 1 C; 0 G; 6 T; 0 U; 0 Other;
XX Query Match      1.2%; Score 13; DB 1; Length 13;
XX Best Local Similarity 100.0%; Pred.No. 2.7e+02;
XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1779 TATATTGTTAAATA 1791
DB 13 TATATTGTTAAATA 1
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RESULT 399
ABCI1783/c
ID ABCI1783 standard; DNA; 13 BP.
XX AC ABCI1783;
XX DT 20-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 17790 for detecting SNP TSC0003802.
XX SNF; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX FN WO200177384-A2.
XX

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XX 18-OCT-2001.  
PD  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PF 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPiG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 17790; 29pp + Sequence Listing; German.  
XX  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABG9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073  
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CC data for this patent did not form part of the printed specification, but  
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CC ftp.wipo.int/pub/published\_pct\_sequences  
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SQ Sequence 13 BP; 6 A; 4 C; 0 G; 3 T; 0 U; 0 Other;  
Query Match 1.2%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1806 GTGTGTGTATATA 1818  
Db 13 GTGTGTGTATATA 1  
RESULT 400  
ABC05415  
ID ABC05415 standard; DNA; 13 BP.  
XX  
AC ABC05415;  
XX  
XX 20-FEB-2002 (first entry)  
DT  
DE Oligonucleotide SEQ ID NO 5406 for detecting SNP TSC0001818.  
XX  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
XX Homo sapiens.  
OS  
XX WO200177384-A2.  
PN  
XX 18-OCT-2001.  
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XX  
XX 06-APR-2001; 2001WO-IB000713.  
PF  
XX 07-APR-2000; 2000DE-01019173.  
PR  
XX (EPiG-) EPIGENOMICS AG.  
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XX Olek A, Piepenbrock C, Berlin K;  
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XX WPI; 2001-657177/75.  
DR  
XX  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 17790; 29pp + Sequence Listing; German.  
XX  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABG9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073  
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XX  
SQ Sequence 13 BP; 6 A; 4 C; 0 G; 3 T; 0 U; 0 Other;  
Query Match 1.2%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
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Db 13 GTGTGTGTATATA 1  
RESULT 400  
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ID ABC05415 standard; DNA; 13 BP.  
XX  
AC ABC05415;  
XX  
XX 20-FEB-2002 (first entry)  
DT  
DE Oligonucleotide SEQ ID NO 5406 for detecting SNP TSC0001818.  
XX  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
XX Homo sapiens.  
OS  
XX WO200177384-A2.  
PN  
XX 18-OCT-2001.  
PD  
XX  
XX 06-APR-2001; 2001WO-IB000713.  
PF  
XX 07-APR-2000; 2000DE-01019173.  
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XX Olek A, Piepenbrock C, Berlin K;  
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PT methylation status.  
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CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABG9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073  
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XX  
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Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1813 TATATATATATAT 1825  
Db 1 TATATATATATAT 13  
RESULT 401  
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XX  
AC ABC05415;  
XX  
XX 20-FEB-2002 (first entry)  
DT  
DE Oligonucleotide SEQ ID NO 5406 for detecting SNP TSC0001818.  
XX  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
XX Homo sapiens.  
OS  
XX WO200177384-A2.  
PN  
XX 18-OCT-2001.  
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XX 06-APR-2001; 2001WO-IB000713.  
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XX 07-APR-2000; 2000DE-01019173.  
PR  
XX (EPiG-) EPIGENOMICS AG.  
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XX WPI; 2001-657177/75.  
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PT designed to detect single-nucleotide polymorphisms and cytosine  
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XX  
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CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
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CC -ABG9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073  
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SQ Sequence 13 BP; 6 A; 0 C; 0 G; 7 T; 0 U; 0 Other;  
Query Match 1.2%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 1 TATATATATATAT 13  
RESULT 401  
ABC05415/C  
ID ABC05415 standard; DNA; 13 BP.  
XX  
AC ABC05415;  
XX  
XX 20-FEB-2002 (first entry)  
DT  
DE Oligonucleotide SEQ ID NO 5406 for detecting SNP TSC0001818.  
XX  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
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XX Homo sapiens.  
OS  
XX WO200177384-A2.  
PN  
XX 18-OCT-2001.  
PD  
XX  
XX 06-APR-2001; 2001WO-IB000713.  
PF  
XX 07-APR-2000; 2000DE-01019173.  
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XX (EPiG-) EPIGENOMICS AG.  
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XX  
PS Claim 1; SEQ ID NO 5406; 29pp + Sequence Listing; German.  
XX  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010

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CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 6 A; 0 C; 0 G; 7 T; 0 U; 0 Other;

Query Match 1.2%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1814 ATATATATATATA 1826
DB 13 ATATATATATATA 1
RESULT 402
ABCI2932
ID ABCI2932 standard; DNA; 13 BP.
XX AC ABCI2932;
XX
DT 20-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 12939 for detecting SNP TSC0003018.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
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XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
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PT methylation status.
XX
PS Claim 1; SEQ ID NO 12939; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 6 A; 0 C; 1 G; 6 T; 0 U; 0 Other;

Query Match 1.2%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1812 GTATATATATATA 1824
DB 12 GTATATATATATA 1
RESULT 404
ABH52395/c
ID ABH52395 standard; DNA; 13 BP.
XX AC ABH52395;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 252372 for detecting SNP TSC0061564.
```

```
Db 1 GTATATATATATA 13
RESULT 403
ABF38750
ID ABF38750 standard; DNA; 13 BP.
XX AC ABF38750;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 138747 for detecting SNP TSC0034761.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 138747; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 5 A; 0 C; 1 G; 7 T; 0 U; 0 Other;

Query Match 1.2%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1817 TATATATATATCT 1829
DB 1 TATATATATATCT 13
RESULT 404
ABH52395/c
ID ABH52395 standard; DNA; 13 BP.
XX AC ABH52395;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 252372 for detecting SNP TSC0061564.
```

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX Homo sapiens.  
 OS WO200177384-A2.  
 XX 18-OCT-2001.  
 XX 06-APR-2001; 2001WO-IB000713.  
 XX 07-APR-2000; 2000DE-01019173.  
 XX (EPIG-) EPIGENOMICS AG.  
 XX Olek A, Piepenbrock C, Berlin K;  
 PI WPI; 2001-657177/75.  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX Claim 1; SEQ ID NO 252372; 29pp + Sequence Listing; German.  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX Sequence 13 BP; 7 A; 4 C; 0 G; 2 T; 0 U; 0 Other;  
 SQ Query Match 1.2%; Score 13; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1805 TGTGTGTGTAT 1817  
 DB 13 TGTGTGTGTAT 1  
 RESULT 405  
 ABC43064  
 ID ABC43064 standard; DNA; 13 BP.  
 XX ABC43064;  
 XX 21-FEB-2002 (first entry)  
 DT Oligonucleotide SEQ ID NO 43081 for detecting SNP TSC0012784.  
 DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX Homo sapiens.  
 OS WO200177384-A2.  
 XX 18-OCT-2001.  
 XX 06-APR-2001; 2001WO-IB000713.  
 XX Claim 1; SEQ ID NO 88230; 29pp + Sequence Listing; German.

PR 07-APR-2000; 2000DE-01019173.  
 XX (EPIG-) EPIGENOMICS AG.  
 XX Olek A, Piepenbrock C, Berlin K;  
 PI WPI; 2001-657177/75.  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX Claim 1; SEQ ID NO 43081; 29pp + Sequence Listing; German.  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX Sequence 13 BP; 2 A; 0 C; 5 G; 6 T; 0 U; 0 Other;  
 SQ Query Match 1.2%; Score 13; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1804 GTGTGTGTAT 1816  
 DB 1 GTGTGTGTAT 13  
 RESULT 406  
 ABC8213/C  
 ID ABC8213 standard; DNA; 13 BP.  
 XX ABC8213;  
 XX 21-FEB-2002 (first entry)  
 DT Oligonucleotide SEQ ID NO 88230 for detecting SNP TSC0022170.  
 DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX Homo sapiens.  
 OS WO200177384-A2.  
 XX 18-OCT-2001.  
 XX 06-APR-2001; 2001WO-IB000713.  
 XX 07-APR-2000; 2000DE-01019173.  
 XX (EPIG-) EPIGENOMICS AG.  
 XX Olek A, Piepenbrock C, Berlin K;  
 PI WPI; 2001-657177/75.  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX Claim 1; SEQ ID NO 88230; 29pp + Sequence Listing; German.

XX CC This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABG99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 13 BP; 8 A; 0 C; 0 G; 5 T; 0 U; 0 Other;

Query Match 1.2%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1769 TTTTAAATTTAT 1781  
DB 13 TTTTAAATTTAT 1

RESULT 407  
ABH52394  
ID ABH52394 standard; DNA; 13 BP.  
XX AC ABH52394;  
XX DT 22-FEB-2002 (first entry)  
XX DE Oligonucleotide SEQ ID NO 252371 for detecting SNP TSC0061564.  
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX OS Homo sapiens.  
XX PN WO200177384-A2.  
XX PD 18-OCT-2001.  
XX PF 06-APR-2001; 2001WO-IB000713.  
XX PR 07-APR-2000; 2000DE-01019173.  
XX PA (EPIG-) EPIGENOMICS AG.  
XX PI Olek A, Piepenbrock C, Berlin K;  
XX WPI; 2001-657177/75.  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.  
XX Claim 1; SEQ ID NO 252371; 29pp + Sequence Listing; German.  
XX This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABG99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 13 BP; 2 A; 0 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 1.2%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1805 TGTGTGTGTATAT 1817  
DB 1 TGTGTGTGTATAT 13

RESULT 408  
ABCI7781/C  
ID ABCI7781 standard; DNA; 13 BP.  
XX AC ABCI7781;  
XX DT 20-FEB-2002 (first entry)  
XX DE Oligonucleotide SEQ ID NO 17788 for detecting SNP TSC0003802.  
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX OS Homo sapiens.  
XX PN WO200177384-A2.  
XX PD 18-OCT-2001.  
XX PF 06-APR-2001; 2001WO-IB000713.  
XX PR 07-APR-2000; 2000DE-01019173.  
XX PA (EPIG-) EPIGENOMICS AG.  
XX PI Olek A, Piepenbrock C, Berlin K;  
XX WPI; 2001-657177/75.  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.  
XX Claim 1; SEQ ID NO 17788; 29pp + Sequence Listing; German.  
XX This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABG99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 13 BP; 6 A; 3 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 1.2%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1808 GTGTGTATATATA 1820  
DB 13 GTGTGTATATATA 1

RESULT 409

ABC28589/c  
ID ABC28589 standard; DNA; 13 BP.

XX AC ABC28589;

XX DT 20-FEB-2002 (first entry)

XX DE Oligonucleotide SEQ ID NO 28606 for detecting SNP TSC0008245.

XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX DR WPI; 2001-657177/75.

XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
XX PT designed to detect single-nucleotide polymorphisms and cytosine  
XX PT methylation status.

XX PS Claim 1; SEQ ID NO 28606; 29pp + Sequence Listing; German.

XX CC This invention describes novel oligonucleotide primers or peptide nucleic  
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The  
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
XX CC range of diseases including immune system, gastrointestinal, respiratory,  
XX CC central nervous system, cardiovascular and metabolic disorders. The  
XX CC oligomers are also used for detecting cell type differentiation. ABC00010  
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
XX CC represent the oligomers described in the invention. NOTE: The sequence  
XX CC data for this patent did not form part of the printed specification, but  
XX CC was obtained in electronic format from WIPO at  
XX CC ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 13 BP; 6 A; 1 C; 0 G; 6 T; 0 U; 0 Other;

Query Match 1.2%; Score 13; DB 1; Length 13;

Best Local Similarity 100.0%; Pred. No. 2.7e+02;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1818 ATATATATATGTA 1830

Db 13 ATATATATATGTA 1

RESULT 410

ABC33894

ID ABC33894 standard; DNA; 13 BP.

XX AC ABC33894;

XX DT 20-FEB-2002 (first entry)

XX DE Oligonucleotide SEQ ID NO 33911 for detecting SNP TSC0010852.

XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX DR WPI; 2001-657177/75.

XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
XX PT designed to detect single-nucleotide polymorphisms and cytosine  
XX PT methylation status.

XX PS Claim 1; SEQ ID NO 33911; 29pp + Sequence Listing; German.

XX CC This invention describes novel oligonucleotide primers or peptide nucleic  
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The  
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
XX CC range of diseases including immune system, gastrointestinal, respiratory,  
XX CC central nervous system, cardiovascular and metabolic disorders. The  
XX CC oligomers are also used for detecting cell type differentiation. ABC00010  
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
XX CC represent the oligomers described in the invention. NOTE: The sequence  
XX CC data for this patent did not form part of the printed specification, but  
XX CC was obtained in electronic format from WIPO at  
XX CC ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 13 BP; 2 A; 0 C; 1 G; 10 T; 0 U; 0 Other;

Query Match 1.2%; Score 13; DB 1; Length 13;

Best Local Similarity 100.0%; Pred. No. 2.7e+02;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1870 ATTATGTTTTTA 1882

Db 1 ATTATGTTTTTA 13

RESULT 411

ABC88036/c

ID ABC88036 standard; DNA; 13 BP.

XX AC ABC88036;

XX DT 21-FEB-2002 (first entry)

XX DE Oligonucleotide SEQ ID NO 88053 for detecting SNP TSC0022135.

XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;



XX WPI; 2001-657177/75.  
XX  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
XX  
PS Claim 1; SEQ ID NO 88053; 29pp + Sequence Listing; German.  
XX  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
XX and cytosine methylation status in chemically pretreated genomic DNA. The  
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
XX range of diseases including immune system, gastrointestinal, respiratory,  
XX central nervous system, cardiovascular and metabolic disorders. The  
XX oligomers are also used for detecting cell type differentiation. ABC00010  
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABT00010-ABT82073  
XX represent the oligomers described in the invention. NOTE: The sequence  
XX data for this patent did not form part of the printed specification, but  
XX was obtained in electronic format from WIPO at  
XX ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 13 BP; 6 A; 1 C; 2 G; 4 T; 0 U; 0 Other;  
  
Query Match 1.2%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1252 TTTTTCGTAATA 1264  
DB 13 TTTTTCGTAATA 1  
  
RESULT 412  
ABF37479/c  
ID ABF37479 standard; DNA; 13 BP.  
XX  
XX AC ABF37479;  
XX  
XX 21-FEB-2002 (first entry)  
XX  
XX Oligonucleotide SEQ ID NO 137476 for detecting SNP TSC0034363.  
XX  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
XX Homo sapiens.  
XX  
XX WO200177384-A2.  
XX  
XX 18-OCT-2001.  
XX  
XX 06-APR-2001; 2001WO-IB000713.  
XX  
XX 07-APR-2000; 2000DE-01019173.  
XX  
XX (EPIG-) EPIGENOMICS AG.  
XX  
XX Olek A, Piepenbrock C, Berlin K;  
XX  
XX WPI; 2001-657177/75.  
XX  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
XX designed to detect single-nucleotide polymorphisms and cytosine  
XX methylation status.  
XX  
XX Claim 1; SEQ ID NO 137476; 29pp + Sequence Listing; German.  
XX  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
XX and cytosine methylation status in chemically pretreated genomic DNA. The  
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a

CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABT00010-ABT82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX Sequence 13 BP; 11 A; 1 C; 0 G; 1 T; 0 U; 0 Other;  
  
Query Match 1.2%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1869 TATTTTGTGTTTT 1881  
DB 13 TATTTTGTGTTTT 1  
  
RESULT 413  
ABC20146  
ID ABC20146 standard; DNA; 13 BP.  
XX  
XX AC ABC20146;  
XX  
XX 20-FEB-2002 (first entry)  
XX  
XX Oligonucleotide SEQ ID NO 20163 for detecting SNP TSC0004136.  
XX  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
XX Homo sapiens.  
XX  
XX WO200177384-A2.  
XX  
XX 18-OCT-2001.  
XX  
XX 06-APR-2001; 2001WO-IB000713.  
XX  
XX 07-APR-2000; 2000DE-01019173.  
XX  
XX (EPIG-) EPIGENOMICS AG.  
XX  
XX Olek A, Piepenbrock C, Berlin K;  
XX  
XX WPI; 2001-657177/75.  
XX  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
XX designed to detect single-nucleotide polymorphisms and cytosine  
XX methylation status.  
XX  
XX Claim 1; SEQ ID NO 20163; 29pp + Sequence Listing; German.  
XX  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
XX and cytosine methylation status in chemically pretreated genomic DNA. The  
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
XX range of diseases including immune system, gastrointestinal, respiratory,  
XX central nervous system, cardiovascular and metabolic disorders. The  
XX oligomers are also used for detecting cell type differentiation. ABC00010  
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABT00010-ABT82073  
XX represent the oligomers described in the invention. NOTE: The sequence  
XX data for this patent did not form part of the printed specification, but  
XX was obtained in electronic format from WIPO at  
XX ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX Sequence 13 BP; 1 A; 0 C; 1 G; 11 T; 0 U; 0 Other;  
  
Query Match 1.2%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1868 TTATTTTGTTTT 1880  
DB 1 TTATTTTGTTTT 13

RESULT 414  
ABC05127/c  
ID ABC05127 standard; DNA; 13 BP.  
XX AC ABC05127;  
XX DT 20-FEB-2002 (first entry)  
XX DE Oligonucleotide SEQ ID NO 20164 for detecting SNP TSC0004136.  
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX OS Homo sapiens.  
XX PN WO200177384-A2.  
XX PD 18-OCT-2001.  
XX PF 06-APR-2001; 2001WO-IB000713.  
XX PR 07-APR-2000; 2000DE-01019173.  
XX PA (EPIG-) EPIGENOMICS AG.  
XX PI Olek A, Piepenbrock C, Berlin K;  
XX DR WPI; 2001-657177/75.  
XX KW Set of oligonucleotides, useful for diagnosis and cell typing, is  
XX KW designed to detect single-nucleotide polymorphisms and cytosine  
XX KW methylation status.  
XX PS Claim 1; SEQ ID NO 20164; 29pp + Sequence Listing; German.  
XX CC This invention describes novel oligonucleotide primers or peptide nucleic  
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The  
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
XX CC range of diseases including immune system, gastrointestinal, respiratory,  
XX CC central nervous system, cardiovascular and metabolic disorders. The  
XX CC oligomers are also used for detecting cell type differentiation. ABC00010  
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
XX CC represent the oligomers described in the invention. NOTE: The sequence  
XX CC data for this patent did not form part of the printed specification, but  
XX CC was obtained in electronic format from WIPO at  
XX CC ftp.wipo.int/pub/published\_pct\_sequences  
XX SQ Sequence 13 BP; 11 A; 1 C; 0 G; 1 T; 0 U; 0 Other;  
Query Match 1.2%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1868 TTATTTTGTTTT 1880  
DB 1 TTATTTTGTTTT 13

RESULT 415  
ABC05127/c  
ID ABC05127 standard; DNA; 13 BP.  
XX AC ABC05127;  
XX DT 20-FEB-2002 (first entry)  
XX DE Oligonucleotide SEQ ID NO 20164 for detecting SNP TSC0004136.  
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX OS Homo sapiens.  
XX PN WO200177384-A2.  
XX PD 18-OCT-2001.  
XX PF 06-APR-2001; 2001WO-IB000713.  
XX PR 07-APR-2000; 2000DE-01019173.  
XX PA (EPIG-) EPIGENOMICS AG.  
XX PI Olek A, Piepenbrock C, Berlin K;  
XX DR WPI; 2001-657177/75.  
XX KW Set of oligonucleotides, useful for diagnosis and cell typing, is  
XX KW designed to detect single-nucleotide polymorphisms and cytosine  
XX KW methylation status.  
XX PS Claim 1; SEQ ID NO 20164; 29pp + Sequence Listing; German.  
XX CC This invention describes novel oligonucleotide primers or peptide nucleic  
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The  
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
XX CC range of diseases including immune system, gastrointestinal, respiratory,  
XX CC central nervous system, cardiovascular and metabolic disorders. The  
XX CC oligomers are also used for detecting cell type differentiation. ABC00010  
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
XX CC represent the oligomers described in the invention. NOTE: The sequence  
XX CC data for this patent did not form part of the printed specification, but  
XX CC was obtained in electronic format from WIPO at  
XX CC ftp.wipo.int/pub/published\_pct\_sequences  
XX SQ Sequence 13 BP; 11 A; 1 C; 0 G; 1 T; 0 U; 0 Other;  
Query Match 1.2%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DT 20-FEB-2002 (first entry)  
XX Oligonucleotide SEQ ID NO 5118 for detecting SNP TSC0001771.  
DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX OS Homo sapiens.  
XX PN WO200177384-A2.  
XX PD 18-OCT-2001.  
XX PF 06-APR-2001; 2001WO-IB000713.  
XX PR 07-APR-2000; 2000DE-01019173.  
XX PA (EPIG-) EPIGENOMICS AG.  
XX PI Olek A, Piepenbrock C, Berlin K;  
XX DR WPI; 2001-657177/75.  
XX KW Set of oligonucleotides, useful for diagnosis and cell typing, is  
XX KW designed to detect single-nucleotide polymorphisms and cytosine  
XX KW methylation status.  
XX PS Claim 1; SEQ ID NO 5118; 29pp + Sequence Listing; German.  
XX CC This invention describes novel oligonucleotide primers or peptide nucleic  
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The  
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
XX CC range of diseases including immune system, gastrointestinal, respiratory,  
XX CC central nervous system, cardiovascular and metabolic disorders. The  
XX CC oligomers are also used for detecting cell type differentiation. ABC00010  
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
XX CC represent the oligomers described in the invention. NOTE: The sequence  
XX CC data for this patent did not form part of the printed specification, but  
XX CC was obtained in electronic format from WIPO at  
XX CC ftp.wipo.int/pub/published\_pct\_sequences  
XX SQ Sequence 13 BP; 7 A; 6 C; 0 G; 0 T; 0 U; 0 Other;  
Query Match 1.2%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGT 1805  
DB 13 TGTGTGTGTGTGT 1

RESULT 416  
ABC05414  
ID ABC05414 standard; DNA; 13 BP.  
XX AC ABC05414;  
XX DT 20-FEB-2002 (first entry)  
XX DE Oligonucleotide SEQ ID NO 5405 for detecting SNP TSC0001818.  
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX OS Homo sapiens.  
XX PN WO200177384-A2.  
XX PD 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.  
 XX 07-APR-2000; 2000DE-01019173.  
 XX (EPIG-) EPIGENOMICS AG.  
 XX Olek A, Piepenbrock C, Berlin K;  
 XX WPI; 2001-657177/75.  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX Claim 1; SEQ ID NO 5405; 29pp + Sequence Listing; German.  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP).  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX Sequence 13 BP; 7 A; 0 C; 0 G; 6 T; 0 U; 0 Other;  
 SQ Query Match 1.2%; Score 13; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1814 ATATATATATATA 1826  
 DB 1 ATATATATATATA 13  
 RESULT 417  
 ABC05414/C  
 ID ABC05414 standard; DNA; 13 BP.  
 XX AC ABC05414;  
 XX 20-FEB-2002 (first entry)  
 DE Oligonucleotide SEQ ID NO 5405 for detecting SNP TSC0001818.  
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX Homo sapiens.  
 XX WO200177384-A2.  
 XX 18-OCT-2001.  
 XX 06-APR-2001; 2001WO-IB000713.  
 XX 07-APR-2000; 2000DE-01019173.  
 XX (EPIG-) EPIGENOMICS AG.  
 XX Olek A, Piepenbrock C, Berlin K;  
 XX WPI; 2001-657177/75.  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine

PT methylation status.  
 XX Claim 1; SEQ ID NO 5405; 29pp + Sequence Listing; German.  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP).  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX Sequence 13 BP; 7 A; 0 C; 0 G; 6 T; 0 U; 0 Other;  
 SQ Query Match 1.2%; Score 13; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1813 TATATATATATAT 1825  
 DB 13 TATATATATATAT 1  
 RESULT 418  
 ABF61048  
 ID ABF61048 standard; DNA; 13 BP.  
 XX AC ABF61048;  
 XX 22-FEB-2002 (first entry)  
 DE Oligonucleotide SEQ ID NO 161045 for detecting SNP TSC0040548.  
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX Homo sapiens.  
 XX WO200177384-A2.  
 XX 18-OCT-2001.  
 XX 06-APR-2001; 2001WO-IB000713.  
 XX 07-APR-2000; 2000DE-01019173.  
 XX (EPIG-) EPIGENOMICS AG.  
 XX Olek A, Piepenbrock C, Berlin K;  
 XX WPI; 2001-657177/75.  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX Claim 1; SEQ ID NO 161045; 29pp + Sequence Listing; German.  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP).  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence

CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 13 BP; 5 A; 0 C; 1 G; 7 T; 0 U; 0 Other;  
SQ

Query Match 1.2%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1774 AAATTATATGT 1786  
|||||  
Db 1 AAATTATATGT 13

RESULT 419  
ABF90363  
ID ABF90363 standard; DNA; 13 BP.  
XX  
AC ABF90363;  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide SEQ ID NO 190360 for detecting SNP TSC0046817.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
WPI; 2001-657177/75.  
XX  
Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
Claim 1; SEQ ID NO 190360; 29pp + Sequence Listing; German.  
XX  
This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 13 BP; 3 A; 1 C; 0 G; 9 T; 0 U; 0 Other;  
SQ

Query Match 1.2%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2265 TATTTTCTATA 2278  
|||||  
Db 1 TATTTTCTATA 13

RESULT 420  
ABF90383/c  
ID ABF90383 standard; DNA; 13 BP.  
XX  
AC ABF90383;  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide SEQ ID NO 190380 for detecting SNP TSC0046825.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
WPI; 2001-657177/75.  
XX  
Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
Claim 1; SEQ ID NO 190380; 29pp + Sequence Listing; German.  
XX  
This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 13 BP; 11 A; 1 C; 0 G; 1 T; 0 U; 0 Other;  
SQ

Query Match 1.2%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1867 TTATTTTGT 1879  
|||||  
Db 13 TTATTTTGT 1

RESULT 421  
ABC79590  
ID ABC79590 standard; DNA; 13 BP.  
XX  
AC ABC79590;  
XX  
DT 21-FEB-2002 (first entry)  
XX  
DE Oligonucleotide SEQ ID NO 79607 for detecting SNP TSC0020218.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;

KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX Homo sapiens.  
 OS  
 XX WO200177384-A2.  
 FN  
 XX 18-OCT-2001.  
 PD  
 XX 06-APR-2001; 2001WO-IB000713.  
 PF  
 XX 07-APR-2000; 2000DE-01019173.  
 XX  
 PR (EPIG-) EPIGENOMICS AG.  
 XX  
 XX Olek A, Piepenbrock C, Berlin K;  
 PI  
 XX WPI; 2001-657177/75.  
 XX  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 PT  
 XX Claim 1; SEQ ID NO 79607; 29pp + Sequence Listing; German.  
 PS  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 CC  
 XX Sequence 13 BP; 1 A; 0 C; 6 G; 6 T; 0 U; 0 Other;  
 SQ  
 Query Match 1.2%; Score 13; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1802 GTGTGTGTGTGTGT 1814  
 DB 1 GTGTGTGTGTGTGT 13  
 RESULT 422  
 ABC05126  
 ID ABC05126 standard; DNA; 13 BP.  
 XX  
 AC ABC05126;  
 XX  
 XX 20-FEB-2002 (first entry)  
 DT  
 XX Oligonucleotide SEQ ID NO 5117 for detecting SNP TSC0001771.  
 DE  
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX Homo sapiens.  
 OS  
 XX WO200177384-A2.  
 FN  
 XX 18-OCT-2001.  
 PD  
 XX 06-APR-2001; 2001WO-IB000713.  
 PF  
 XX 07-APR-2000; 2000DE-01019173.  
 XX  
 PR This invention describes novel oligonucleotide primers or peptide nucleic

PA (EPIG-) EPIGENOMICS AG.  
 XX Olek A, Piepenbrock C, Berlin K;  
 XX  
 XX WPI; 2001-657177/75.  
 XX  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 PT  
 XX Claim 1; SEQ ID NO 5117; 29pp + Sequence Listing; German.  
 PS  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 CC  
 XX Sequence 13 BP; 0 A; 0 C; 6 G; 7 T; 0 U; 0 Other;  
 SQ  
 Query Match 1.2%; Score 13; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1793 TGTGTGTGTGTGT 1805  
 DB 1 TGTGTGTGTGTGT 13  
 RESULT 423  
 ABF37478  
 ID ABF37478 standard; DNA; 13 BP.  
 XX  
 AC ABF37478;  
 XX  
 XX 21-FEB-2002 (first entry)  
 DT  
 XX Oligonucleotide SEQ ID NO 137475 for detecting SNP TSC0034363.  
 DE  
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX Homo sapiens.  
 OS  
 XX WO200177384-A2.  
 FN  
 XX 18-OCT-2001.  
 PD  
 XX 06-APR-2001; 2001WO-IB000713.  
 PF  
 XX 07-APR-2000; 2000DE-01019173.  
 XX  
 PR (EPIG-) EPIGENOMICS AG.  
 XX  
 XX Olek A, Piepenbrock C, Berlin K;  
 PI  
 XX WPI; 2001-657177/75.  
 XX  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 PT  
 XX Claim 1; SEQ ID NO 137475; 29pp + Sequence Listing; German.  
 PS  
 XX This invention describes novel oligonucleotide primers or peptide nucleic

CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX

XX Sequence 13 BP; 1 A; 0 C; 1 G; 11 T; 0 U; 0 Other;

Query Match 1.2%; Score 13; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1869 TATTTTGTGTTT 1881

Db 1 TATTTTGTGTTT 13

RESULT 424

ABF96134

ID ABF96134 standard; DNA; 13 BP.

XX AC ABF96134;

XX DT 22-FEB-2002 (first entry)

XX DE Oligonucleotide SEQ ID NO 196131 for detecting SNP TSC0048267.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX FA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX DR WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.

XX Claim 1; SEQ ID NO 196131; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX

XX Sequence 13 BP; 3 A; 0 C; 3 G; 7 T; 0 U; 0 Other;

Query Match 1.2%; Score 13; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2202 TTATTTGTTGAGA 2214

Db 1 TTATTTGTTGAGA 13

RESULT 425

ABH13186

ID ABH13186 standard; DNA; 13 BP.

XX AC ABH13186;

XX DT 22-FEB-2002 (first entry)

XX DE Oligonucleotide SEQ ID NO 213163 for detecting SNP TSC0010105.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX DR WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.

XX Claim 1; SEQ ID NO 213163; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX

XX Sequence 13 BP; 5 A; 0 C; 0 G; 8 T; 0 U; 0 Other;

Query Match 1.2%; Score 13; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1768 TTTTAAATTTA 1780

Db 1 TTTTAAATTTA 13

RESULT 426

ABF90362/C

ID ABF90362 standard; DNA; 13 BP.

XX ABF90362;  
AC  
XX  
DT 22-FEB-2002 (first entry)  
XX  
XX  
DE Oligonucleotide SEQ ID NO 190359 for detecting SNP TSC0046817.  
XX  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
XX Homo sapiens.  
XX  
XX  
XX WO200177384-A2.  
XX  
XX 18-OCT-2001.  
XX  
XX  
XX 06-APR-2001; 2001WO-IB000713.  
XX  
XX  
XX 07-APR-2000; 2000DE-01019173.  
XX  
XX (EPIG-) EPIGENOMICS AG.  
XX  
XX Olek A, Piepenbrock C, Berlin K;  
XX  
XX WPI; 2001-657177/75.  
XX  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
XX designed to detect single-nucleotide polymorphisms and cytosine  
XX methylation status.  
XX  
XX Claim 1; SEQ ID NO 190359; 29pp + Sequence Listing; German.  
XX  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
XX and cytosine methylation status in chemically pretreated genomic DNA. The  
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
XX range of diseases including immune system, gastrointestinal, respiratory,  
XX central nervous system, cardiovascular and metabolic disorders. The  
XX oligomers are also used for detecting cell type differentiation. ABC00010  
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073  
XX represent the oligomers described in the invention. NOTE: The sequence  
XX data for this patent did not form part of the printed specification, but  
XX was obtained in electronic format from WIPO at  
XX ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX SQ Sequence 13 BP; 9 A; 0 C; 1 G; 3 T; 0 U; 0 Other;  
XX  
XX Query Match 1.2%; Score 13; DB 1; Length 13;  
XX Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX  
XX 2266 TATTTTTCCTATA 2278  
XX 13 TATTTTTCCTATA 1  
XX  
XX  
XX RESULT 427  
XX ABH60366  
XX ID ABH60366 standard; DNA; 13 BP.  
XX  
XX AC ABH60366;  
XX  
XX  
XX 22-FEB-2002 (first entry)  
XX  
XX Oligonucleotide SEQ ID NO 260343 for detecting SNP TSC0063217.  
XX  
XX  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
XX Homo sapiens.  
XX

PN WO200177384-A2.  
XX  
XX 18-OCT-2001.  
XX  
XX 06-APR-2001; 2001WO-IB000713.  
XX  
XX 07-APR-2000; 2000DE-01019173.  
XX  
XX (EPIG-) EPIGENOMICS AG.  
XX  
XX Olek A, Piepenbrock C, Berlin K;  
XX  
XX WPI; 2001-657177/75.  
XX  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
XX designed to detect single-nucleotide polymorphisms and cytosine  
XX methylation status.  
XX  
XX Claim 1; SEQ ID NO 260343; 29pp + Sequence Listing; German.  
XX  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
XX and cytosine methylation status in chemically pretreated genomic DNA. The  
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
XX range of diseases including immune system, gastrointestinal, respiratory,  
XX central nervous system, cardiovascular and metabolic disorders. The  
XX oligomers are also used for detecting cell type differentiation. ABC00010  
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073  
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XX was obtained in electronic format from WIPO at  
XX ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX SQ Sequence 13 BP; 5 A; 0 C; 1 G; 7 T; 0 U; 0 Other;  
XX  
XX Query Match 1.2%; Score 13; DB 1; Length 13;  
XX Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX  
XX 1765 GATTTTAAAAAT 1777  
XX 1 GATTTTAAAAAT 13  
XX  
XX  
XX RESULT 428  
XX ABC28588  
XX ID ABC28588 standard; DNA; 13 BP.  
XX  
XX AC ABC28588;  
XX  
XX  
XX 20-FEB-2002 (first entry)  
XX  
XX Oligonucleotide SEQ ID NO 28605 for detecting SNP TSC0008245.  
XX  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
XX Homo sapiens.  
XX  
XX WO200177384-A2.  
XX  
XX 18-OCT-2001.  
XX  
XX 06-APR-2001; 2001WO-IB000713.  
XX  
XX 07-APR-2000; 2000DE-01019173.  
XX  
XX (EPIG-) EPIGENOMICS AG.  
XX  
XX Olek A, Piepenbrock C, Berlin K;  
XX  
XX WPI; 2001-657177/75.  
XX

XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX Claim 1; SEQ ID NO 28605; 29pp + Sequence Listing; German.  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX SQ Sequence 13 BP; 6 A; 0 C; 1 G; 6 T; 0 U; 0 Other;  
 Query Match 1.2%; Score 13; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1818 ATATATATATGTA 1830  
 Db 1 ATATATATATGTA 13  
 RESULT 429  
 ABC13480/c  
 ID ABC13480 standard; DNA; 13 BP.  
 AC ABC13480;  
 AC ABC13480;  
 DT 20-FEB-2002 (first entry)  
 XX Oligonucleotide SEQ ID NO 13487 for detecting SNP TSC0003116.  
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX Homo sapiens.  
 OS WO200177384-A2.  
 PN 18-OCT-2001.  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX Claim 1; SEQ ID NO 13487; 29pp + Sequence Listing; German.  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX SQ Sequence 13 BP; 6 A; 0 C; 1 G; 6 T; 0 U; 0 Other;  
 Query Match 1.2%; Score 13; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1818 ATATATATATGTA 1830  
 Db 1 ATATATATATGTA 13  
 RESULT 429  
 ABC13480/c  
 ID ABC13480 standard; DNA; 13 BP.  
 AC ABC13480;  
 AC ABC13480;  
 DT 20-FEB-2002 (first entry)  
 XX Oligonucleotide SEQ ID NO 13487 for detecting SNP TSC0003116.  
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX Homo sapiens.  
 OS WO200177384-A2.  
 PN 18-OCT-2001.  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX Claim 1; SEQ ID NO 13487; 29pp + Sequence Listing; German.  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
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 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX SQ Sequence 13 BP; 6 A; 0 C; 1 G; 6 T; 0 U; 0 Other;  
 Query Match 1.2%; Score 13; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX SQ Sequence 13 BP; 9 A; 0 C; 0 G; 4 T; 0 U; 0 Other;  
 Query Match 1.2%; Score 13; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1767 TTTTAAAAATTT 1779  
 Db 13 TTTTAAAAATTT 1  
 RESULT 430  
 ABF48195/c  
 ID ABF48195 standard; DNA; 13 BP.  
 AC ABF48195;  
 AC ABF48195;  
 DT 21-FEB-2002 (first entry)  
 XX Oligonucleotide SEQ ID NO 148192 for detecting SNP TSC0037417.  
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX Homo sapiens.  
 OS WO200177384-A2.  
 PN 18-OCT-2001.  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX Claim 1; SEQ ID NO 148192; 29pp + Sequence Listing; German.  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX SQ Sequence 13 BP; 8 A; 0 C; 0 G; 5 T; 0 U; 0 Other;  
 Query Match 1.2%; Score 13; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



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QY 1766 ATTATTTAAATTT 1778
Db 13 ATTATTTAAATTT 1
RESULT 431
ABC43065/c
ID ABC43065 standard; DNA; 13 BP.
XX
AC ABC43065;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 43082 for detecting SNP TSC0012784.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIC-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 43082; 29pp + Sequence Listing; German.
XX
This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
Sequence 13 BP; 6 A; 5 C; 0 G; 2 T; 0 U; 0 Other;
XX
This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
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CC ftp.wipo.int/pub/published_pct_sequences
XX
Query Match 1.2%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1804 GTGTGTGTGTATA 1816
Db 13 GTGTGTGTGTATA 1
RESULT 432
ABC58806
ID ABC58806 standard; DNA; 13 BP.
XX
AC ABC58806;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 119127 for detecting SNP TSC0029745.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.

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DE Oligonucleotide SEQ ID NO 58923 for detecting SNP TSC0015758.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIC-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 58923; 29pp + Sequence Listing; German.
XX
This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
Sequence 13 BP; 1 A; 0 C; 5 G; 7 T; 0 U; 0 Other;
XX
Query Match 1.2%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1803 TGTGTGTGTAT 1815
Db 1 TGTGTGTGTAT 13
RESULT 433
ABF19130
ID ABF19130 standard; DNA; 13 BP.
XX
AC ABF19130;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 119127 for detecting SNP TSC0029745.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.

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XX 07-APR-2000; 2000DE-01019173.  
XX (EPIG-) EPIGENOMICS AG.  
XX Olek A, Piepenbrock C, Berlin K;  
XX WPI; 2001-657177/75.  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
XX designed to detect single-nucleotide polymorphisms and cytosine  
XX methylation status.  
XX Claim 1; SEQ ID NO 119127; 29pp + Sequence Listing; German.  
XX  
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XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
XX and cytosine methylation status in chemically pretreated genomic DNA. The  
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XX central nervous system, cardiovascular and metabolic disorders. The  
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XX  
XX Sequence 13 BP; 6 A; 0 C; 1 G; 6 T; 0 U; 0 Other;  
XX  
XX Query Match 1.2%; Score 13; DB 1; Length 13;  
XX Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 1816 ATATATATATATG 1828  
DB 1 ATATATATATATG 13  
|||||  
RESULT 434  
ID ABH60367/c  
XX ABH60367 standard; DNA; 13 BP.  
XX  
XX ABH60367;  
XX  
XX 22-FEB-2002 (first entry)  
XX  
XX Oligonucleotide SEQ ID NO 260344 for detecting SNP TSC0063217.  
XX  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
XX Homo sapiens.  
XX  
XX WO200177384-A2.  
XX  
XX 18-OCT-2001.  
XX  
XX 06-APR-2001; 2001WO-IB000713.  
XX  
XX 07-APR-2000; 2000DE-01019173.  
XX  
XX (EPIG-) EPIGENOMICS AG.  
XX  
XX Olek A, Piepenbrock C, Berlin K;  
XX  
XX WPI; 2001-657177/75.  
XX  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
XX designed to detect single-nucleotide polymorphisms and cytosine  
XX methylation status.

PS Claim 1; SEQ ID NO 260344; 29pp + Sequence Listing; German.  
XX  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
XX and cytosine methylation status in chemically pretreated genomic DNA. The  
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
XX range of diseases including immune system, gastrointestinal, respiratory,  
XX central nervous system, cardiovascular and metabolic disorders. The  
XX oligomers are also used for detecting cell type differentiation. ABC00010  
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073  
XX represent the oligomers described in the invention. NOTE: The sequence  
XX data for this patent did not form part of the printed specification, but  
XX was obtained in electronic format from WIPO at  
XX ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX Sequence 13 BP; 7 A; 1 C; 0 G; 5 T; 0 U; 0 Other;  
XX  
XX Query Match 1.2%; Score 13; DB 1; Length 13;  
XX Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 1765 GATTTTAAAAAT 1777  
DB 13 GATTTTAAAAAT 1  
|||||  
RESULT 435  
ID ABC29728  
XX ABC29728 standard; DNA; 13 BP.  
XX  
XX ABC29728;  
XX  
XX 20-FEB-2002 (first entry)  
XX  
XX Oligonucleotide SEQ ID NO 29745 for detecting SNP TSC0008989.  
XX  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
XX Homo sapiens.  
XX  
XX WO200177384-A2.  
XX  
XX 18-OCT-2001.  
XX  
XX 06-APR-2001; 2001WO-IB000713.  
XX  
XX 07-APR-2000; 2000DE-01019173.  
XX  
XX (EPIG-) EPIGENOMICS AG.  
XX  
XX Olek A, Piepenbrock C, Berlin K;  
XX  
XX WPI; 2001-657177/75.  
XX  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
XX designed to detect single-nucleotide polymorphisms and cytosine  
XX methylation status.  
XX  
XX Claim 1; SEQ ID NO 29745; 29pp + Sequence Listing; German.  
XX  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
XX and cytosine methylation status in chemically pretreated genomic DNA. The  
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
XX range of diseases including immune system, gastrointestinal, respiratory,  
XX central nervous system, cardiovascular and metabolic disorders. The  
XX oligomers are also used for detecting cell type differentiation. ABC00010  
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073  
XX represent the oligomers described in the invention. NOTE: The sequence  
XX data for this patent did not form part of the printed specification, but  
XX was obtained in electronic format from WIPO at

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CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 0 A; 0 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 1.2%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1794 GTGTGTGTGTGTG 1806
Db 1 GTGTGTGTGTGTG 13

RESULT 436
ABC91692
ID ABC91692 standard; DNA; 13 BP.
XX
AC ABC91692;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 91709 for detecting SNP TSC0022946.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
WPI; 2001-657177/75.
XX
DR Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 91709; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 4 A; 0 C; 2 G; 7 T; 0 U; 0 Other;

Query Match 1.2%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2259 AAGTGATATTTT 2271
Db 1 AAGTGATATTTT 13

RESULT 437
ABF04284
ID ABF04284 standard; DNA; 13 BP.
XX
AC ABF04284;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 104281 for detecting SNP TSC0026066.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
WPI; 2001-657177/75.
XX
DR Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 104281; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 3 A; 0 C; 3 G; 7 T; 0 U; 0 Other;

Query Match 1.2%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1849 TAAAGTTGTTGT 1861
Db 1 TAAAGTTGTTGT 13

RESULT 438
ABC55254
ID ABC55254 standard; DNA; 13 BP.
XX
AC ABC55254;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 55271 for detecting SNP TSC0015107.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
```

XX OS Homo sapiens.  
 XX PN WO200177384-A2.  
 XX PD 18-OCT-2001.  
 XX XX  
 XX PF 06-APR-2001; 2001WO-IB000713.  
 XX PR 07-APR-2000; 2000DE-01019173.  
 XX PA (EPIG-) EPIGENOMICS AG.  
 XX PI Olek A, Piepenbrock C, Berlin K;  
 XX PI WPI; 2001-657177/75.  
 XX DR  
 XX XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX PS Claim 1; SEQ ID NO 55271; 29pp + Sequence Listing; German.  
 XX CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABG9989, ABF00010-ABF9989, ABH00010-ABH9989 and AB100010-AB182073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX SQ Sequence 13 BP; 6 A; 0 C; 0 G; 7 T; 0 U; 0 Other;  
 Query Match 1.2%; Score 13; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1771 TTAATAATTTATAT 1783  
 DB 1 TTAATAATTTATAT 13  
 RESULT 439  
 ABF06850  
 ID ABF06850 standard; DNA; 13 BP.  
 AC ABF06850;  
 XX AC  
 XX DT 21-FEB-2002 (first entry)  
 XX DE Oligonucleotide SEQ ID NO 106847 for detecting SNP TSC0026750.  
 XX SN; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX OS Homo sapiens.  
 XX PN WO200177384-A2.  
 XX PD 18-OCT-2001.  
 XX PF 06-APR-2001; 2001WO-IB000713.  
 XX PR 07-APR-2000; 2000DE-01019173.  
 XX PA (EPIG-) EPIGENOMICS AG.  
 XX PI Olek A, Piepenbrock C, Berlin K;  
 XX PI WPI; 2001-657177/75.  
 XX DR  
 XX XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX PS Claim 1; SEQ ID NO 55271; 29pp + Sequence Listing; German.  
 XX CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABG9989, ABF00010-ABF9989, ABH00010-ABH9989 and AB100010-AB182073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX SQ Sequence 13 BP; 6 A; 0 C; 0 G; 7 T; 0 U; 0 Other;  
 Query Match 1.2%; Score 13; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1771 TTAATAATTTATAT 1783  
 DB 1 TTAATAATTTATAT 13  
 RESULT 439  
 ABF06850  
 ID ABF06850 standard; DNA; 13 BP.  
 AC ABF06850;  
 XX AC  
 XX DT 21-FEB-2002 (first entry)  
 XX DE Oligonucleotide SEQ ID NO 106847 for detecting SNP TSC0026750.  
 XX SN; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX OS Homo sapiens.  
 XX PN WO200177384-A2.  
 XX PD 18-OCT-2001.  
 XX PF 06-APR-2001; 2001WO-IB000713.  
 XX PR 07-APR-2000; 2000DE-01019173.  
 XX PA (EPIG-) EPIGENOMICS AG.  
 XX PI Olek A, Piepenbrock C, Berlin K;  
 XX PI WPI; 2001-657177/75.  
 XX DR  
 XX XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX PS Claim 1; SEQ ID NO 55271; 29pp + Sequence Listing; German.  
 XX CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABG9989, ABF00010-ABF9989, ABH00010-ABH9989 and AB100010-AB182073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX SQ Sequence 13 BP; 6 A; 0 C; 0 G; 7 T; 0 U; 0 Other;

PI Olek A, Piepenbrock C, Berlin K;  
 XX WPI; 2001-657177/75.  
 XX XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX PS Claim 1; SEQ ID NO 106847; 29pp + Sequence Listing; German.  
 XX CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABG9989, ABF00010-ABF9989, ABH00010-ABH9989 and AB100010-AB182073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX SQ Sequence 13 BP; 2 A; 0 C; 1 G; 10 T; 0 U; 0 Other;  
 Query Match 1.2%; Score 13; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1871 TTTTGTGTTTAA 1883  
 DB 1 TTTTGTGTTTAA 13  
 RESULT 440  
 ABC82325/c  
 ID ABC82325 standard; DNA; 13 BP.  
 AC ABC82325;  
 XX AC  
 XX DT 21-FEB-2002 (first entry)  
 XX DE Oligonucleotide SEQ ID NO 82342 for detecting SNP TSC0020792.  
 XX SN; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX OS Homo sapiens.  
 XX PN WO200177384-A2.  
 XX PD 18-OCT-2001.  
 XX PF 06-APR-2001; 2001WO-IB000713.  
 XX PR 07-APR-2000; 2000DE-01019173.  
 XX PA (EPIG-) EPIGENOMICS AG.  
 XX PI Olek A, Piepenbrock C, Berlin K;  
 XX PI WPI; 2001-657177/75.  
 XX DR  
 XX XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX PS Claim 1; SEQ ID NO 82342; 29pp + Sequence Listing; German.  
 XX CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABG9989, ABF00010-ABF9989, ABH00010-ABH9989 and AB100010-AB182073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX SQ Sequence 13 BP; 2 A; 0 C; 1 G; 10 T; 0 U; 0 Other;

CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX Sequence 13 BP; 7 A; 1 C; 0 G; 5 T; 0 U; 0 Other;  
 SQ Query Match 1.2%; Score 13; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1778 TTATATTTGTAAT 1790  
 DB 13 TTATATTTGTAAT 1  
 RESULT 441  
 ABF38751/C  
 ID ABF38751 standard; DNA; 13 BP.  
 XX AC ABF38751;  
 XX DT 21-FEB-2002 (first entry)  
 DE Oligonucleotide SEQ ID NO 138748 for detecting SNP TSC0034761.  
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX Homo sapiens.  
 XX WO200177384-A2.  
 XX PD 18-OCT-2001.  
 XX PF 06-APR-2001; 2001WO-IB000713.  
 XX PR 07-APR-2000; 2000DE-01019173.  
 XX PA (EPIC-) EPIGENOMICS AG.  
 XX PI Olek A, Piepenbrock C, Berlin K;  
 XX WPI; 2001-657177/75.  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX Claim 1; SEQ ID NO 138748; 29pp + Sequence Listing; German.  
 CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX Sequence 13 BP; 7 A; 1 C; 0 G; 5 T; 0 U; 0 Other;  
 SQ Query Match 1.2%; Score 13; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1817 TATATATATATGT 1829  
 DB 13 TATATATATATGT 1  
 RESULT 442  
 ABF61494  
 ID ABF61494 standard; DNA; 13 BP.  
 XX AC ABF61494;  
 XX DT 22-FEB-2002 (first entry)  
 DE Oligonucleotide SEQ ID NO 161491 for detecting SNP TSC0040647.  
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX Homo sapiens.  
 XX WO200177384-A2.  
 XX PD 18-OCT-2001.  
 XX PF 06-APR-2001; 2001WO-IB000713.  
 XX PR 07-APR-2000; 2000DE-01019173.  
 XX PA (EPIC-) EPIGENOMICS AG.  
 XX PI Olek A, Piepenbrock C, Berlin K;  
 XX WPI; 2001-657177/75.  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX Claim 1; SEQ ID NO 161491; 29pp + Sequence Listing; German.  
 CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX Sequence 13 BP; 1 A; 0 C; 1 G; 11 T; 0 U; 0 Other;  
 SQ Query Match 1.2%; Score 13; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1865 TTTTATTTTGT 1877  
 DB 1 TTTTATTTTGT 13  
 RESULT 443  
 ABH13187/C  
 ID ABH13187 standard; DNA; 13 BP.  
 XX AC ABH13187;  
 Query Match 1.2%; Score 13; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
PS Claim 1; SEQ ID NO 196132; 29pp + Sequence Listing; German.  
XX

CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABG99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

XX  
SQ Sequence 13 BP; 7 A; 3 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 1.2%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2202 TTATTGTGAGA 2214

Db 13 TTATTGTGAGA 1

#### RESULT 446

ABF61049/C  
ID ABF61049 standard; DNA; 13 BP.

XX AC  
XX ABF61049;

DT 22-FEB-2002 (first entry)

DE Oligonucleotide SEQ ID NO 161046 for detecting SNP TSC0040548.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX Homo sapiens.

XX WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.

XX Claim 1; SEQ ID NO 161046; 29pp + Sequence Listing; German.

CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABG99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073

CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

XX  
SQ Sequence 13 BP; 7 A; 1 C; 0 G; 5 T; 0 U; 0 Other;

Query Match 1.2%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1774 AAATTATATGTT 1786

Db 13 AAATTATATGTT 1

#### RESULT 447

ABK70590  
ID ABK70590 standard; DNA; 13 BP.

XX AC  
XX ABK70590;

DT 15-JUL-2002 (first entry)

DE Ligand binding affinity determining oligonucleotide #32.

XX KW Ligand binding affinity; ss.

XX OS Synthetic.

XX US6355428-B1.

XX PD 12-MAR-2002.

XX PF 10-SEP-1999; 99US-00393783.

XX PR 11-SEP-1998; 98US-00151890.

XX PA (GENE-) GENELABS TECHNOLOGIES INC.

XX PI Schroth GP, Bruice TW, Suh YJ;

XX WPI; 2002-380936/41.

XX Determining relative affinity of ligands for oligonucleotides, from  
PT ability to separate a duplex of oligonucleotides, one labeled and the  
PT other having a signal modifying group.

XX Disclosure; Col 16; Sipp; English.

XX The invention relates to a method for determining the relative binding  
XX affinities of a ligand to different oligonucleotides. A mixture is formed  
XX from two oligonucleotides, one carrying a label and a second containing a  
XX group that alters the signal from the label, when the sequences  
XX hybridise. In the absence of the ligand, the oligonucleotides exist  
XX mainly in single-stranded form and the signal is recorded in this state.  
XX The ligand is then added and the signal measured again, and the effect  
XX compared with that observed for a different pair of oligos. The relative  
XX binding affinities of the ligands are determined by comparing their  
XX effects. Sequences ABK70559-ABK70529 represent oligonucleotides used for  
XX determining relative binding affinities of ligands

XX  
SQ Sequence 13 BP; 0 A; 0 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 1.2%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTG 1806

Db 1 GTGTGTGTGTGTG 13

```
RESULT 448
AAD45600
ID AAD45600 standard; DNA; 13 BP.
XX
XX
AC AAD45600;
XX
XX 27-DEC-2002 (first entry)
XX
XX Competitor oligo used in the invention #1.
XX
XX Competitive binding assay; binding affinity; ligand; indicator;
XX competitor; ss.
XX
XX Unidentified.
XX
XX US6420109-B1.
XX
XX 16-JUL-2002.
XX
XX 11-SEP-1998; 98US-00151890.
XX
XX 11-SEP-1998; 98US-00151890.
XX
XX (GENE-) GENELABS TECHNOLOGIES INC.
XX
XX Schroth GP, Bruce TW, Suh YJ;
XX
XX WPI; 2002-626078/67.
XX
XX New assay for determining relative binding affinities of a ligand to
XX different oligonucleotide sequences is useful to determine nucleic acid
XX binding specificities and base pair determinants of particularly ligands.
XX
XX Disclosure; Col 11; 32pp; English.
XX
XX The invention relates to methods for determining relative binding
XX affinities of a ligand to different oligonucleotide sequences, using
XX indicator oligonucleotide pairs having a signal and a signal-altering
XX group attached in direct or competitive binding assays. The method is
XX used to determine nucleic acid binding specificities and base pair
XX determinants of particular ligands. The present sequence is a competitor
XX oligonucleotide used to illustrate the method of the invention
XX
XX Sequence 13 BP; 0 A; 0 C; 7 G; 6 T; 0 U; 0 Other;
XX
Query Match 1.2%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTG 1806
Db 1 GTGTGTGTGTGTG 13

RESULT 449
ABX79758
ID ABX79758 standard; cDNA; 15 BP.
XX
XX
AC ABX79758;
XX
XX 17-APR-2003 (first entry)
XX
XX EST polymorphic DNA repeat polynucleotide #83.
XX
XX EST; expressed sequence tag; ss; polymorphic repeat; tandem repeat;
XX polymorphic marker prediction of ubiquitous simple sequences; POMPOUS;
XX Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;
XX Haw River syndrome; Huntington's disease; fragile-X syndrome;
XX Friedrich's ataxia; myotonic dystrophy; hyperandrogenaemia;
XX spinal atrophy; bulbar atrophy; spinocerebellar ataxia.
XX
XX Homo sapiens.
XX
XX

RESULT 450
AAT55014/c
ID AAT55014 standard; RNA; 15 BP.
XX
XX
AC AAT55014;
XX
XX 25-MAR-2003 (revised)
XX 18-APR-1997 (first entry)
XX
XX Human rela hammerhead ribozyme target sequence (nt. position 562).
XX
XX Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
XX gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
XX intercellular adhesion molecule; rel A; tumor necrosis factor;
XX TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
XX translocation; chronic myelogenous leukaemia; CML; cancer;
XX Philadelphia chromosome; inflammation; autoimmune disease;
XX atherosclerosis; myocardial infarction; stroke; restenosis;
XX transplant rejection; rheumatoid arthritis; psoriasis;
XX myocardial ischaemia; Kawasaki disease; septic shock; HIV;
XX human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
XX
XX Homo sapiens.
XX
XX

US6472154-B1.
XX
XX 29-OCT-2002.
XX
XX 31-DEC-1999; 99US-00475947.
XX
XX 31-DEC-1999; 99US-00475947.
XX
XX (TEXA ) UNIV TEXAS SYSTEM.
XX
XX Garner HR, Wren JD, Minna JD, Fondon JW;
XX
XX WPI; 2003-208818/20.
XX
XX Identifying a candidate polymorphic repeat within a coding sequence, for
XX understanding or treating genetic disease, comprises detecting tandem
XX repeats in a target coding sequence and scoring the repeats for
XX polymorphic probability.
XX
XX Example; Col 309; 588pp; English.
XX
XX The invention discloses a method for identifying a candidate polymorphic
XX repeat within a coding sequence (expressed sequence tag, EST), which
XX comprises detecting tandem repeats in a target coding sequence, scoring
XX the repeats for polymorphic probability and generating a dataset
XX correlating the repeats with polymorphic probability to identify a
XX candidate polymorphic repeat. The computational methods (polymorphic,
XX marker prediction of ubiquitous simple sequences, POMPOUS, and Rep-X) are
XX useful for identifying and detecting candidate polymorphic repeats in
XX human genes, which can be used to understand, treat or eliminate genetic
XX diseases, predispositions or adverse drug-treatment reactions. Examples
XX of diseases linked to nucleotide repeats are Machado-Joseph, Haw River
XX syndrome, Huntington's disease, fragile-X syndrome, Friedrich's ataxia,
XX myotonic dystrophy, hyperandrogenaemia, spinal and bulbar atrophy and
XX spinocerebellar ataxia. The sequences presented in ABX79676-ABX80022 are
XX the polymorphic repeats identified for a search of human ESTs
XX
XX Sequence 15 BP; 9 A; 0 C; 0 G; 6 T; 0 U; 0 Other;
XX
Query Match 1.2%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1814 ATATATATATATA 1826
Db 1 ATATATATATATA 13

RESULT 450
AAT55014/c
ID AAT55014 standard; RNA; 15 BP.
XX
XX
AC AAT55014;
XX
XX 25-MAR-2003 (revised)
XX 18-APR-1997 (first entry)
XX
XX Human rela hammerhead ribozyme target sequence (nt. position 562).
XX
XX Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
XX gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
XX intercellular adhesion molecule; rel A; tumor necrosis factor;
XX TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
XX translocation; chronic myelogenous leukaemia; CML; cancer;
XX Philadelphia chromosome; inflammation; autoimmune disease;
XX atherosclerosis; myocardial infarction; stroke; restenosis;
XX transplant rejection; rheumatoid arthritis; psoriasis;
XX myocardial ischaemia; Kawasaki disease; septic shock; HIV;
XX human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
XX
XX Homo sapiens.
XX
XX
```



PN WO9523225-A2.  
XX 31-AUG-1995.  
XX 23-FEB-1995; 95WO-IB000156.  
XX 23-FEB-1994; 94US-00201109.  
XX 29-MAR-1994; 94US-00218934.  
XX 04-APR-1994; 94US-00222795.  
XX 07-APR-1994; 94US-00224483.  
XX 15-APR-1994; 94US-00227958.  
XX 18-APR-1994; 94US-00228041.  
XX 18-MAY-1994; 94US-00245736.  
XX 06-JUL-1994; 94US-00271280.  
XX 16-AUG-1994; 94US-00291433.  
XX 17-AUG-1994; 94US-00292620.  
XX 19-AUG-1994; 94US-00293520.  
XX 02-SEP-1994; 94US-00300000.  
XX 08-SEP-1994; 94US-00303039.  
XX 23-SEP-1994; 94US-00311486.  
XX 28-SEP-1994; 94US-00311749.  
XX 03-OCT-1994; 94US-00314397.  
XX 07-OCT-1994; 94US-00316771.  
XX 11-OCT-1994; 94US-00319492.  
XX 04-NOV-1994; 94US-00321993.  
XX 10-NOV-1994; 94US-00324847.  
XX 28-NOV-1994; 94US-00337608.  
XX 16-DEC-1994; 94US-00345516.  
XX 23-DEC-1994; 94US-00357577.  
XX 30-JAN-1995; 94US-00363233.  
XX 95US-00380734.  
XX (RIBO-) RIBOZYME PHARM INC.  
XX Stinchcomb DT, Chowrira B, Drenzo A, Draper KG, Dudycz LW;  
XX Grimm S, Karpeisky A, Kisch K, Matulic-Adamic J, Mcswiggen JA;  
XX Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;  
XX Tracz D, Usman N, Wincott FE, Woolf T;  
XX WPI; 1995-351090/45.  
XX Ribozyms having modified bases and methods for producing them - for use  
XX in inhibiting disease related genes.  
XX Claim 2; Page 228; 407pp; English.  
XX The present sequence represents a preferred target sequence for an  
XX enzymatic nucleic acid (i.e. a ribozyme) which cleaves relA mRNA at the  
XX nucleotide base position indicated in the DE line. The relA gene product  
XX is a subunit of the transcriptional regulator NF-kappaB and is implicated  
XX specifically in the induction of inflammatory responses. Regions of the  
XX mRNA that do not form secondary folding structures and that contain  
XX potential hammerhead and hairpin ribozyme cleavage sites were identified  
XX by computer analysis. Ribozymes directed against these mRNA sequences  
XX were designed and synthesised with modifications that improve their  
XX nuclease resistance. The ribozymes are designed to cleave the target  
XX sequences and thereby inhibit relA expression, making them potentially  
XX useful for treating rheumatoid arthritis, restenosis and asthma as well  
XX as for increasing tolerance to transplanted tissues. The potential  
XX immunosuppressive properties of a ribozyme that cleaves relA mRNA means  
XX that uses are limited to local delivery, acute indications or ex vivo  
XX treatment. (Updated on 25-MAR-2003 to correct PI field.)  
XX Sequence 15 BP; 2 A; 4 C; 4 G; 0 T; 5 U; 0 Other;  
XX Query Match 1.2%; Score 13; DB 1; Length 15;  
XX Best Local Similarity 100.0%; Pred. No. 3e+02;  
XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2152 TCACCTGGAGCA 2164  
DB 15 TCACCTGGAGCA 3

RESULT 451  
AAT54825/c  
ID AAT54825 standard; RNA; 15 BP.  
XX  
XX AAT54825;  
XX AC  
XX 25-MAR-2003 (revised)  
XX 07-APR-1997 (first entry)  
XX  
XX Mouse relA hammerhead ribozyme target sequence (nt. position 562).  
XX  
XX Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;  
XX gene expression; downregulation; interleukin-5; IL-5; ICAM-1;  
XX intercellular adhesion molecule; rel A; tumour necrosis factor;  
XX TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;  
XX translocation; chronic myelogenous leukaemia; CML; cancer;  
XX Philadelphia chromosome; inflammation; autoimmune disease;  
XX atherosclerosis; myocardial infarction; stroke; restenosis;  
XX myocardial rejection; rheumatoid arthritis; psoriasis;  
XX myocardial ischaemia; Kawasaki disease; septic shock; HIV;  
XX human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;  
XX ss.  
XX  
XX Mus musculus.  
XX OS  
XX WO9523225-A2.  
XX  
XX 31-AUG-1995.  
XX  
XX 23-FEB-1995; 95WO-IB000156.  
XX  
XX 23-FEB-1994; 94US-00201109.  
XX 29-MAR-1994; 94US-00218934.  
XX 04-APR-1994; 94US-00222795.  
XX 07-APR-1994; 94US-00224483.  
XX 15-APR-1994; 94US-00227958.  
XX 18-MAY-1994; 94US-00228041.  
XX 06-JUL-1994; 94US-00245736.  
XX 16-AUG-1994; 94US-00291433.  
XX 17-AUG-1994; 94US-00292620.  
XX 19-AUG-1994; 94US-00293520.  
XX 02-SEP-1994; 94US-00300000.  
XX 08-SEP-1994; 94US-00303039.  
XX 23-SEP-1994; 94US-00311486.  
XX 28-SEP-1994; 94US-00311749.  
XX 03-OCT-1994; 94US-00314397.  
XX 07-OCT-1994; 94US-00316771.  
XX 11-OCT-1994; 94US-00319492.  
XX 04-NOV-1994; 94US-00321993.  
XX 10-NOV-1994; 94US-00324847.  
XX 28-NOV-1994; 94US-00345516.  
XX 16-DEC-1994; 94US-00357577.  
XX 23-DEC-1994; 94US-00363233.  
XX 30-JAN-1995; 95US-00380734.  
XX (RIBO-) RIBOZYME PHARM INC.  
XX  
XX Stinchcomb DT, Chowrira B, Drenzo A, Draper KG, Dudycz LW;  
XX Grimm S, Karpeisky A, Kisch K, Matulic-Adamic J, Mcswiggen JA;  
XX Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;  
XX Tracz D, Usman N, Wincott FE, Woolf T;  
XX WPI; 1995-351090/45.  
XX Ribozyms having modified bases and methods for producing them - for use  
XX in inhibiting disease related genes.  
XX Claim 2; Page 225; 407pp; English.  
XX

XX The present sequence represents a preferred target sequence for an  
 CC enzymatic nucleic acid (i.e. a ribozyme) which cleaves relA mRNA at the  
 CC nucleotide base position indicated in the DE line. The relA gene product  
 CC is a subunit of the transcriptional regulator NF-kappaB and is implicated  
 CC specifically in the induction of inflammatory responses. Regions of the  
 CC mRNA that do not form secondary folding structures and that contain  
 CC potential hammerhead and hairpin ribozyme cleavage sites were identified  
 CC by computer analysis. Ribozymes directed against these mRNA sequences  
 CC were designed and synthesized with modifications that improve their  
 CC nuclease resistance. The ribozymes are designed to cleave the target  
 CC sequences and thereby inhibit relA expression, making them potentially  
 CC useful for treating rheumatoid arthritis, restenosis and asthma as well  
 CC as for increasing tolerance to transplanted tissues. The potential  
 CC immunosuppressive properties of a ribozyme that cleaves relA mRNA means  
 CC that uses are limited to local delivery, acute indications or ex vivo  
 CC treatment. (Updated on 25-MAR-2003 to correct PI field.)  
 XX  
 XX SQ Sequence 15 BP; 2 A; 4 C; 4 G; 0 T; 5 U; 0 Other;  
 Query Match 1.2%; Score 13; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 3e+02;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 2152 TCACCTGGAGCA 2164  
 Db 15 TCACCTGGAGCA 3  
 RESULT 452  
 AAT54971/C  
 ID AAT54971 standard; RNA; 15 BP.  
 XX  
 AC AAT54971;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 07-APR-1997 (first entry)  
 XX  
 DE Mouse relA hammerhead ribozyme target sequence (nt. position 1664).  
 XX  
 KW Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;  
 KW gene expression; downregulation; interleukin-5; IL-5; ICAM-1;  
 KW intercellular adhesion molecule; rel A; tumour necrosis factor;  
 KW TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;  
 KW translocation; chronic myelogenous leukaemia; CML; cancer;  
 KW Philadelphia chromosome; inflammation; autoimmune disease;  
 KW atherosclerosis; myocardial infarction; stroke; restenosis;  
 KW transplant rejection; rheumatoid arthritis; psoriasis;  
 KW myocardial ischaemia; Kawasaki disease; septic shock; HIV;  
 KW human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;  
 KW ss.  
 XX  
 OS Mus musculus.  
 XX  
 PN W09523225-A2.  
 XX  
 PD 31-AUG-1995.  
 XX  
 PF 23-FEB-1995; 95WO-IB000156.  
 XX  
 PR 23-FEB-1994; 94US-00201109.  
 PR 29-MAR-1994; 94US-00218934.  
 PR 04-APR-1994; 94US-00222795.  
 PR 07-APR-1994; 94US-00224483.  
 PR 15-APR-1994; 94US-00227958.  
 PR 15-APR-1994; 94US-00228041.  
 PR 18-MAY-1994; 94US-00245736.  
 PR 06-JUL-1994; 94US-00271280.  
 PR 15-AUG-1994; 94US-00291932.  
 PR 16-AUG-1994; 94US-00291433.  
 PR 17-AUG-1994; 94US-00292620.  
 PR 19-AUG-1994; 94US-00293520.  
 PR 02-SEP-1994; 94US-00300000.

PR 08-SEP-1994; 94US-00303039.  
 PR 23-SEP-1994; 94US-00311486.  
 PR 28-SEP-1994; 94US-00311749.  
 PR 03-OCT-1994; 94US-00314397.  
 PR 07-OCT-1994; 94US-00316771.  
 PR 11-OCT-1994; 94US-00319492.  
 PR 04-NOV-1994; 94US-00321993.  
 PR 10-NOV-1994; 94US-00334847.  
 PR 28-NOV-1994; 94US-00337608.  
 PR 16-DEC-1994; 94US-00345516.  
 PR 23-DEC-1994; 94US-00357577.  
 PR 30-JAN-1995; 94US-00363233.  
 XX  
 XX (RIBO-) RIBOZYME PHARM INC.  
 PI Stinchcomb DT, Chowira B, Dhirenzo A, Draper KG, Dudycz LW;  
 PI Grimm S, Karpeisky A, Kisich K, Matulic-Adamic J, Mcawiggen JA;  
 PI Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;  
 PI Tracz D, Usman N, Wincott FE, Woolf T;  
 XX WPT; 1995-35i090/45.  
 XX  
 XX Ribozymes having modified bases and methods for producing them - for use  
 PT in inhibiting disease related genes.  
 PS  
 PS Claim 2; Page 226; 407pp; English.  
 XX  
 CC The present sequence represents a preferred target sequence for an  
 CC enzymatic nucleic acid (i.e. a ribozyme) which cleaves relA mRNA at the  
 CC nucleotide base position indicated in the DE line. The relA gene product  
 CC is a subunit of the transcriptional regulator NF-kappaB and is implicated  
 CC specifically in the induction of inflammatory responses. Regions of the  
 CC mRNA that do not form secondary folding structures and that contain  
 CC potential hammerhead and hairpin ribozyme cleavage sites were identified  
 CC by computer analysis. Ribozymes directed against these mRNA sequences  
 CC were designed and synthesized with modifications that improve their  
 CC nuclease resistance. The ribozymes are designed to cleave the target  
 CC sequences and thereby inhibit relA expression, making them potentially  
 CC useful for treating rheumatoid arthritis, restenosis and asthma as well  
 CC as for increasing tolerance to transplanted tissues. The potential  
 CC immunosuppressive properties of a ribozyme that cleaves relA mRNA means  
 CC that uses are limited to local delivery, acute indications or ex vivo  
 CC treatment. (Updated on 25-MAR-2003 to correct PI field.)  
 XX  
 XX SQ Sequence 15 BP; 2 A; 4 C; 4 G; 0 T; 5 U; 0 Other;  
 Query Match 1.2%; Score 13; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 3e+02;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 2152 TCACCTGGAGCA 2164  
 Db 15 TCACCTGGAGCA 3  
 RESULT 453  
 AAZ90176  
 ID AAZ90176 standard; cDNA; 15 BP.  
 XX  
 AC AAZ90176;  
 XX  
 DT 19-MAY-2000 (first entry)  
 XX  
 DE 3-nitrotyrrole-containing primer.  
 XX  
 KW Chemokine receptor; interleukin-8 compound inhibitor; chromosome 7p22;  
 KW inflammation; wound healing; neutropenia; myeloid leukaemia; tumour;  
 KW toxin delivery; hypermegakaryocytopoietic disease; polycythemia vera;  
 KW primer; ss.  
 XX  
 OS Synthetic.  
 XX

PH Key modified\_base Location/Qualifiers  
 FT 8  
 FT /\*tag= a  
 FT /note= "Optionally A, T, G, C or 1-(2-deoxy-D-  
 FT riburanosyl)-3-nitropyrolole"  
 XX  
 XX WO200000515-A2.  
 XX  
 XX 06-JAN-2000.  
 XX  
 XX 29-JUN-1999; 99WO-US012829.  
 XX  
 XX 29-JUN-1998; 98US-00106800.  
 XX  
 XX 22-JAN-1999; 99US-00236166.  
 XX  
 XX (HYSE-) HYSEQ INC.  
 XX  
 XX WPI; 2000-170907/15.  
 XX  
 XX New nucleic acid encoding chemokine receptor, useful for diagnosis and  
 XX treatment of e.g. neutropenia, inflammation and leukemia.  
 XX  
 XX Example 2; Page 52; 138pp; English.  
 XX  
 XX This sequence represents a 3-nitropyrolole-containing primer which is used  
 XX in the course of the invention. The invention relates to a polynucleotide  
 XX sequence which encodes a human chemokine receptor. The nucleotide  
 XX sequence (see AA290174) is derived from a human foetal liver-spleen cDNA  
 XX library. The chemokine receptor (see AA78856) encoded by the nucleotide  
 XX sequence inhibits the activity of interleukin-8-type compounds through  
 XX competition for cell binding sites. The chemokine receptor gene is  
 XX located on the short arm of chromosome 7 at 7p22. The polynucleotide  
 XX encoding the chemokine receptor is useful as a hybridization probe or a  
 XX PCR primer. The nucleotide sequence may also be used for chromosome/gene  
 XX mapping or in the recombinant production of polypeptides and the  
 XX production of antisense or triplex-forming molecules for the control of  
 XX gene expression. The chemokine receptor polypeptides are used to raise  
 XX specific antibodies, also for purification, detection or modulation of  
 XX interleukin-8-type chemokines (for diagnosis or prognosis, or monitoring  
 XX chemokine recruitment at a site of infection or inflammation). The  
 XX protein sequence can also be used as molecular weight markers or food  
 XX supplements, and to screen compound libraries for specific binding  
 XX agents, potential agonists or antagonists. Antibodies raised against the  
 XX chemokine receptor polypeptide sequence are used to detect or purify the  
 XX polypeptide, also for the diagnosis and treatment of activated or  
 XX inflamed cells or tissues, and to promote the healing of wounds. The  
 XX polypeptide and antibodies are also used to prevent neutropenia  
 XX (associated with chemotherapy or radiation treatment to protect myeloid  
 XX precursors), inflammation or other immune responses; also conditions  
 XX associated with hyperproliferation of progenitor cells (e.g. some  
 XX myelogenous leukaemias, polycythaemia vera and hypermegakaryocytopenic  
 XX diseases). The antibodies are potentially useful therapeutically; e.g. to  
 XX carry toxins to tumour cells  
 XX  
 XX SQ Sequence 15 BP; 0 A; 2 C; 2 G; 10 T; 0 U; 1 Other;  
 Query Match 1.2%; Score 13; DB 1; Length 15;  
 Best Local Similarity 92.9%; Pred. No. 3e+02;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1863 CCCTTTTATTGTTT 1876  
 1 CCCTTTTATTGTTT 14  
 Db  
 RESULT 454  
 ABK55502  
 ID ABK55502 standard; DNA; 15 BP.  
 XX  
 XX AC ABK55502;  
 XX  
 XX 18-JUN-2002 (first entry)  
 XX

DE Selectin L Lymphocyte Adhesion Molecule 1 (SELL) oligonucleotide #38.  
 XX  
 XX Human; Selectin L Lymphocyte Adhesion Molecule 1; SELL;  
 KW neonatal pertussis; whooping cough; haplotyping; primer;  
 KW allele-specific oligonucleotide; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200216654-A1.  
 XX  
 XX 28-FEB-2002.  
 XX  
 XX 27-AUG-2001; 2001WO-US026675.  
 XX  
 XX 25-AUG-2000; 2000US-0228262P.  
 XX  
 XX (GENA-) GENAISSANCE PHARM INC.  
 XX  
 XX Anastasio AE, Bieglecki KM, Kliem SE, Koshiy B, Kumar AM;  
 XX WPI; 2002-292071/33.  
 XX  
 XX Novel genetic variants of selectin L lymphocyte adhesion molecule 1  
 XX (SELL) gene useful for therapeutic purposes and for expressing SELL  
 XX protein useful in identifying drugs to treat whooping cough.  
 XX  
 XX Claim 17; Page 14; 137pp; English.  
 XX  
 XX The invention relates to an isolated polynucleotide (I) comprising a  
 XX nucleotide sequence which is a polymorphic variant of a reference  
 XX sequence for Selectin L Lymphocyte Adhesion Molecule 1 (SELL) gene. SELL  
 XX polypeptide is useful for screening for drugs targeting the polypeptide.  
 XX Oligonucleotides derived from (I) are used to target SELL and a haplotype  
 XX or haplotype pair of SELL gene. These are useful in developing diagnostic  
 XX tests and therapeutic treatments for neonatal pertussis (whooping cough).  
 XX (I) is useful for studying the expression and function of SELL and  
 XX expressing SELL protein for use in screening for candidate drugs to treat  
 XX diseases related to SELL activity. The polymorphism and haplotype data  
 XX are useful for validating whether SELL is a suitable target for drugs to  
 XX treat whooping cough, screening for such drugs and reducing bias in  
 XX clinical trials of such drugs. Establishing the SELL haplotype or  
 XX haplotype pair of an individual is useful for improving the efficiency  
 XX and reliability of several steps in the discovery and development of  
 XX drugs for treating diseases associated with SELL activity e.g. neonatal  
 XX pertussis (whooping cough). The haplotyping method is useful to validate  
 XX SELL as a candidate target for treating a specific condition or disease  
 XX in screening for compounds targeting SELL to treat a specific condition  
 XX or disease predicted to be associated with SELL activity, e.g. detecting  
 XX which of the SELL haplotypes or haplotype pairs present in individual  
 XX members of a population with the specific disease of interest enables one  
 XX to screen for compounds that display the highest desired agonist or  
 XX antagonist activity for each of the most frequent SELL isoforms present  
 XX in the disease population. A polymorphic variant of SELL is useful in  
 XX studying the effect of the variation on the biological activity of SELL,  
 XX on the binding affinity of candidate drugs targeting SELL for the  
 XX treatment of neonatal pertussis (whooping cough) and in assays to measure  
 XX the binding affinities of one or more candidate drugs targeting the SELL  
 XX protein. ABK5545-ABK5559 represent SELL gene allele-specific  
 XX oligonucleotides of the invention  
 XX  
 XX SQ Sequence 15 BP; 2 A; 5 C; 4 G; 3 T; 0 U; 1 Other;  
 Query Match 1.2%; Score 13; DB 1; Length 15;  
 Best Local Similarity 86.7%; Pred. No. 3e+02;  
 Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1584 GCCCCAGTGCAGCT 1598  
 1 GCCCCAGTGCAGT 15  
 Db  
 RESULT 455

ACH50832  
ID ACH50832 standard; DNA; 15 BP.  
XX  
AC ACH50832;  
XX  
DT 13-OCT-2003 (first entry)  
XX  
XX 3-nitropyrrole containing oligonucleotide #1.  
DE  
XX  
KW Primer; ss; sequencing by hybridisation; SBH; 3-nitropyrrole;  
KW genome mapping; biodiversity; genetic disorder.  
XX  
OS Synthetic.  
XX  
XX US2003073623-A1.  
XX  
XX 17-APR-2003.  
XX  
XX 30-JUL-2001; 2001US-00918995.  
XX  
XX 30-JUL-2001; 2001US-00918995.  
XX  
XX (DRMA/) DRMANAC R T.  
XX (LABA/) LABAT I.  
XX (STAC/) STACHE-CRAIN B.  
XX (DICK/) DICKSON M C.  
XX (JONE/) JONES L W.  
XX  
XX Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;  
XX WPI; 2003-615964/58.  
XX  
XX New polynucleotide sequences obtained from various cDNA libraries, useful  
XX as hybridization probes, as oligomers for PCR, for chromosome and gene  
XX mapping, in the recombinant production of protein, or in generating  
XX antisense DNA or RNA.  
XX  
XX Example 2; Page 16; 44pp; English.  
XX  
XX The invention relates to an isolated polynucleotide comprising any one of  
XX 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was  
XX determined by the technique of SBH (sequencing by hybridisation). Also  
XX included is a purified polypeptide comprising a sequence corresponding to  
XX a reading frame of the novel polynucleotide. The nucleic acid sequences  
XX are useful in diagnostics as expressed sequence tags (EST) for  
XX identifying expressed genes or for physical mapping of the human genome,  
XX in forensics, in assessing biodiversity, or in identifying mutations  
XX responsible for genetic disorders and other traits. The nucleotide  
XX sequences are also useful as hybridisation probes, as oligomers for PCR,  
XX for chromosome and gene mapping, in the recombinant production of  
XX protein, or in generating antisense DNA or RNA. The purified polypeptide  
XX is useful for generating antibodies specific for it. The present sequence  
XX is an example of an oligonucleotide containing a 3-nitropyrrole base  
XX analogue which may be used in the SBH technique  
XX  
XX Sequence 15 BP; 0 A; 2 C; 2 G; 10 T; 0 U; 1 Other;  
SQ  
Query Match 1.2%; Score 13; DB 1; Length 15;  
Best Local Similarity 92.9%; Pred. No. 3e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1863 CCTTTTATTTTG 1876  
DB 1 CCTTTTNTTTTG 14  
RESULT 456  
ACH50832/c  
ID ACH50833 standard; DNA; 15 BP.  
XX  
AC ACH50833;  
XX  
DT 13-OCT-2003 (first entry)

XX  
DE 3-nitropyrrole containing oligonucleotide #2.  
XX  
KW Primer; ss; sequencing by hybridisation; SBH; 3-nitropyrrole;  
KW genome mapping; biodiversity; genetic disorder.  
XX  
OS Synthetic.  
XX  
XX US2003073623-A1.  
XX  
XX 17-APR-2003.  
XX  
XX 30-JUL-2001; 2001US-00918995.  
XX  
XX 30-JUL-2001; 2001US-00918995.  
XX  
XX (DRMA/) DRMANAC R T.  
XX (LABA/) LABAT I.  
XX (STAC/) STACHE-CRAIN B.  
XX (DICK/) DICKSON M C.  
XX (JONE/) JONES L W.  
XX  
XX Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;  
XX WPI; 2003-615964/58.  
XX  
XX New polynucleotide sequences obtained from various cDNA libraries, useful  
XX as hybridization probes, as oligomers for PCR, for chromosome and gene  
XX mapping, in the recombinant production of protein, or in generating  
XX antisense DNA or RNA.  
XX  
XX Example 2; Page 16; 44pp; English.  
XX  
XX The invention relates to an isolated polynucleotide comprising any one of  
XX 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was  
XX determined by the technique of SBH (sequencing by hybridisation). Also  
XX included is a purified polypeptide comprising a sequence corresponding to  
XX a reading frame of the novel polynucleotide. The nucleic acid sequences  
XX are useful in diagnostics as expressed sequence tags (EST) for  
XX identifying expressed genes or for physical mapping of the human genome,  
XX in forensics, in assessing biodiversity, or in identifying mutations  
XX responsible for genetic disorders and other traits. The nucleotide  
XX sequences are also useful as hybridisation probes, as oligomers for PCR,  
XX for chromosome and gene mapping, in the recombinant production of  
XX protein, or in generating antisense DNA or RNA. The purified polypeptide  
XX is useful for generating antibodies specific for it. The present sequence  
XX is an example of an oligonucleotide containing a 3-nitropyrrole base  
XX analogue which may be used in the SBH technique  
XX  
XX Sequence 15 BP; 10 A; 2 C; 2 G; 0 T; 0 U; 1 Other;  
SQ  
Query Match 1.2%; Score 13; DB 1; Length 15;  
Best Local Similarity 92.9%; Pred. No. 3e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1863 CCTTTTATTTTG 1876  
DB 15 CCTTTTNTTTTG 2  
RESULT 457  
ACF63345  
ID ACF63345 standard; DNA; 16 BP.  
XX  
AC ACF63345;  
XX  
XX 09-OCT-2003 (first entry)  
XX  
XX Human CD40L antisense oligonucleotide SEQ ID NO:67.  
XX  
XX Human; pharmacological; hypotensive; antilipaeamic; vasotropic; laxative;  
KW dermatological; antidepressant; tranquiliser; antiinflammatory; eczema;  
KW antiulcer; antimigraine; neuroprotective; antiparkinsonian; analgesic;

KW gynaecological; virucide; vulnary; antiarthritic; antipsoriatic; cold;  
 KW antimicrobial; cytostatic; litholytic; pathological disorder; depression;  
 KW abnormal appetite; hypertension; hypercholesterolaemia; hyperlipidaemia;  
 KW erectile dysfunction; anxiety; stress; inflammatory bowel syndrome;  
 KW ulcerative colitis; Crohn's disease; renal stone; gall stone; migraine;  
 KW constipation; headache; seizure; multiple sclerosis; polymyositis;  
 KW fibromyalgia; Parkinson's disease; amyotrophic lateral sclerosis; trauma;  
 KW chronic pain; pre-menstrual syndrome; sinusitis; carpal tunnel syndrome;  
 KW chronic fatigue syndrome; rosacea; arthritis; psoriasis; prostatitis;  
 KW inflammation; heart burn; infection; colon cancer; malignant melanoma;  
 KW skin disorder; antisense oligonucleotide; ss.

XX Homo sapiens.  
 OS Synthetic.

XX WO2003006478-A1.

XX 23-JAN-2003.

XX 10-JUL-2002; 2002WO-US021664.

XX 10-JUL-2001; 2001US-0303820P.

XX (OLIG-) OLIGOS ETC INC.

XX Dale RMK, Arrow A, Thompson T;

XX WPI; 2003-221709/21.

XX Composition with a modified oligonucleotide useful for treating a patient  
 PT with a pathological disorder such as abnormal appetite, hypertension,  
 PT eczema, anxiety, stress, and cancer.

XX Claim 17; Page 9; 173pp; English.

XX The present invention describes a composition (I) suitable for  
 CC administration in a mammal, which comprises a modified oligonucleotide  
 CC (I) of 7-75 nucleotides containing 7 or more contiguous ribose groups  
 CC linked by achiral 5'-3' internucleoside phosphate linkages, where the  
 CC modified oligonucleotide is complementary to a region of a gene  
 CC associated with a pathological disorder. Also described: (1) a  
 CC nutritional supplement comprising (II); and (2) a cosmetic composition  
 CC comprising (II), where the modified oligonucleotide is complementary to a  
 CC region of a gene associated with a skin disorder. (I) and (II) can have  
 CC hypotensive, antilipemic, vasotropic, dermatological, antidepressant,  
 CC tranquiliser, antiinflammatory, antitumor, laxative, antimigraine,  
 CC neuroprotective, antiparkinsonian, analgesic, gynaecological, virucide,  
 CC litholytic activities. (I) can be used for treating a patient with a  
 CC pathological disorder selected from abnormal appetite, hypertension,  
 CC hypercholesterolaemia, hyperlipidaemia, erectile dysfunction, eczema,  
 CC depression, anxiety, stress, inflammatory bowel syndrome, ulcerative  
 CC colitis, Crohn's disease, renal stones, gall stones, constipation, colds,  
 CC migraine headache, seizure multiple sclerosis, polymyositis, sinusitis,  
 CC fibromyalgia, Parkinson's disease, amyotrophic lateral sclerosis (ALS),  
 CC chronic pain, pre-menstrual syndrome, trauma, carpal tunnel syndrome,  
 CC chronic fatigue syndrome, rosacea, arthritis, psoriasis, prostatitis,  
 CC inflammation, heart burn, infection, poison ivy, colon cancer, malignant  
 CC melanoma, and malignant nasal polyps. The nutritional supplement is  
 CC useful for supplementing the diet of an individual, and the cosmetic  
 CC composition is useful for improving the appearance of the skin in an  
 CC individual with a skin disorder. ACF63279 to ACF63410 represent  
 CC nucleotide sequence given in the exemplification of the present invention

XX Sequence 16 BP; 4 A; 3 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 1.2%; Score 13; DB 1; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1688 TCACACTGTTTCAG 1700

DB 4 TCACACTGTTTCAG 16

RESULT 458

AAQ27968

ID AAQ27968 standard; DNA; 16 BP.

XX AAQ27968;

XX AC

DT 11-FEB-1993 (first entry)

DE Primer V810.

XX Polymerase chain reaction; PCR; amplify; Staphylococcus; ss.

XX Synthetic.

XX JP04211370-A.

XX 03-AUG-1992.

XX 19-FEB-1991; 91JP-00024633.

XX 20-FEB-1990; 90JP-00040398.

XX (SHIO) SHIONOGI & CO LTD.

XX WPI; 1992-304938/37.

XX Novel protease prepd. using Bacillus or Saccharomyces host - capable of  
 PT cleaving peptide bond at carboxyl terminus of glutamic acid residues in  
 PT polypeptide(s).

XX Disclosure; Page 4; 25pp; Japanese.

XX The sequences given in AAQ27960-86 are primers which were used in the  
 CC construction of the DNA encoding a Staphylococcus protease. The protease  
 CC (see also AAQ27987) specifically cleaves the peptide bond at the C-  
 CC terminus of the glutamic acid residue in polypeptide

XX Sequence 16 BP; 5 A; 0 C; 3 G; 8 T; 0 U; 0 Other;

Query Match 1.2%; Score 12.8; DB 1; Length 16;  
 Best Local Similarity 87.5%; Pred. No. 3.3e+02;  
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2200 GTTATTGTTGAGAG 2215

DB 1 GTTATTGTTAAAG 16

RESULT 459

AAQ07568/C

ID AAQ07568 standard; cDNA; 16 BP.

XX AAQ07568;

XX 21-JUN-1999 (first entry)

XX Homo sapiens fetal kidney clone AK647 secreted protein gene 3' end.

XX Secreted protein; fetal kidney; ds.

XX Homo sapiens.

XX WO9900405-A1.

XX 07-JAN-1999.

XX 29-JUN-1998; 98WO-US013530.

XX 30-JUN-1997; 97US-00685610.

XX (GEM) GENETICS INST INC.

XX Jacobs K, McCoy JM, Lavallie ER, Racie LA, Merberg D, Treacy M;  
 PI Evans C, Agostino MJ;  
 XX WPI; 1999-095671/08.  
 XX New polynucleotides encoding secreted human proteins - are derived from  
 PT foetal kidney or adult retina cDNA libraries, used as, e.g. potential  
 PT vaccines.  
 XX  
 XX Disclosure; Page 54; 76pp; English.  
 XX The sequence is that of the 3' end of a sequence encoding a secreted  
 CC protein from a human fetal kidney clone AX296. Such a sequence is  
 CC predicted to have biological activities which would make them suitable  
 CC for treating, preventing or ameliorating medical conditions in humans and  
 CC animals, although no supporting data is given. Suggested activities  
 CC include nutritional activity, cytokine and cell  
 CC proliferation/differentiation activity, immune stimulating (e.g. as  
 CC vaccines) or suppressing activity, haematopoiesis regulating activity,  
 CC tissue growth activity, activin/inhibin activity, and thrombolytic activity,  
 CC chemotactic/chemokinetic activity, haemostatic and thrombolytic activity,  
 CC receptor/ligand activity, anti-inflammatory activity, cadherin/tumour  
 CC invasion suppressor activity, and tumour inhibition activity. It is also  
 CC stated to be useful for gene therapy  
 XX  
 XX Sequence 16 BP; 16 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
 SQ  
 Query Match 1.2%; Score 12.8; DB 1; Length 16;  
 Best Local Similarity 87.5%; Pred. No. 3.3e+02;  
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1865 TTTTATTTTGTGTTT 1880  
 DB 16 TTTTATTTTGTGTTT 1  
 RESULT 460  
 AAZ98510/c  
 ID AAZ98510 standard; DNA; 16 BP.  
 XX  
 AC AAZ98510;  
 XX  
 DT 19-JUN-2000 (first entry)  
 XX  
 XX H. discus derived sequence #28.  
 DE  
 DE Satellite sequence; DNA fragmentation; microsatellite DNA; DNA marker;  
 KW Hallotis discus; ss.  
 XX  
 OS Hallotis discus.  
 XX  
 PN WO200011156-A1.  
 XX  
 PD 02-MAR-2000.  
 XX  
 XX 01-JUL-1999; 99WO-JP003551.  
 PF  
 XX 18-AUG-1998; 98JP-00232153.  
 PR  
 XX (NORQ) JAPAN MIN AGRIC FORESTRY & FISHERIES.  
 PA  
 XX Takahashi H, Sekino M;  
 PI  
 XX WPI; 2000-224692/19.  
 DR  
 XX Isolation of satellite sequences from genomic DNA for use as DNA markers  
 PT comprises isolating a library with high homogeneity by DNA fragmentation.  
 PT  
 XX Example 5; Page 15; 35pp; Japanese.  
 PS  
 XX The invention provides a novel method for isolation of satellite  
 CC sequences from genomic DNA that comprises fragmentation of the DNA by a

CC method which is not dependent on base sequences, then selection of the  
 CC satellite sequences from the obtained genomic library of high  
 CC homogeneity. The method is useful for the isolation of microsatellite DNA  
 CC sequences which can be used as DNA markers. The new method markedly  
 CC improves the efficiency of isolation of satellite sequences in comparison  
 CC to prior art methods which are reliant on base sequences. Sequences  
 CC AAZ98483-514 represent sequences from Hallotis discus, used in the method  
 CC of the invention  
 XX  
 SQ Sequence 16 BP; 8 A; 6 C; 2 G; 0 T; 0 U; 0 Other;  
 Query Match 1.2%; Score 12.8; DB 1; Length 16;  
 Best Local Similarity 87.5%; Pred. No. 3.3e+02;  
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1793 TGTGTGTGTGTGTGTG 1808  
 DB 16 TCTCTGTGTGTGTGTG 1  
 RESULT 461  
 AAC66068/c  
 ID AAC66068 standard; DNA; 16 BP.  
 XX  
 AC AAC66068;  
 XX  
 DT 22-FEB-2001 (first entry)  
 XX  
 XX DNA chip primer #4.  
 DE  
 XX DNA chip; primer; nucleoside derivative; photolabile protecting group;  
 KW photolithographic nucleic acid chip; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200061594-A2.  
 XX  
 PD 19-OCT-2000.  
 XX  
 XX 07-APR-2000; 2000WO-DE001148.  
 PF  
 XX 08-APR-1999; 99DE-01015867.  
 PR  
 XX 28-JAN-2000; 2000DE-01003631.  
 PR  
 XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.  
 PA  
 XX Beier M, Hoheisel J;  
 PI  
 XX WPI; 2000-679457/66.  
 DR  
 XX New nucleoside derivatives with photolabile protecting groups, useful in  
 PT oligonucleotide synthesis, particularly on solid phases, e.g. for  
 PT hybridization testing.  
 XX  
 PS Disclosure; Fig 9; 48pp; German.  
 XX  
 XX This invention describes nucleoside derivatives (I) with photolabile  
 CC protecting groups. (I) are used to synthesize oligonucleotides using the  
 CC photolithographic nucleic acid chip method, particularly where these are  
 CC intended for performing enzymatic reactions initiated from a free 3'-  
 CC hydroxy (especially solid-phase polymerase reactions or ligase reactions,  
 CC but also reverse transcription, cDNA synthesis etc.), also for  
 CC hybridization testing, sequencing and in DNA computing. (I) are produced  
 CC with high selectivity by reaction with a mild acylating agent that has  
 CC high specificity for the 3'-position, without significant side-reactions  
 CC (cf. more reactive acylating agents such as chloroformates)  
 XX  
 SQ Sequence 16 BP; 16 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
 Query Match 1.2%; Score 12.8; DB 1; Length 16;  
 Best Local Similarity 87.5%; Pred. No. 3.3e+02;  
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1865 TTTTATTTTGTGTTT 1880  
 Db 16 TTTTATTTTGTGTTT 1

RESULT 462  
 ABA04585  
 ID ABA04585 standard; DNA; 16 BP.  
 XX AC ABA04585;  
 XX DT 15-FEB-2002 (first entry)  
 XX DE Oligonucleotide #5.  
 XX KW Analytical support; genomic sequencing; mutation detection;  
 XX KW pharmaceutical development; ss.  
 XX OS Synthetic.  
 XX PH Key Location/Qualifiers  
 FT modified\_base 1 /\*tag= a  
 FT /mod\_base= OTHER  
 FT /note= "OTHER = Fl(CH2)6-PO-thymine, where Fl is flavine  
 FT and PO is a phosphate group"  
 XX PN FR2805348-A1.  
 XX PD 24-AUG-2001.  
 XX PF 23-FEB-2000; 2000FR-00002236.  
 XX PR 23-FEB-2000; 2000FR-00002236.  
 XX PA (COMS ) COMMISSARIAT ENERGIE ATOMIQUE.  
 XX PI Cuzin M, Peltie P, Fontecave M, Decout JL, Dueymes C;  
 XX DR WPI; 2001-628265/73.  
 XX Support for hybridization analysis of nucleic acids for sequencing  
 FT techniques, comprises an array of oligonucleotides having a label where  
 FT the fluorescence changes follow hybridization.  
 XX Example 1; Page 12; 33pp; French.  
 XX The present invention relates to an analytical support, to which a number  
 CC of oligonucleotides are fixed. The oligonucleotides are labelled with a  
 CC fluorescent compound, the fluorescence of which varies when the  
 CC oligonucleotide hybridises to its complement. The analytical support is  
 CC useful in hybridisation testing for identification of specific nucleic  
 CC acids, such as genomic sequencing, detecting mutations or pharmaceutical  
 CC development. The present oligonucleotide was used to illustrate the  
 CC invention  
 XX Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;  
 SQ Query Match 1.2%; Score 12.8; DB 1; Length 16;  
 Best Local Similarity 87.5%; Pred. No. 3.3e-02;  
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1865 TTTTATTTTGTGTTT 1880  
 Db 1 TTTTATTTTGTGTTT 16

RESULT 463  
 AAF30895  
 ID AAF30895 standard; DNA; 16 BP.  
 XX AC AAF30895;  
 XX DT 09-JUL-2001 (first entry)  
 XX DE Oligonucleotide portion of ODN-MGB-LF conjugate.  
 XX KW ODN-MGB-LF; oligonucleotide; minor groove binder; latent fluorophore;  
 XX KW hybridisation; detection; fluorescence; probe; ss.

DT 09-JUL-2001 (first entry)  
 XX Oligonucleotide-minor groove binder complex.  
 XX ODN-MGB-LF; oligonucleotide; minor groove binder; latent fluorophore;  
 KW hybridisation; detection; fluorescence; probe; ss.  
 XX OS Synthetic.  
 XX PH Key Location/Qualifiers  
 FT modified\_base 1 /\*tag= a  
 FT /note= "thymine modified by a minor groove binder (2-  
 FT dimethylaminonaphthalene-6- sulfonamide"  
 XX PN WO200131063-A1.  
 XX PD 03-MAY-2001.  
 XX PF 26-OCT-2000; 2000WO-US029786.  
 XX PR 26-OCT-1999; 99US-00428236.  
 XX PA (EPOC-) EPOCH BIOSCIENCES INC.  
 XX PI Dempcy RO, Afonina IA, Vermeulen NMJ;  
 XX DR WPI; 2001-328656/34.  
 XX Conjugate of oligonucleotide, minor groove binder and latent fluorophore,  
 FT useful for detecting specific nucleic acids, e.g. for single-nucleotide  
 FT mismatch discrimination.  
 XX Disclosure; Page 101; 105pp; English.  
 XX The present sequence is that of an oligonucleotide (ODN) -minor groove  
 CC binder (MGB) complex. MGBs bind in a non-intercalating manner to the  
 CC minor groove of non-single-stranded DNA, RNA or their hybrids. ODN-MGB-LF  
 CC conjugates of the invention also comprise a latent fluorophore (LF), lies  
 CC which binds similarly to the MGB but in an intercalating manner, or lies  
 CC in the minor groove, or is oriented in some other way to the DNA molecule  
 CC by MGB, such that it becomes fluorescent (or its fluorescent properties  
 CC change detectably). The conjugates are used as hybridisation probes and  
 CC amplification primers for fluorescent detection of specifically  
 CC hybridising sequences, for analysis or diagnosis, especially (real-time)  
 CC PCR, for single-nucleotide mismatch discrimination, target or signal  
 CC amplification, array-based assays and sequencing, including detection of  
 CC double-stranded DNA by triplex formation  
 XX Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;  
 SQ Query Match 1.2%; Score 12.8; DB 1; Length 16;  
 Best Local Similarity 87.5%; Pred. No. 3.3e-02;  
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1865 TTTTATTTTGTGTTT 1880  
 Db 1 TTTTATTTTGTGTTT 16

RESULT 464  
 AAF30880  
 ID AAF30880 standard; DNA; 16 BP.  
 XX AC AAF30880;  
 XX DT 09-JUL-2001 (first entry)  
 XX DE Oligonucleotide portion of ODN-MGB-LF conjugate.  
 XX KW ODN-MGB-LF; oligonucleotide; minor groove binder; latent fluorophore;  
 XX KW hybridisation; detection; fluorescence; probe; ss.





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XX Bimov V, Fernandez J, Archdeacon D, Archdeacon J;
PI Chakhmakhechev O, Buryakova A, Choob M, Hondorp K;
XX WPI; 2002-041177/05.
XX
XX Oligonucleotides analogs useful in detection, separation and purification
PT of nucleic acid molecules, comprise monomers, dimers and oligomers.
XX
XX Example 17; Page 118; 197pp; English.
XX
XX This invention relates to oligonucleotide analogues comprising a protein
CC nucleic acid molecule (PNA) monomer. They are used in the detection and
CC separation of nucleic acid molecules and as probes, primers, linkers,
CC adapters and antisense agents on solid supports. Modifications enhance
CC their use as capture and detection probes e.g. by the incorporation of
CC biotin, digoxigenin, radioisotopes, fluorescent labels such as
CC fluorescein and reporter molecules such as alkaline phosphatase. They are
CC also used for enhancing or inhibiting the activity of an enzyme or
CC cellular activity. The compounds are stable to nucleases and proteases,
CC have high affinity, binding specificity and solubility. The polyamide
CC backbone of PNAs is resistant to both nucleases and proteases. PNAs bind
CC nucleic acid molecules with greater affinity than DNA or RNA
CC concentration. The compounds are relatively simple to synthesize and are
CC used in a wide variety of applications. This sequence represents a DNA
CC oligomer which is used to represent the thermal stability of the
CC oligomers of the invention
XX
XX Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;
SQ
Query Match 1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 3.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTGTTT 1880
    |||||
    1 TTTTATTGTTT 16

Db
RESULT 467
AAL56451
ID AAL56451 standard; DNA; 16 BP.
XX
AC AAL56451;
XX
DT 07-AUG-2003 (first entry)
XX
DE 2'-P-ANA antisense oligo #6, to elicit RNase H degradation of target RNA.
XX
DE Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;
XX antisense; ss.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT modified_base 1..16
FT /tag= a
FT /mod_base= OTHER
FT /note= "2'-deoxy-2'-fluorocarabinothymidine"
FT misc_feature 8..9
FT /tag= b
FT /note= "Bases 8 and 9 are linked by two secouridine
FT linkers which is represented as S in page 49 and X in
FT page 57 and Fig 7 and 8 of the specification"
XX
PN WO2003037909-A1.
XX
PD 08-MAY-2003.
XX
XX 29-OCT-2002; 2002WO-CA001628.
XX
XX 29-OCT-2001; 2001US-0330719P.
XX

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PA (UYMC-) UNIV MCGILL.
XX
XX Damha MJ, Viazovkina E, Mangos MM, Parniak MA, Min K;
XX WPI; 2003-421516/39.
XX
XX Novel acyclic linker-containing oligonucleotide useful for preventing or
PT decreasing translation, reverse transcription and/or replication of a
PT target RNA in a system, comprises a modified deoxyribonucleotide.
XX
XX Example 2; Fig 7; 104pp; English.
XX
XX The invention relates to an acyclic linker-containing oligonucleotide
CC comprising at least one modified deoxyribonucleotide. Oligonucleotides of
CC the invention are useful for preventing or decreasing translation,
CC reverse transcription and/or replication of a target RNA in a system.
CC They are useful for selectively preventing gene expression in a sequence-
CC specific manner, for hybridising to complementary RNA such as cellular
CC mRNA or viral RNA, to hybridise to and induce cleavage of complementary
CC RNA. They are also useful therapeutically in formulations or medicaments
CC to prevent or treat a disease characterised by the expression of a
CC particular target RNA. The invention is used in gene therapy. The present
CC sequence is an antisense oligo used to elicit human RNase (ribonuclease)
CC H degradation of target RNA. This sequence is used in the exemplification
CC of the invention
XX
XX Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;
SQ
Query Match 1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 3.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTGTTT 1880
    |||||
    1 TTTTATTGTTT 16

Db
RESULT 468
AAL54078
ID AAL54078 standard; DNA; 16 BP.
XX
AC AAL54078;
XX
DT 06-MAR-2003 (first entry)
XX
DE Oligo-homodeoxyribonucleotide sequence, oligo dt.
XX
DE Detection; single-stranded sensor; detectable fluorescence emission;
XX forensic testing; paternity testing; tissue typing; hereditary disorder;
XX human population genetics; human evolutionary history; cystic fibrosis;
XX human haplotype diversity; Tay-Sachs; sickle-cell anaemia; ss.
XX
OS Unidentified.
XX
XX WO200284271-A2.
XX
XX 24-OCT-2002.
XX
XX 16-APR-2002; 2002WO-US012176.
XX
XX 16-APR-2001; 2001US-00836579.
XX
XX (REGC ) UNIV CALIFORNIA.
XX (CHAJ/) CHA J N.
XX
XX Cha JN, Morse DE, Stucky GD;
XX WPI; 2003-103378/09.
XX
XX Detecting polynucleotides, for pharmacogenetic testing, comprises
PT contacting a target polynucleotide with a complementary single-stranded
PT sensor polynucleotide and an agent that allows the sensor to fluoresce
PT upon excitation.

```



CC the human c-myb sequence at the base position indicated in the descriptor  
 CC line. The c-myb sequence was screened for optimal ribozyme target sites  
 CC using a computer folding algorithm, and regions of the mRNA which did not  
 CC form secondary folding structures and contained potential ribozyme  
 CC cleavage sites were identified. Ribozymes were synthesised and their  
 CC activities optimised by either varying the length of the binding arms or  
 CC by modification to prevent degradation by nucleases. The ribozymes cleave  
 CC the c-myb sequence and can be used to prevent smooth muscle cell  
 CC hyperproliferation in restenosis, especially after coronary angioplasty,  
 CC and in cancers  
 CC  
 SQ Sequence 17 BP; 7 A; 1 C; 0 G; 0 T; 9 U; 0 Other;

Query Match 1.2%; Score 12.8; DB 1; Length 17;  
 Best Local Similarity 43.8%; Pred. No. 3.4e+02;  
 Matches 7; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 1811 TGTATATATATATATA 1826  
 Db 2 UUUUAUAUAUAUA 17

RESULT 471  
 ABK55689  
 ID ABK55689 standard; RNA; 17 BP.

AC ABK55689;  
 AC  
 DT 02-JUL-2002 (first entry)  
 XX  
 DE Human CLCA1 gene enzymatic nucleic acid #60.

XX Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic;  
 KW antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;  
 KW chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;  
 KW oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;  
 KW acetylcysteine.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200211674-A2.  
 XX  
 PD 14-FEB-2002.

XX 09-AUG-2001; 2001WO-US024970.  
 XX  
 XX 09-AUG-2000; 2000US-0224383P.  
 XX  
 XX (RIBO-) RIBOZYME PHARM INC.  
 PA (SYNT) SYNTAX USA LLC.  
 PA (THOM) THOMPSON J.

XX Thompson J, Mcawiggen J, McKenzie T, Ayers D, Szymkowski DE;  
 PI Grupe A;  
 PI  
 XX WPI; 2002-217145/27.

XX Enzymatic polynucleotide that down regulates expression of chloride  
 PT channel calcium activated gene, useful for treating chronic obstructive  
 PT pulmonary disease (COPD), chronic bronchitis and asthma.  
 XX  
 XX Claim 4; Page 54; 152pp; English.

XX The invention relates to enzymatic nucleic acid molecules that down  
 CC regulate expression of chloride channel calcium activated 1 (CLCA1) genes  
 CC by cleaving RNA derived from the genes. The nucleic acid sequences are  
 CC useful as pharmaceutical agents for treating conditions such as chronic  
 CC obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic  
 CC fibrosis, obstructive bowel syndrome and any other diseases or conditions  
 CC that are related to or will respond to the levels of CLCA1 in a cell or  
 CC tissue. The sequences are useful for reducing CLCA1 activity in a cell,  
 CC hence, are useful for treatment of a patient having a condition  
 CC associated with the level of CLCA1, where the invention further comprises

CC the use of one or more therapies under conditions suitable for the  
 CC treatment, for example, oxygen therapy, bronchodilators, corticosteroids,  
 CC antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The  
 CC nucleic acids of the invention are also used as diagnostic tools to  
 CC examine genetic drift and mutations within diseased cells or to detect  
 CC the presence of CLCA1 RNA in a cell. This sequence represents an  
 CC enzymatic nucleic acid molecule of the invention  
 CC  
 SQ Sequence 17 BP; 7 A; 1 C; 1 G; 0 T; 8 U; 0 Other;

Query Match 1.2%; Score 12.8; DB 1; Length 17;  
 Best Local Similarity 37.5%; Pred. No. 3.4e+02;  
 Matches 6; Conservative 8; Mismatches 2; Indels 0; Gaps 0;

QY 1807 TGTGTATATATATA 1822  
 Db 2 UAUCUGUAUAUAUA 17

RESULT 472  
 ABC05097/C  
 ID ABC05097 standard; DNA; 13 BP.

XX ABC05097;  
 AC  
 DT 20-FEB-2002 (first entry)  
 XX  
 DE Oligonucleotide SEQ ID NO 5088 for detecting SNP TSC0001769.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200177384-A2.  
 XX  
 PD 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.  
 XX  
 XX 07-APR-2000; 2000DE-01019173.  
 XX  
 XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;  
 XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX  
 PS Claim 1; SEQ ID NO 5088; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF0010-ABF99989, ABH0010-ABH99989 and AB10010-AB182073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 13 BP; 10 A; 1 C; 0 G; 1 T; 0 U; 1 Other;  
 Query Match 1.2%; Score 12.6; DB 1; Length 13;  
 Best Local Similarity 92.3%; Pred. No. 3e+02;  
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

OY 1869 TATTTTGTGTTT 1881
DB 13 TATTTTGTGTTT 1

RESULT 473
ABF15464/c
ID ABF15464 standard; DNA; 13 BP.
XX AC ABF15464;
XX XX
DT 21-FEB-2002 (first entry)
XX XX
DE Oligonucleotide SEQ ID NO 115461 for detecting SNP TSC0028934.
XX XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX XX
XX WO200177384-A2.
XX PN
XX AC ABF15464;
XX XX
DT 21-FEB-2002 (first entry)
XX XX
DE Oligonucleotide SEQ ID NO 115461 for detecting SNP TSC0028934.
XX XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX XX
XX WO200177384-A2.
XX PN
XX AC ABF15464;
XX XX
DT 18-OCT-2001.
XX PD
XX AC ABF15464;
XX XX
DT 06-APR-2001; 2001WO-IB000713.
XX PF
XX AC ABF15464;
XX XX
DT 07-APR-2000; 2000DE-01019173.
XX PR
XX (EPIC-) EPIGENOMICS AG.
XX PA
XX Olek A, Piepenbrock C, Berlin K;
XX PI
XX WPI; 2001-657177/75.
XX DR
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX PT
XX Claim 1; SEQ ID NO 115461; 29pp + Sequence Listing; German.
XX PS
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX CC
XX Sequence 13 BP; 4 A; 0 C; 4 G; 4 T; 0 U; 1 Other;
XX SQ
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX CC
XX Query Match 1.2%; Score 12.6; DB 1; Length 13;
XX Best Local Similarity 92.3%; Pred. No. 3e+02; 0; Indels 0; Gaps 0;
XX Matches 12; Conservative 1; Mismatches 0;
XX OY 1239 GATTCACATCTCA 1251
XX DB 13 GATTCACATCTCA 1
XX RESULT 474
XX ABF82715
XX ID ABF82715 standard; DNA; 13 BP.
XX XX
XX AC ABF82715;
XX XX
DT 22-FEB-2002 (first entry)
XX DT

```

```

XX Oligonucleotide SEQ ID NO 182712 for detecting SNP TSC0045154.
DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX XX
XX WO200177384-A2.
XX PN
XX AC ABF15464;
XX XX
DT 18-OCT-2001.
XX PD
XX AC ABF15464;
XX XX
DT 06-APR-2001; 2001WO-IB000713.
XX PF
XX AC ABF15464;
XX XX
DT 07-APR-2000; 2000DE-01019173.
XX PR
XX (EPIC-) EPIGENOMICS AG.
XX PA
XX Olek A, Piepenbrock C, Berlin K;
XX PI
XX WPI; 2001-657177/75.
XX DR
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX PT
XX Claim 1; SEQ ID NO 182712; 29pp + Sequence Listing; German.
XX PS
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX CC
XX Sequence 13 BP; 4 A; 0 C; 0 G; 8 T; 0 U; 1 Other;
XX SQ
XX Query Match 1.2%; Score 12.6; DB 1; Length 13;
XX Best Local Similarity 92.3%; Pred. No. 3e+02; 0; Indels 0; Gaps 0;
XX Matches 12; Conservative 1; Mismatches 0;
XX OY 1766 ATTTTAAATTT 1778
XX DB 1 RTTTTAAATTT 13
XX RESULT 475
XX ABF60174
XX ID ABF60174 standard; DNA; 13 BP.
XX XX
XX AC ABF60174;
XX XX
DT 22-FEB-2002 (first entry)
XX DT
DE Oligonucleotide SEQ ID NO 160171 for detecting SNP TSC0040332.
XX XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX XX
XX WO200177384-A2.
XX PN
XX AC ABF82715;
XX XX
DT 18-OCT-2001.
XX DT

```

PF 06-APR-2001; 2001WO-IB000713.  
 XX PR 07-APR-2000; 2000DE-01019173.  
 XX PA (EPIC-) EPIGENOMICS AG.  
 XX PI Olek A, Piepenbrock C, Berlin K;  
 XX WPI; 2001-657177/75.  
 DR XX  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX PS  
 XX Claim 1; SEQ ID NO 160171; 29pp + Sequence Listing; German.  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX SQ Sequence 13 BP; 1 A; 0 C; 1 G; 10 T; 0 U; 1 Other;  
 Query Match 1.2%; Score 12.6; DB 1; Length 13;  
 Best Local Similarity 92.3%; Pred. No. 3e+02; 0; Indels 0; Gaps 0;  
 Matches 12; Conservative 1; Mismatches 0; Gaps 0;  
 QY 1866 TTTTATTTTGGT 1878  
 DB 1 TTTTATTTTGT 13  
 RESULT 476  
 ABC68366  
 ID ABC68366 standard; DNA; 13 BP.  
 AC ABC68366;  
 XX 21-FEB-2002 (first entry)  
 DT Oligonucleotide SEQ ID NO 68383 for detecting SNP TSC0017833.  
 DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX Homo sapiens.  
 OS WO200177384-A2.  
 PN 18-OCT-2001.  
 PD 06-APR-2001; 2001WO-IB000713.  
 PF 07-APR-2000; 2000DE-01019173.  
 PR (EPIC-) EPIGENOMICS AG.  
 PA Olek A, Piepenbrock C, Berlin K;  
 XX WPI; 2001-657177/75.  
 DR Set of oligonucleotides, useful for diagnosis and cell typing, is  
 XX designed to detect single-nucleotide polymorphisms and cytosine  
 XX methylation status.  
 XX PS  
 XX Claim 1; SEQ ID NO 160171; 29pp + Sequence Listing; German.  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX SQ Sequence 13 BP; 1 A; 0 C; 1 G; 10 T; 0 U; 1 Other;  
 Query Match 1.2%; Score 12.6; DB 1; Length 13;  
 Best Local Similarity 92.3%; Pred. No. 3e+02; 0; Indels 0; Gaps 0;  
 Matches 12; Conservative 1; Mismatches 0; Gaps 0;  
 QY 1866 TTTTATTTTGGT 1878  
 DB 1 TTTTATTTTGT 13  
 RESULT 476  
 ABC68366  
 ID ABC68366 standard; DNA; 13 BP.  
 AC ABC68366;  
 XX 21-FEB-2002 (first entry)  
 DT Oligonucleotide SEQ ID NO 68383 for detecting SNP TSC0017833.  
 DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX Homo sapiens.  
 OS WO200177384-A2.  
 PN 18-OCT-2001.  
 PD 06-APR-2001; 2001WO-IB000713.  
 PF 07-APR-2000; 2000DE-01019173.  
 PR (EPIC-) EPIGENOMICS AG.  
 PA Olek A, Piepenbrock C, Berlin K;  
 XX WPI; 2001-657177/75.  
 DR Set of oligonucleotides, useful for diagnosis and cell typing, is  
 XX designed to detect single-nucleotide polymorphisms and cytosine  
 XX methylation status.

XX Claim 1; SEQ ID NO 68383; 29pp + Sequence Listing; German.  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX SQ Sequence 13 BP; 2 A; 0 C; 2 G; 8 T; 0 U; 1 Other;  
 Query Match 1.2%; Score 12.6; DB 1; Length 13;  
 Best Local Similarity 92.3%; Pred. No. 3e+02; 0; Indels 0; Gaps 0;  
 Matches 12; Conservative 1; Mismatches 0; Gaps 0;  
 QY 2261 GTGTATATTTT 2273  
 DB 1 GTGTATATTTT 13  
 RESULT 477  
 ABC68367/C  
 ID ABC68367 standard; DNA; 13 BP.  
 AC ABC68367;  
 XX 21-FEB-2002 (first entry)  
 DT Oligonucleotide SEQ ID NO 68384 for detecting SNP TSC0017833.  
 DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX Homo sapiens.  
 OS WO200177384-A2.  
 PN 18-OCT-2001.  
 PD 06-APR-2001; 2001WO-IB000713.  
 PF 07-APR-2000; 2000DE-01019173.  
 PR (EPIC-) EPIGENOMICS AG.  
 PA Olek A, Piepenbrock C, Berlin K;  
 XX WPI; 2001-657177/75.  
 DR Set of oligonucleotides, useful for diagnosis and cell typing, is  
 XX designed to detect single-nucleotide polymorphisms and cytosine  
 XX methylation status.  
 XX PS  
 XX Claim 1; SEQ ID NO 68384; 29pp + Sequence Listing; German.  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 13 BP; 8 A; 2 C; 0 G; 2 T; 0 U; 1 Other;

Query Match 1.2%; Score 12.6; DB 1; Length 13;  
Best Local Similarity 92.3%; Pred. No. 3e+02;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2261 GTGTATATTTT 2273  
DB 13 GTGTATATTTT 1

RESULT 478  
AB14215/C  
ID ABC14215 standard; DNA; 13 BP.  
XX  
AC ABC14215;  
XX  
DT 20-FEB-2002 (first entry)  
XX  
DE Oligonucleotide SEQ ID NO 14222 for detecting SNP TSC0003234.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.

Claim 1; SEQ ID NO 14222; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABIS2073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

Sequence 13 BP; 6 A; 6 C; 0 G; 0 T; 0 U; 1 Other;  
XX  
SQ  
Query Match 1.2%; Score 12.6; DB 1; Length 13;  
Best Local Similarity 92.3%; Pred. No. 3e+02;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGT 1805  
DB 13 TGTGTGTGTGT 1

RESULT 479  
ABF96635  
ID ABF96635 standard; DNA; 13 BP.  
XX  
AC ABF96635;  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide SEQ ID NO 196632 for detecting SNP TSC0048388.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.

Claim 1; SEQ ID NO 196632; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABIS2073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

Sequence 13 BP; 4 A; 1 C; 0 G; 7 T; 0 U; 1 Other;  
XX  
SQ  
Query Match 1.2%; Score 12.6; DB 1; Length 13;  
Best Local Similarity 92.3%; Pred. No. 3e+02;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1283 GTTATTTAAATCT 1295  
DB 1 RTTATTTAAATCT 13

RESULT 480  
ABF87882  
ID ABF87882 standard; DNA; 13 BP.  
XX  
AC ABF87882;  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide SEQ ID NO 187879 for detecting SNP TSC0046259.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;

KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX Homo sapiens.  
XX WO200177384-A2.  
XX 18-OCT-2001.  
XX 06-APR-2001; 2001WO-IB000713.  
XX 07-APR-2000; 2000DE-01019173.  
XX (EPIG-) EPIGENOMICS AG.  
XX Olek A, Piepenbrock C, Berlin K;  
XX WPI; 2001-657177/75.  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX Claim 1; SEQ ID NO 187879; 29pp + Sequence Listing; German.  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX Sequence 13 BP; 1 A; 0 C; 5 G; 6 T; 0 U; 1 Other;  
SQ  
Query Match 1.2%; Score 12.6; DB 1; Length 13;  
Best Local Similarity 92.3%; Pred. No. 3e+02;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1803 TGTGTCGTGTAT 1815  
DB 1 TGTGTCGTGTAT 13  
RESULT 481  
ABCE9602  
ID ABC99602 standard; DNA; 13 BP.  
XX ABC99602;  
XX 21-FEB-2002 (first entry)  
XX Oligonucleotide SEQ ID NO 89619 for detecting SNP TSC0022467.  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX Homo sapiens.  
XX WO200177384-A2.  
XX 18-OCT-2001.  
XX 06-APR-2001; 2001WO-IB000713.  
XX 07-APR-2000; 2000DE-01019173.  
XX (EPIG-) EPIGENOMICS AG.  
PA

KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX Homo sapiens.  
XX WO200177384-A2.  
XX 18-OCT-2001.  
XX 06-APR-2001; 2001WO-IB000713.  
XX 07-APR-2000; 2000DE-01019173.  
XX (EPIG-) EPIGENOMICS AG.  
XX Olek A, Piepenbrock C, Berlin K;  
XX WPI; 2001-657177/75.  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX Claim 1; SEQ ID NO 89619; 29pp + Sequence Listing; German.  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX Sequence 13 BP; 1 A; 0 C; 5 G; 6 T; 0 U; 1 Other;  
SQ  
Query Match 1.2%; Score 12.6; DB 1; Length 13;  
Best Local Similarity 92.3%; Pred. No. 3e+02;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1803 TGTGTCGTGTAT 1815  
DB 1 TGTGTCGTGTAT 13  
RESULT 481  
ABCE9602  
ID ABC99602 standard; DNA; 13 BP.  
XX ABC99602;  
XX 21-FEB-2002 (first entry)  
XX Oligonucleotide SEQ ID NO 89619 for detecting SNP TSC0022467.  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX Homo sapiens.  
XX WO200177384-A2.  
XX 18-OCT-2001.  
XX 06-APR-2001; 2001WO-IB000713.  
XX 07-APR-2000; 2000DE-01019173.  
XX (EPIG-) EPIGENOMICS AG.  
PA

XX Olek A, Piepenbrock C, Berlin K;  
XX WPI; 2001-657177/75.  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX Claim 1; SEQ ID NO 89619; 29pp + Sequence Listing; German.  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX Sequence 13 BP; 5 A; 0 C; 1 G; 6 T; 0 U; 1 Other;  
SQ  
Query Match 1.2%; Score 12.6; DB 1; Length 13;  
Best Local Similarity 92.3%; Pred. No. 3e+02;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1817 TATATATATATGT 1829  
DB 1 TATATATATATGY 13  
RESULT 482  
ABH25451/C  
ID ABH25451 standard; DNA; 13 BP.  
XX ABH25451;  
XX 22-FEB-2002 (first entry)  
XX Oligonucleotide SEQ ID NO 225428 for detecting SNP TSC0054949.  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX Homo sapiens.  
XX WO200177384-A2.  
XX 18-OCT-2001.  
XX 06-APR-2001; 2001WO-IB000713.  
XX 07-APR-2000; 2000DE-01019173.  
XX (EPIG-) EPIGENOMICS AG.  
XX Olek A, Piepenbrock C, Berlin K;  
XX WPI; 2001-657177/75.  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX Claim 1; SEQ ID NO 225428; 29pp + Sequence Listing; German.  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, cardiovascular and metabolic disorders. The  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligonucleotides are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 13 BP; 6 A; 4 C; 0 G; 2 T; 0 U; 1 Other;

Query Match 1.2%; Score 12.6; DB 1; Length 13;  
 Best Local Similarity 92.3%; Pred. No. 3e+02;  
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1805 TGTGTGTGTAT 1817  
 |||||  
 Db 13 TGTGTGTGTAT 1

## RESULT 483

ABF87883/C  
 ID ABF87883 standard; DNA; 13 BP.

XX AC ABF87883;

XX 22-FEB-2002 (first entry)

XX Oligonucleotide SEQ ID NO 187880 for detecting SNP TSC0046259.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.

XX Claim 1; SEQ ID NO 187880; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 13 BP; 6 A; 5 C; 0 G; 1 T; 0 U; 1 Other;

Query Match 1.2%; Score 12.6; DB 1; Length 13;  
 Best Local Similarity 92.3%; Pred. No. 3e+02;  
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1803 TGTGTGTGTAT 1815  
 |||||  
 Db 13 TGTGTGTGTAT 1

## RESULT 484

ABF64975/C  
 ID ABF64975 standard; DNA; 13 BP.

XX AC ABF64975;

XX 22-FEB-2002 (first entry)

XX Oligonucleotide SEQ ID NO 164972 for detecting SNP TSC0006375.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.

XX Claim 1; SEQ ID NO 164972; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 13 BP; 10 A; 1 C; 0 G; 1 T; 0 U; 1 Other;

Query Match 1.2%; Score 12.6; DB 1; Length 13;  
 Best Local Similarity 92.3%; Pred. No. 3e+02;  
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1867 TTTATTTTGT 1879  
 |||||  
 Db 13 TTTATTTTGT 1

## RESULT 485

ABF82714/C  
 ID ABF82714 standard; DNA; 13 BP.

XX



```

AC ABF82714;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 182711 for detecting SNP TSC0045154.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 182711; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 8 A; 0 C; 0 G; 4 T; 0 U; 1 Other;
XX
Query Match 1.2%; Score 12.6; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 3e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1766 ATTTTAAATTT 1778
DB 13 RTTTTAAATTT 1
:|||||
:|||||

RESULT 486
ABC25106
ID ABC25106 standard; DNA; 13 BP.
XX
AC ABC25106;
XX
DT 20-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 25123 for detecting SNP TSC0006116.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.

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XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 25123; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 4 A; 0 C; 0 G; 8 T; 0 U; 1 Other;
XX
Query Match 1.2%; Score 12.6; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 3e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1767 TTTTAAATTT 1779
DB 1 TTTTAAATTT 13
:|||||
:|||||

RESULT 487
ABH25450
ID ABH25450 standard; DNA; 13 BP.
XX
AC ABH25450;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 225427 for detecting SNP TSC0054949.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX

```

PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.

XX Claim 1; SEQ ID NO 225427; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 13 BP; 2 A; 0 C; 4 G; 6 T; 0 U; 1 Other;

Query Match 1.2%; Score 12.6; DB 1; Length 13;  
Best Local Similarity 92.3%; Pred. No. 3e+02;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1805 TGTGTGTGTAT 1817

Db 1 TGTGTGTGTAT 13

RESULT 488

ABF64974

ID ABF64974 standard; DNA; 13 BP.

XX ABF64974;

XX 22-FEB-2002 (first entry)

XX Oligonucleotide SEQ ID NO 164971 for detecting SNP TSC006375.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;

XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;

XX central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is

XX designed to detect single-nucleotide polymorphisms and cytosine

XX methylation status.

XX Claim 1; SEQ ID NO 164971; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic

XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

XX and cytosine methylation status in chemically pretreated genomic DNA. The

XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a

XX range of diseases including immune system, gastrointestinal, respiratory,

XX central nervous system, cardiovascular and metabolic disorders. The

XX oligomers are also used for detecting cell type differentiation. ABC00010

CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 13 BP; 1 A; 0 C; 1 G; 10 T; 0 U; 1 Other;

Query Match 1.2%; Score 12.6; DB 1; Length 13;

Best Local Similarity 92.3%; Pred. No. 3e+02;

Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1867 TTTATTTTGT 1879

Db 1 TTTATTTTGT 13

RESULT 489

ABC28716

ID ABC28716 standard; DNA; 13 BP.

XX ABC28716;

XX 20-FEB-2002 (first entry)

XX Oligonucleotide SEQ ID NO 28733 for detecting SNP TSC0008353.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;

XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;

XX central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is

XX designed to detect single-nucleotide polymorphisms and cytosine

XX methylation status.

XX Claim 1; SEQ ID NO 28733; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic

XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

XX and cytosine methylation status in chemically pretreated genomic DNA. The

XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a

XX range of diseases including immune system, gastrointestinal, respiratory,

XX central nervous system, cardiovascular and metabolic disorders. The

XX oligomers are also used for detecting cell type differentiation. ABC00010

CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073

CC represent the oligomers described in the invention. NOTE: The sequence

CC data for this patent did not form part of the printed specification, but

CC was obtained in electronic format from WIPO at

CC ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 13 BP; 5 A; 0 C; 1 G; 6 T; 0 U; 1 Other;

Query Match 1.2%; Score 12.6; DB 1; Length 13;

Best Local Similarity 92.3%; Pred. No. 3e+02;

Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1774 AAATTATATGT 1786

Db 1 AAATTATATGY 13

RESULT 490

ABC59000  
ID ABC59000 standard; DNA; 13 BP.

AC ABC59000;

DT 21-FEB-2002 (first entry)

DE Cligonucleotide SEQ ID NO 59017 for detecting SNP TSC0015817.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens.

XX PN WO200177384-A2

XX  
PD  
18-OCT-2001.

XX  
PF 06-APR-2001: 2001WO-TB000713XX  
PR 07-APR-2000: 2000DE-01019173.

XX PA (EPTG-) EPTGENOMICS AG

Pi Olek A. Piepenbrock C. Berlin K:

XX  
DR  
WPI: 2001-657177/75.

Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.

PS Claim 1; SEQ ID NO 59017; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC000010-ABC99989, ABF00010-ABF99989 and ABH00010-ABH99989 and AB100010-AB182073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at [ftp.wipo.int/pub/published/pat](http://wipo.int/pub/published/pat) sequences

Sequence 13 BP; 6 A; 0 C; 0 G; 6 T; 0 U; 1 Other;

```
Query Match      1.2%; Score 12.6; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 3e+02;
Matches 12; Conservative 1; Mismatches 0; Indels
```

Qy 1813 TATATATATAT 1825

Db 1 TATATATATATAY 13

RESULT 491

ABC59000/c  
ID ABC59000 standard; DNA; 13 BP.

AA ABC59000;

DT 21-FEB-2002 (first entry)

DE Oligonucleotide SEQ ID NO 59017 for detecting SNP TSC0015817.

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PR 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
PA Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
DR Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 239455; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 5 A; 0 C; 0 G; 7 T; 0 U; 1 Other;
Query Match 1.2%; Score 12.6; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 3e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1769 TTTTAAATTTAT 1781
Db 1 TTTTAAATTTAT 13
RESULT 493
ABC47718
ID ABC47718 standard; DNA; 13 BP.
XX AC ABC47718;
XX DT 21-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 47735 for detecting SNP TSC0013684.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX OS WO200177384-A2.
XX PN 18-OCT-2001.
XX PD 06-APR-2001; 2001WO-IB000713.
XX PF 07-APR-2000; 2000DE-01019173.
XX PR (EPIG-) EPIGENOMICS AG.
XX PA Olek A, Piepenbrock C, Berlin K;
XX PI WPI; 2001-657177/75.
XX DR Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX Claim 1; SEQ ID NO 47735; 29pp + Sequence Listing; German.

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```

XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 1 A; 0 C; 1 G; 10 T; 0 U; 1 Other;
Query Match 1.2%; Score 12.6; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 3e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1865 TTTTATTTTGT 1877
Db 1 TTTTATTTTGT 13
RESULT 494
ABC05096
ID ABC05096 standard; DNA; 13 BP.
XX AC ABC05096;
XX DT 20-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 5087 for detecting SNP TSC0001768.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX OS WO200177384-A2.
XX PN 18-OCT-2001.
XX PD 06-APR-2001; 2001WO-IB000713.
XX PF 07-APR-2000; 2000DE-01019173.
XX PR (EPIG-) EPIGENOMICS AG.
XX PA Olek A, Piepenbrock C, Berlin K;
XX PI WPI; 2001-657177/75.
XX DR Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX Claim 1; SEQ ID NO 5087; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX

```

```

XX SQ Sequence 13 BP; 1 A; 0 C; 1 G; 10 T; 0 U; 1 Other;
XX
XX Query Match 1.2%; Score 12.6; DB 1; Length 13;
XX Best Local Similarity 92.3%; Pred. No. 3e+02; 0; Indels 0; Gaps 0;
XX Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1869 TATTTTGTGTTT 1881
XX |||||
XX 1 TATTTTGTGTTT 13
XX
XX
XX RESULT 495
XX ABC14214
XX ID ABC14214 standard; DNA; 13 BP.
XX
XX AC ABC14214;
XX
XX XX
XX DT 20-FEB-2002 (first entry)
XX
XX DE Oligonucleotide SEQ ID NO 14221 for detecting SNP TSC0003234.
XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX PN WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX
XX PR 07-APR-2000; 2000DE-01019173.
XX
XX PA (EPITG-) EPIGENOMICS AG.
XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX
XX DR WPI; 2001-657177/75.
XX
XX XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX PS Claim 1; SEQ ID NO 14221; 29pp + Sequence Listing; German.
XX
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 13 BP; 0 A; 0 C; 6 G; 6 T; 0 U; 1 Other;
XX
XX Query Match 1.2%; Score 12.6; DB 1; Length 13;
XX Best Local Similarity 92.3%; Pred. No. 3e+02; 0; Indels 0; Gaps 0;
XX Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1793 TGTGTGTGTGTGT 1805
XX |||||
XX 1 TGTGTGTGTGTGT 13
XX
XX
XX RESULT 496

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ABF15465
XX ID ABF15465 standard; DNA; 13 BP.
XX
XX AC ABF15465;
XX
XX DT 21-FEB-2002 (first entry)
XX
XX DE Oligonucleotide SEQ ID NO 115462 for detecting SNP TSC0028934.
XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX PN WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX
XX PR 07-APR-2000; 2000DE-01019173.
XX
XX PA (EPITG-) EPIGENOMICS AG.
XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX
XX DR WPI; 2001-657177/75.
XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX PS Claim 1; SEQ ID NO 115462; 29pp + Sequence Listing; German.
XX
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 13 BP; 4 A; 4 C; 0 G; 4 T; 0 U; 1 Other;
XX
XX Query Match 1.2%; Score 12.6; DB 1; Length 13;
XX Best Local Similarity 92.3%; Pred. No. 3e+02; 0; Indels 0; Gaps 0;
XX Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1239 GATTTCATCTCA 1251
XX |||||
XX 1 TATTTCATCTCA 13
XX
XX
XX RESULT 497
XX ABF60175/C
XX ID ABF60175 standard; DNA; 13 BP.
XX
XX AC ABF60175;
XX
XX DT 22-FEB-2002 (first entry)
XX
XX DE Oligonucleotide SEQ ID NO 160172 for detecting SNP TSC0040332.
XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX

```



CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 13 BP; 8 A; 0 C; 0 G; 4 T; 0 U; 1 Other;  
Query Match 1.2%; Score 12.6; DB 1; Length 13;  
Best Local Similarity 92.3%; Pred. No. 3e+02;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 1767 TTTTAAAAATTT 1779  
Db 13 TTTTAAAAATTT 1  
RESULT 500  
ABC59001  
ID ABC59001 standard; DNA; 13 BP.  
XX  
AC ABC59001;  
XX  
DT 21-FEB-2002 (first entry)  
XX  
DE Oligonucleotide SEQ ID NO 59018 for detecting SNP TSC0015817.  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 59018; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 13 BP; 6 A; 0 C; 0 G; 6 T; 0 U; 1 Other;  
Query Match 1.2%; Score 12.6; DB 1; Length 13;  
Best Local Similarity 92.3%; Pred. No. 3e+02;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 1812 GTATATATATATA 1824  
Db 13 TATATATATATA 13  
RESULT 501  
ABC59001/c  
ID ABC59001 standard; DNA; 13 BP.  
XX  
AC ABC59001;  
XX  
DT 21-FEB-2002 (first entry)  
XX  
DE Oligonucleotide SEQ ID NO 59018 for detecting SNP TSC0015817.  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 59018; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 13 BP; 6 A; 0 C; 0 G; 6 T; 0 U; 1 Other;  
Query Match 1.2%; Score 12.6; DB 1; Length 13;  
Best Local Similarity 92.3%; Pred. No. 3e+02;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 1813 TATATATATATAT 1825  
Db 13 TATATATATATAT 1  
RESULT 502  
ABC89603/c  
ID ABC89603 standard; DNA; 13 BP.  
XX  
AC ABC89603;  
XX

DT 21-FEB-2002 (first entry)  
XX Oligonucleotide SEQ ID NO 89620 for detecting SNP TSC0022467.  
DE  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX WO200177384-A2.  
PN  
XX 18-OCT-2001.  
PD  
XX  
XX 06-APR-2001; 2001WO-IB000713.  
PF  
XX 07-APR-2000; 2000DE-01019173.  
PR  
XX (EPIG-) EPIGENOMICS AG.  
PA  
XX Olek A, Piepenbrock C, Berlin K;  
PI  
XX WPI; 2001-657177/75.  
DR  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
XX Claim 1; SEQ ID NO 89620; 29pp + Sequence Listing; German.  
PS  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 13 BP; 6 A; 1 C; 0 G; 5 T; 0 U; 1 Other;  
Query Match 1.2%; Score 12.6; DB 1; Length 13;  
Best Local Similarity 92.3%; Pred. No. 3e+02; Mismatches 0; Gaps 0;  
Matches 12; Conservative 1; Indels 0;  
QY 1817 TATATATATGCT 1829  
DB 13 TATATATATGCT 1  
RESULT 503  
ABC28717/C  
ID ABC28717 standard; DNA; 13 BP.  
AC  
XX ABC28717;  
XX  
XX 20-FEB-2002 (first entry)  
DT  
XX Oligonucleotide SEQ ID NO 28734 for detecting SNP TSC0008353.  
DE  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX WO200177384-A2.  
PN  
XX 18-OCT-2001.  
PD

XX 06-APR-2001; 2001WO-IB000713.  
PF  
XX 07-APR-2000; 2000DE-01019173.  
PR  
XX (EPIG-) EPIGENOMICS AG.  
PA  
XX Olek A, Piepenbrock C, Berlin K;  
PI  
XX WPI; 2001-657177/75.  
DR  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
XX Claim 1; SEQ ID NO 28734; 29pp + Sequence Listing; German.  
PS  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 13 BP; 6 A; 1 C; 0 G; 5 T; 0 U; 1 Other;  
Query Match 1.2%; Score 12.6; DB 1; Length 13;  
Best Local Similarity 92.3%; Pred. No. 3e+02; Mismatches 0; Gaps 0;  
Matches 12; Conservative 1; Indels 0;  
QY 1774 AAATTTATATGCT 1786  
DB 13 AAATTTATATGCT 1  
RESULT 504  
ABC47719/C  
ID ABC47719 standard; DNA; 13 BP.  
AC  
XX ABC47719;  
XX  
XX 21-FEB-2002 (first entry)  
DT  
XX Oligonucleotide SEQ ID NO 47736 for detecting SNP TSC0013684.  
DE  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX WO200177384-A2.  
PN  
XX 18-OCT-2001.  
PD  
XX 06-APR-2001; 2001WO-IB000713.  
PF  
XX 07-APR-2000; 2000DE-01019173.  
PR  
XX (EPIG-) EPIGENOMICS AG.  
PA  
XX Olek A, Piepenbrock C, Berlin K;  
PI  
XX WPI; 2001-657177/75.  
DR  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT



PT methylation status.  
 XX Claim 1; SEQ ID NO 47736; 29pp + Sequence Listing; German.  
 XX  
 CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 XX Sequence 13 BP; 10 A; 1 C; 0 G; 1 T; 0 U; 1 Other;  
 XX  
 XX Query Match 1.2%; Score 12.6; DB 1; Length 13;  
 XX Best Local Similarity 92.3%; Pred. No. 3e+02;  
 XX Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 QY 1865 TTTTATTATTGT 1877  
 Db 13 TTTTATTATTGT 1  
 RESULT 505  
 ABF9634/C  
 ID ABF9634 standard; DNA; 13 BP.  
 XX  
 XX ABF9634;  
 XX  
 XX 22-FEB-2002 (first entry)  
 XX  
 XX Oligonucleotide SEQ ID NO 196631 for detecting SNP TSC0048388.  
 XX  
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX  
 XX Homo sapiens.  
 XX  
 XX WO200177384-A2.  
 XX  
 XX 18-OCT-2001.  
 XX  
 XX 06-APR-2001; 2001WO-IB000713.  
 XX  
 XX 07-APR-2000; 2000DE-01019173.  
 XX  
 XX (EPIG-) EPIGENOMICS AG.  
 XX  
 XX Olek A, Piepenbrock C, Berlin K;  
 XX  
 XX WPI; 2001-657177/75.  
 XX  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 XX designed to detect single-nucleotide polymorphisms and cytosine  
 XX methylation status.  
 XX  
 XX Claim 1; SEQ ID NO 196631; 29pp + Sequence Listing; German.  
 XX  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 XX and cytosine methylation status in chemically pretreated genomic DNA. The  
 XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 XX range of diseases including immune system, gastrointestinal, respiratory,  
 XX central nervous system, cardiovascular and metabolic disorders. The  
 XX oligomers are also used for detecting cell type differentiation. ABC00010  
 XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 XX represent the oligomers described in the invention. NOTE: The sequence

CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 XX Sequence 13 BP; 7 A; 0 C; 1 G; 4 T; 0 U; 1 Other;  
 XX  
 XX Query Match 1.2%; Score 12.6; DB 1; Length 13;  
 XX Best Local Similarity 92.3%; Pred. No. 3e+02;  
 XX Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 QY 1283 GTTATTATAAATCT 1295  
 Db 13 RTTATTATAAATCT 1  
 RESULT 506  
 AAT96309  
 ID AAT96309 standard; DNA; 14 BP.  
 XX  
 XX AAT96309;  
 XX  
 XX 25-MAR-2003 (revised)  
 XX  
 XX 08-APR-1998 (first entry)  
 XX  
 XX Fungal telomeric nucleic acid sequence.  
 XX  
 XX Detection; eukaryotic pathogen; telomeric nucleic acid sequence;  
 XX telomerase activity; diagnosis; fungal infection; fungus; fungi;  
 XX malarial infection; malaria; ss.  
 XX  
 XX Saccharomyces cerevisiae.  
 XX  
 XX US5695932-A.  
 XX  
 XX 09-DEC-1997.  
 XX  
 XX 13-MAY-1993; 93US-00060952.  
 XX  
 XX 13-MAY-1992; 92US-00882438.  
 XX  
 XX 24-MAR-1993; 93US-00038766.  
 XX  
 XX (UYCA-) UNIV CALIFORNIA SAN FRANCISCO.  
 XX (TEXA) UNIV TEXAS SYSTEM.  
 XX  
 XX Blackburn EH, Shay J, Mceachern MJ, West MD, Wright W;  
 XX  
 XX WPI; 1998-041292/04.  
 XX  
 XX Detection of eukaryotic pathogens, especially fungal or Plasmodium spp. -  
 XX by detecting telomerase activity.  
 XX  
 XX Claim 5; Col 93-94; 82pp; English.  
 XX  
 XX The present sequence can be used in a novel method for detecting a  
 XX eukaryotic pathogen in a patient. The method comprises obtaining a sample  
 XX of somatic tissue or cells from the patient, determining if telomerase  
 XX activity is present and correlating this with the presence of the  
 XX pathogen. The method is useful for diagnosis of fungal infections,  
 XX especially a fungus of the genus Candida, Kluyveromyces, Saccharomyces,  
 XX Sporothrix, Coccioides, Histoplasma Blastomyces, Paracoccidioides,  
 XX Cryptococcus, Aspergillus, Mucor or Rhizopus, or malarial infections,  
 XX especially Plasmodium vivax, P. ovale, P. malariae or P. falciparum.  
 XX (Updated on 25-MAR-2003 to correct PA field.)  
 XX  
 XX Sequence 14 BP; 0 A; 0 C; 8 G; 6 T; 0 U; 0 Other;  
 XX  
 XX Query Match 1.2%; Score 12.4; DB 1; Length 14;  
 XX Best Local Similarity 92.3%; Pred. No. 3.3e+02;  
 XX Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 XX  
 QY 1793 TGTGTGTGTGTGTG 1806  
 Db 1 TGGGTGTGTGTGTG 14

telomerase activity; cel replication; neoplasia; cancer;  
age-related macular degeneration; Alzheimer's disease; atherosclerosis;  
telomerase; telomerase inhibitor; immortalised cell; ss.

Synthetic.

US2002127634-A1.

12-SEP-2002.

05-JUN-1995; 95US-00463404.

13-MAY-1992; 92US-00892438.

24-MAR-1993; 93US-00038766.

13-MAY-1993; 93US-00060952.

(WEST/) WEST M D.

(SHAY/) SHAY J.

(WRIGHT/) WRIGHT W.

(BLAC/) BLACKBURN E H.

West MD, Shay J, Wright W, Blackburn EH;

WPI; 2003-066996/06.

Disclosure; Page 51; 86pp; English.

The invention describes a method use for treating increased rate of proliferation of a cell or extending the ability of a cell to replicate, or treating a disease associated with cell senescence. The method comprises administering an agent to reduce loss of telomere length within the cell during proliferation or replication, or to derepress telomerase in the senescing cells. The method is useful for treating a condition associated with an increased rate of proliferation of a cell extending the ability of a cell to replicate, or for treating a disease or condition associated with cell senescence e.g. neoplasia. A second method disclosed in the invention is useful for treating a condition associated with an elevated level of telomerase activity within a cell e.g. cancer. Also disclosed is a method useful for diagnosis of a condition associated with an increased rate of proliferation in a cell in an individual e.g. age-related macular degeneration, astrocytes associated with Alzheimer's disease and endothelial cells associated with atherosclerosis. This sequence represents a polynucleotide used in the study of telomere length and telomerase activity described in the invention

Sequence 14 BP; 0 A; 0 C; 8 G; 6 T; 0 U; 0 Other;

Query Match 1.2%; Score 12.4; DB 1; Length 14;  
Best Local Similarity 92.9%; Pred. No. 3.3e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTGTG 1806

Db 1 TGGGTGTGTGTGTG 14

RESULT 509

AAT54694

ID AAT54694 standard; RNA; 15 BP.

XX AC AAT54694;

XX 25-MAR-2003 (revised)

DT 22-APR-1997 (first entry)

DE Mouse IL-5 hammerhead ribozyme target sequence (nt. position 1350).

XX Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;

RESULT 507

AAV95611

ID AAV95611 standard; RNA; 14 BP.

XX AC AAV95611;

DT 24-FEB-1999 (first entry)

XX Human c-fos target sequence nucleotide position 756.

XX Human; c-fos; hammerhead ribozyme; hairpin ribozyme; target site; cancer;

XX oncogene; leukaemia; neuroblastoma; diagnosis; genetic drift; mutation;

XX diseased cell; ss.

XX Homo sapiens.

XX WO9832846-A2.

XX 30-JUL-1998.

XX 20-JAN-1998; 98WO-US001017.

XX 23-JAN-1997; 97US-0037658P.

XX 24-DEC-1997; 97US-00998099.

XX (RIBO-) RIBOZYME PHARM INC.

XX Jarvis T, Mcswiggen JA, Stinchcomb DT;

XX WPI; 1998-427942/36.

XX Enzymatic nucleic acid molecules which specifically cleave RNA derived

XX from a c-fos gene - useful for treating conditions related to levels of c

XX -fos, especially cancer.

XX Claim 5; Page 53; 72pp; English.

XX The present invention describes an enzymatic nucleic acid molecule which specifically cleaves RNA derived from a c-fos gene. AAV95401 to AAV95540 and AAV95541 to AAV95584 represent hammerhead ribozymes and hairpin ribozymes, respectively, which specifically cleave human c-fos. AAV95261 to AAV95400 and AAV95585 to AAV95628 represent human c-fos target sequences. The enzymatic nucleic acid molecules can be used for treating cancer associated with elevated levels of c-fos oncogene, especially leukaemia, neuroblastomas and lung, breast and colon cancers. The ribozymes may also be used as diagnostic tools to examine genetic drift and mutations within diseased cells, or to detect the presence of c-fos RNA in a cell

XX Sequence 14 BP; 2 A; 7 C; 2 G; 0 T; 3 U; 0 Other;

Query Match 1.2%; Score 12.4; DB 1; Length 14;

Best Local Similarity 71.4%; Pred. No. 3.3e+02;

Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1567 TCACTGACCTGCT 1580

Db 1 UCACCGACCGCCU 14

RESULT 508

ABX50033

ID ABX50033 standard; DNA; 14 BP.

XX AC ABX50033;

XX 12-FEB-2003 (first entry)

DE Telomere length and/or telomerase activity related polynucleotide #56.

XX Cell proliferation; cell senescence; telomere length;

gene expression; downregulation; interleukin-5; IL-5; ICAM-1;  
intercellular adhesion molecule; rel A; tumour necrosis factor;  
TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;  
translocation; chronic myelogenous leukaemia; CML; cancer;  
Philadelphia chromosome; inflammation; autoimmune disease;  
atherosclerosis; myocardial infarction; stroke; restenosis;  
transplant rejection; rheumatoid arthritis; psoriasis;  
myocardial ischaemia; Kawasaki disease; septic shock; HIV;  
human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;  
SS.

Mus musculus.

WO9523225-A2.

31-AUG-1995.

23-FEB-1995; 95WO-IB000156.

23-FEB-1994; 94US-00201109.  
29-MAR-1994; 94US-00218934.  
04-APR-1994; 94US-00222795.  
07-APR-1994; 94US-00224483.  
15-APR-1994; 94US-00227958.  
15-APR-1994; 94US-00228041.  
15-APR-1994; 94US-00245736.  
18-MAY-1994; 94US-00271280.  
06-JUL-1994; 94US-00291433.  
15-AUG-1994; 94US-00291932.  
17-AUG-1994; 94US-00291433.  
16-AUG-1994; 94US-00292620.  
19-AUG-1994; 94US-00293520.  
02-SEP-1994; 94US-00300000.  
08-SEP-1994; 94US-00303039.  
23-SEP-1994; 94US-00311486.  
23-SEP-1994; 94US-00311749.  
23-SEP-1994; 94US-00314397.  
23-SEP-1994; 94US-00316771.  
07-OCT-1994; 94US-00319492.  
11-OCT-1994; 94US-00321993.  
04-NOV-1994; 94US-00334847.  
10-NOV-1994; 94US-00337608.  
28-NOV-1994; 94US-00345516.  
16-DEC-1994; 94US-00357577.  
23-DEC-1994; 94US-00363233.  
30-JAN-1995; 95US-00380734.

(RIBO-) RIBOZYME PHARM INC.

Stinchcomb DT, Chowrira B, Drenzo A, Draper KG, Dudycz LW;  
Grimm S, Karpeisky A, Kisch K, Matulic-Adamic J, Mcswiggen JA;  
Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;  
Tracz D, Usman N, Wincott PE, Woolf T;  
WPI; 1995-351090/45.

Ribozymes having modified bases and methods for producing them - for use  
in inhibiting disease related genes.

Claim 2; Page 221; 407pp; English.

The present sequence represents a preferred target sequence for an  
enzymatic nucleic acid (i.e. a ribozyme) which cleaves interleukin-5 (IL-  
5) mRNA at the nucleotide base position indicated in the DE line. Regions  
of the mRNA that do not form secondary folding structures and that  
contain potential hammerhead and hairpin ribozyme cleavage sites were  
identified by computer analysis. Ribozymes directed against these mRNA  
sequences were designed and synthesised with modifications that improve  
their nuclease resistance. The ribozymes cleave the IL-5 target sequences  
and thereby inhibit IL-5 expression, making them useful for treating  
chronic asthma, e.g. by inhibiting the synthesis of IL-5 in lymphocytes  
and preventing the recruitment and activation of eosinophils. The  
ribozymes can also be used to treat eosinophilia (related to parasitic  
infection or with pulmonary infiltration) and L-tryptophan-associated

CC eosinophilia-myalgia syndrome. (Updated on 25-MAR-2003 to correct PI  
CC field.)  
XX  
SQ Sequence 15 BP; 8 A; 1 C; 3 G; 0 T; 3 U; 0 Other;  
Query Match 1.2%; Score 12.4; DB 1; Length 15;  
Best Local Similarity 78.6%; Pred. No. 3.5e+02;  
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 1956 AAAGCATGAAATGG 1969  
Db 1 AAAGCAUAAAUUGG 14  
RESULT 510  
AAT56843/C  
ID AAT56843 standard; RNA; 15 BP.  
XX  
AC AAT56843;  
XX  
DT 27-AUG-2003 (revised)  
DT 25-MAR-2003 (revised)  
DT 04-APR-1997 (first entry)  
XX  
DE RSV 1B hammerhead ribozyme target sequence (nt. position 421).  
XX  
KW Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;  
KW gene expression; downregulation; interleukin-5; IL-5; ICAM-1;  
KW intercellular adhesion molecule; rel A; tumour necrosis factor;  
KW TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;  
KW translocation; chronic myelogenous leukaemia; CML; cancer;  
KW Philadelphia chromosome; inflammation; autoimmune disease;  
KW atherosclerosis; myocardial infarction; stroke; restenosis;  
KW transplant rejection; rheumatoid arthritis; psoriasis;  
KW myocardial ischaemia; Kawasaki disease; septic shock; HIV;  
KW human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;  
SS.  
XX  
OS Respiratory syncytial virus.  
XX  
PN WO9523225-A2.  
XX  
PD 31-AUG-1995.  
XX  
PF 23-FEB-1995; 95WO-IB000156.  
XX  
PR 23-FEB-1994; 94US-00201109.  
PR 23-MAR-1994; 94US-00218934.  
PR 04-APR-1994; 94US-00222795.  
PR 07-APR-1994; 94US-00224483.  
PR 15-APR-1994; 94US-00227958.  
PR 15-APR-1994; 94US-00228041.  
PR 18-MAY-1994; 94US-00245736.  
PR 06-JUL-1994; 94US-00271280.  
PR 13-AUG-1994; 94US-00291433.  
PR 16-AUG-1994; 94US-00291932.  
PR 17-AUG-1994; 94US-00292620.  
PR 19-AUG-1994; 94US-00293520.  
PR 02-SEP-1994; 94US-00300000.  
PR 08-SEP-1994; 94US-00303039.  
PR 23-SEP-1994; 94US-00311486.  
PR 23-SEP-1994; 94US-00311749.  
PR 28-SEP-1994; 94US-00314397.  
PR 03-OCT-1994; 94US-00316771.  
PR 07-OCT-1994; 94US-00319492.  
PR 11-OCT-1994; 94US-00321993.  
PR 04-NOV-1994; 94US-00334847.  
PR 10-NOV-1994; 94US-00337608.  
PR 28-NOV-1994; 94US-00345516.  
PR 16-DEC-1994; 94US-00357577.  
PR 23-DEC-1994; 94US-00363233.  
PR 30-JAN-1995; 95US-00380734.  
XX

PA (RIBO-) RIBOZYME PHARM INC.  
 XX Stinchcomb DT, Chowrira B, Drenzo A, Draper KG, Dudycz LW;  
 PI Grimm S, Karpeisky A, Kisch K, Matulic-Adamic J, Mcswiggen JA;  
 PI Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;  
 PI Tracz D, Usman N, Wincott FE, Woolf T;  
 XX WPI; 1995-351090/45.  
 XX Ribozymes having modified bases and methods for producing them - for use  
 PT in inhibiting disease related genes.  
 XX Claim 2; Page 265; 407pp; English.  
 XX The present sequence represents a preferred target sequence for an  
 CC enzymatic nucleic acid (i.e. a ribozyme) which cleaves mRNA coding for a  
 CC protein of respiratory syncytial virus (RSV) at the nucleotide base  
 CC position indicated in the DE line. Regions of the mRNA that do not form  
 CC secondary folding structures and that contain potential hammerhead and  
 CC hairpin ribozyme cleavage sites were identified by computer analysis.  
 CC Ribozymes directed against these mRNA sequences were designed and  
 CC synthesised with modifications that improve their nuclease resistance.  
 CC The ribozymes cleave the target sequences and can be used for treatment  
 CC and diagnosis of RSV infection. (Updated on 25-MAR-2003 to correct PI  
 CC field.) (Updated on 27-AUG-2003 to correct OS field.)  
 XX Sequence 15 BP; 7 A; 5 C; 0 G; 0 T; 3 U; 0 Other;  
 SQ Query Match 1.2%; Score 12.4; DB 1; Length 15;  
 Best Local Similarity 92.9%; Pred. No. 3.5e+02;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1784 TGTAAATATTGTGT 1797  
 DB 14 TGTGAATATTGTGT 1  
 RESULT 511  
 AAT54631  
 ID AAT54631 standard; RNA; 15 BP.  
 XX AC AAT54631;  
 XX 25-MAR-2003 (revised)  
 DT 22-APR-1997 (first entry)  
 XX Mouse IL-5 hammerhead ribozyme target sequence (nt. position 1439).  
 DE Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;  
 KW gene expression; downregulation; interleukin-5; IL-5; ICAM-1;  
 KW intercellular adhesion molecule; rel A; tumour necrosis factor;  
 KW TNF-alpha; respiratory syncytial virus; RSV; bor-abl; oncogene;  
 KW translocation; chronic myelogenous leukaemia; CML; cancer;  
 KW Philadelphia chromosome; inflammation; autoimmune disease;  
 KW atherosclerosis; myocardial infarction; stroke; restenosis;  
 KW transplant rejection; rheumatoid arthritis; psoriasis;  
 KW myocardial ischaemia; Kawasaki disease; septic shock; HIV;  
 KW human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;  
 KW ss.  
 XX Mus musculus.  
 OS WO9523225-A2.  
 XX 31-AUG-1995.  
 PD 23-FEB-1995; 95WO-IB000156.  
 PF 23-FEB-1994; 94US-00201109.  
 PR 29-MAR-1994; 94US-00218934.  
 PR 04-APR-1994; 94US-00222795.  
 PR 07-APR-1994; 94US-00224483.  
 PR 15-APR-1994; 94US-00227958.

PR 15-APR-1994; 94US-00228041.  
 PR 18-MAY-1994; 94US-00245736.  
 PR 06-JUL-1994; 94US-00271280.  
 PR 15-AUG-1994; 94US-00291932.  
 PR 16-AUG-1994; 94US-00291433.  
 PR 17-AUG-1994; 94US-00292620.  
 PR 19-AUG-1994; 94US-00293520.  
 PR 02-SEP-1994; 94US-00300000.  
 PR 08-SEP-1994; 94US-00303039.  
 PR 23-SEP-1994; 94US-00311486.  
 PR 28-SEP-1994; 94US-00311749.  
 PR 03-OCT-1994; 94US-00314397.  
 PR 07-OCT-1994; 94US-00316771.  
 PR 11-OCT-1994; 94US-00319492.  
 PR 04-NOV-1994; 94US-00321993.  
 PR 10-NOV-1994; 94US-00334847.  
 PR 28-NOV-1994; 94US-00337608.  
 PR 16-DEC-1994; 94US-00345516.  
 PR 23-DEC-1994; 94US-00357577.  
 PR 30-JAN-1995; 94US-00363233.  
 XX 95US-00380734.  
 XX (RIBO-) RIBOZYME PHARM INC.  
 PA Stinchcomb DT, Chowrira B, Drenzo A, Draper KG, Dudycz LW;  
 PI Grimm S, Karpeisky A, Kisch K, Matulic-Adamic J, Mcswiggen JA;  
 PI Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;  
 PI Tracz D, Usman N, Wincott FE, Woolf T;  
 XX WPI; 1995-351090/45.  
 XX Ribozymes having modified bases and methods for producing them - for use  
 PT in inhibiting disease related genes.  
 XX Claim 2; Page 221; 407pp; English.  
 XX The present sequence represents a preferred target sequence for an  
 CC enzymatic nucleic acid (i.e. a ribozyme) which cleaves interleukin-5 (IL-  
 CC 5) mRNA at the nucleotide base position indicated in the DE line. Regions  
 CC of the mRNA that do not form secondary folding structures and that  
 CC contain potential hammerhead and hairpin ribozyme cleavage sites were  
 CC identified by computer analysis. Ribozymes directed against these mRNA  
 CC sequences were designed and synthesised with modifications that improve  
 CC their nuclease resistance. The ribozymes cleave the IL-5 target sequences  
 CC and thereby inhibit IL-5 expression, making them useful for treating  
 CC chronic asthma, e.g. by inhibiting the synthesis of IL-5 in lymphocytes  
 CC and preventing the recruitment and activation of eosinophils. The  
 CC ribozymes can also be used to treat eosinophilia (related to parasitic  
 CC infection or with pulmonary infiltration) and L-tryptophan-associated  
 CC eosinophilia-myalgia syndrome. (Updated on 25-MAR-2003 to correct PI  
 CC field.)  
 XX Sequence 15 BP; 3 A; 1 C; 1 G; 0 T; 10 U; 0 Other;  
 SQ Query Match 1.2%; Score 12.4; DB 1; Length 15;  
 Best Local Similarity 35.7%; Pred. No. 3.5e+02;  
 Matches 5; Conservative 8; Mismatches 1; Indels 0; Gaps 0;  
 QY 1284 TTATTAAATCTGT 1297  
 DB 2 UUAUUAUUCUGU 15  
 RESULT 512  
 AAT52173  
 ID AAT52173 standard; RNA; 15 BP.  
 XX AC AAT52173;  
 XX 25-MAR-2003 (revised)  
 DT 25-MAR-1997 (first entry)  
 XX Human ICAM hammerhead ribozyme target sequence (nt. position 2744).  
 DE

XX Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;  
 KW gene expression; downregulation; interleukin-5; IL-5; ICAM-1;  
 KW intercellular adhesion molecule; rel A; tumour necrosis factor;  
 KW TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;  
 KW translocation; chronic myelogenous leukaemia; CML; cancer;  
 KW Philadelphia chromosome; inflammation; autoimmune disease;  
 KW atherosclerosis; myocardial infarction; stroke; restenosis;  
 KW transplant rejection; rheumatoid arthritis; psoriasis;  
 KW myocardial ischaemia; Kawasaki disease; septic shock; HIV;  
 KW human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;  
 KW ss.

XX Homo sapiens.  
 OS  
 XX  
 XX WO9523225-A2.  
 PN  
 XX  
 XX 31-AUG-1995.  
 PD  
 XX  
 XX 23-FEB-1995; 95WO-18000156.  
 PF  
 XX  
 XX 23-FEB-1994; 94US-00201109.  
 PR  
 XX 29-MAR-1994; 94US-00218934.  
 PR  
 XX 04-APR-1994; 94US-00222795.  
 PR  
 XX 07-APR-1994; 94US-00224483.  
 PR  
 XX 15-APR-1994; 94US-00227958.  
 PR  
 XX 18-APR-1994; 94US-00228041.  
 PR  
 XX 18-MAY-1994; 94US-00245736.  
 PR  
 XX 06-JUL-1994; 94US-00271280.  
 PR  
 XX 15-AUG-1994; 94US-00291932.  
 PR  
 XX 16-AUG-1994; 94US-00291433.  
 PR  
 XX 17-AUG-1994; 94US-00292620.  
 PR  
 XX 19-AUG-1994; 94US-00293520.  
 PR  
 XX 02-SEP-1994; 94US-00300000.  
 PR  
 XX 08-SEP-1994; 94US-00303039.  
 PR  
 XX 23-SEP-1994; 94US-00311486.  
 PR  
 XX 28-SEP-1994; 94US-00311749.  
 PR  
 XX 03-OCT-1994; 94US-00314397.  
 PR  
 XX 07-OCT-1994; 94US-00315771.  
 PR  
 XX 11-OCT-1994; 94US-00321993.  
 PR  
 XX 04-NOV-1994; 94US-00334847.  
 PR  
 XX 10-NOV-1994; 94US-00337608.  
 PR  
 XX 28-NOV-1994; 94US-00345516.  
 PR  
 XX 16-DEC-1994; 94US-00357577.  
 PR  
 XX 23-DEC-1994; 94US-00363233.  
 PR  
 XX 30-JAN-1995; 95US-00380734.  
 PR  
 XX (RIBO-) RIBOZYME PHARM INC.  
 PA  
 XX  
 XX Stinchcomb DT, Chowrira B, Dizenzo A, Draper KG, Dudycz LW;  
 PI Grimm S, Karpeisky A, Kisich K, Matulic-Adamic J, McSwiggen JA;  
 PI Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;  
 PI Tracz D, Usman N, Wincott FE, Woolf T;  
 XX  
 XX WPI; 1995-351090/45.  
 DR  
 XX  
 XX Ribozymes having modified bases and methods for producing them - for use  
 PT in inhibiting disease related genes.  
 XX  
 XX Claim 2; Page 175; 407pp; English.  
 PS  
 XX  
 XX The present sequence represents a preferred target sequence for an  
 CC enzymatic nucleic acid (i.e. a ribozyme) which cleaves ICAM-1 mRNA at the  
 CC nucleotide base position indicated in the DE line. Regions of the mRNA  
 CC that do not form secondary folding structures and that contain potential  
 CC hammerhead and hairpin ribozyme cleavage sites were identified by  
 CC computer analysis. Ribozymes directed against these mRNA sequences were  
 CC designed and synthesised with modifications that improve their nuclease  
 CC resistance. The ribozymes cleave the ICAM-1 target sequences and thereby  
 CC inhibit ICAM-1 expression, making them useful for reducing transplant  
 CC rejection and alleviating symptoms in patients with rheumatoid arthritis,  
 CC asthma and other inflammatory disorders. (Updated on 25-MAR-2003 to

CC correct PI field.)  
 XX  
 SQ Sequence 15 BP; 2 A; 0 C; 6 G; 0 T; 7 U; 0 Other;  
 Query Match 1.2%; Score 12.4; DB 1; Length 15;  
 Best Local Similarity 42.9%; Pred. No. 3.5e+02;  
 Matches 6; Conservative 7; Mismatches 1; Indels 0; Gaps 0;  
 QY 1801 TGTGTCGTGTCGTGA 1814  
 Db 1 UGUGUGUAUGUGUA 14

RESULT 513  
 AAF47616/c  
 ID AAF47616 standard; DNA; 15 BP.  
 XX  
 XX AAF47616;  
 AC  
 XX 30-MAR-2001 (first entry)  
 DT  
 XX IGFBP3 oligonucleotide #1036.  
 DE  
 XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;  
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;  
 KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;  
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;  
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;  
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;  
 KW hyperneovascular condition; hyperplasia; kidney disease;  
 KW neovascular condition of the retina; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200078341-A1.  
 PN  
 XX 28-DEC-2000.  
 PD  
 XX 21-JUN-2000; 2000WO-AU000693.  
 XX  
 XX 21-JUN-1999; 99US-0140345P.  
 PR  
 XX (MURD-) MURDOCH CHILDRENS RES INST.  
 PA  
 XX Wright CJ, Werther GA, Edmondson SR;  
 PI WPI; 2001-041421/05.  
 DR  
 XX  
 XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering  
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that  
 PT inhibits or reduces growth factor mediated cell proliferation and/or  
 PT inflammation.  
 PS  
 XX Example 7; Page 50; 201pp; English.  
 XX  
 XX The present invention relates to a method for ameliorating the effects of  
 CC skin disorders. The method comprises contacting the skin with an  
 CC antisense oligonucleotide (for insulin-like Growth Factor [IGF]-1  
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of  
 CC inhibiting or reducing growth factor mediated cell proliferation,  
 CC inflammation and/or other disorders. The present sequence is an  
 CC oligonucleotide which can be used to design the antisense  
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-  
 CC F45161). The method is useful for ameliorating the effects of psoriasis,  
 CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,  
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a  
 CC hyperneovascular condition such as a neovascular condition of the retina,  
 CC brain or skin, growth factor-mediated malignancies, other sclerotic  
 CC disease, kidney disease, hyperproliferation of the inside of blood  
 CC vessels or any other hyperplasia  
 XX  
 SQ Sequence 15 BP; 6 A; 4 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 1.2%; Score 12.4; DB 1; Length 15;  
 Best Local Similarity 92.9%; Pred. No. 3.5e+02;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2046 GTCCTGGCAGGCT 2059  
 DB 15 GTCCTGGCAGGCT 2

RESULT 514  
 AAF50118  
 ID AAF50118 standard; DNA; 15 BP.  
 XX AC AAF50118;  
 XX 30-MAR-2001 (first entry)  
 DT IGF-I oligonucleotide #1078.  
 DE  
 XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;  
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;  
 KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;  
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;  
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;  
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;  
 KW hyperneovascular condition; hyperplasia; kidney disease;  
 KW neovascular condition of the retina; ss.  
 XX Homo sapiens.  
 OS WO200078341-A1.  
 XX 28-DEC-2000.  
 XX 21-JUN-2000; 2000WO-AU000693.  
 XX 21-JUN-1999; 99US-0140345P.  
 PR (MURD-) MURDOCH CHILDRENS RES INST.  
 XX Wright CJ, Werther GA, Edmondson SR;  
 WPI; 2001-041421/05.  
 XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering  
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that  
 PT inhibits or reduces growth factor mediated cell proliferation and/or  
 PT inflammation.  
 XX Example 8; Page 67; 201pp; English.  
 XX The present invention relates to a method for ameliorating the effects of  
 CC skin disorders. The method comprises contacting the skin with an  
 CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1  
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of  
 CC inhibiting or reducing growth factor mediated cell proliferation,  
 CC inflammation and/or other disorders. The present sequence is an  
 CC oligonucleotide which can be used to design the antisense  
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-  
 CC F45161). The method is useful for ameliorating the effects of psoriasis,  
 CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,  
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a  
 CC hyperneovascular condition such as a neovascular condition of the retina,  
 CC brain or skin, growth factor-mediated malignancies, other sclerotic  
 CC disease, kidney disease, hyperproliferation of the inside of blood  
 CC vessels or any other hyperplasia  
 XX Sequence 15 BP; 3 A; 4 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 1.2%; Score 12.4; DB 1; Length 15;  
 Best Local Similarity 92.9%; Pred. No. 3.5e+02;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1983 AATTCTGCTCAGAT 1996  
 DB 1 ACTTCTGCTCAGAT 14

RESULT 515  
 AAF46653/C  
 ID AAF46653 standard; DNA; 15 BP.  
 XX AC AAF46653;  
 XX 30-MAR-2001 (first entry)  
 DT IGFBP3 oligonucleotide #73.  
 DE  
 XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;  
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;  
 KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;  
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;  
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;  
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;  
 KW hyperneovascular condition; hyperplasia; kidney disease;  
 KW neovascular condition of the retina; ss.  
 XX Homo sapiens.  
 OS WO200078341-A1.  
 XX 28-DEC-2000.  
 XX 21-JUN-2000; 2000WO-AU000693.  
 XX 21-JUN-1999; 99US-0140345P.  
 PR (MURD-) MURDOCH CHILDRENS RES INST.  
 XX Wright CJ, Werther GA, Edmondson SR;  
 WPI; 2001-041421/05.  
 XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering  
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that  
 PT inhibits or reduces growth factor mediated cell proliferation and/or  
 PT inflammation.  
 XX Example 7; Page 44; 201pp; English.  
 XX The present invention relates to a method for ameliorating the effects of  
 CC skin disorders. The method comprises contacting the skin with an  
 CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1  
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of  
 CC inhibiting or reducing growth factor mediated cell proliferation,  
 CC inflammation and/or other disorders. The present sequence is an  
 CC oligonucleotide which can be used to design the antisense  
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-  
 CC F45161). The method is useful for ameliorating the effects of psoriasis,  
 CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,  
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a  
 CC hyperneovascular condition such as a neovascular condition of the retina,  
 CC brain or skin, growth factor-mediated malignancies, other sclerotic  
 CC disease, kidney disease, hyperproliferation of the inside of blood  
 CC vessels or any other hyperplasia  
 XX Sequence 15 BP; 4 A; 7 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 1.2%; Score 12.4; DB 1; Length 15;  
 Best Local Similarity 92.9%; Pred. No. 3.5e+02;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2047 TCCTTGGCAGGCTG 2060  
 DB 15 TGCTTGGCAGGCTG 2

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XX AC RESULT 516
XX AAF48749/c
XX ID AAF48749 standard; DNA; 15 BP.
XX AC
XX AC AAF48749;
XX DT
XX DT 30-MAR-2001 (first entry)
XX DE
XX DE IGFBP3 oligonucleotide #2169.
XX KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
XX KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
XX KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
XX KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
XX KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
XX KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
XX KW hyperneovascular condition of the retina; ss.
XX KW neovascular condition of the retina; ss.
XX OS Homo sapiens.
XX PN WO200078341-A1.
XX PD 28-DEC-2000.
XX PF 21-JUN-2000; 2000WO-AU000693.
XX PR 21-JUN-1999; 99US-0140345P.
XX PA (MURD-) MURDOCH CHILDRENS RES INST.
XX PI Wright CJ, Werther GA, Edmondson SR;
XX DR WPI; 2001-041421/05.
XX KW Ameliorating the effects of a disorder, e.g. psoriasis, by administering
XX KW UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
XX KW inhibits or reduces growth factor mediated cell proliferation and/or
XX KW inflammation.
XX PS Example 7; Page 58; 201pp; English.
XX CC The present invention relates to a method for ameliorating the effects of
XX CC skin disorders. The method comprises contacting the skin with an
XX CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
XX CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
XX CC inhibiting or reducing growth factor mediated cell proliferation,
XX CC inflammation and/or other disorders. The present sequence is an
XX CC oligonucleotide which can be used to design the antisense
XX CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
XX CC F45161). The method is useful for ameliorating the effects of psoriasis,
XX CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
XX CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
XX CC hyperneovascular condition such as a neovascular condition of the retina,
XX CC brain or skin, growth factor-mediated malignancies, other sclerotic
XX CC disease, kidney disease, hyperproliferation of the inside of blood
XX CC vessels or any other hyperplasia
XX SQ Sequence 15 BP; 6 A; 1 C; 3 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 1.2%; Score 12.4; DB 1; Length 15;
XX Best Local Similarity 92.9%; Pred. No. 3.5e+02;
XX Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1495 ATCAGATAGCATCT 1508
XX DB |||||
XX . 14 ATCATATAGCATCT 1
XX
XX RESULT 517
XX AAF47618/c
XX ID AAF47618 standard; DNA; 15 BP.

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XX AAF47618;
XX DT
XX DT 30-MAR-2001 (first entry)
XX DE
XX DE IGFBP3 oligonucleotide #1038.
XX KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
XX KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
XX KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
XX KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
XX KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
XX KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
XX KW hyperneovascular condition; hyperplasia; kidney disease;
XX KW neovascular condition of the retina; ss.
XX OS Homo sapiens.
XX PN WO200078341-A1.
XX PD 28-DEC-2000.
XX PF 21-JUN-2000; 2000WO-AU000693.
XX PR 21-JUN-1999; 99US-0140345P.
XX PA (MURD-) MURDOCH CHILDRENS RES INST.
XX PI Wright CJ, Werther GA, Edmondson SR;
XX DR WPI; 2001-041421/05.
XX KW Ameliorating the effects of a disorder, e.g. psoriasis, by administering
XX KW UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
XX KW inhibits or reduces growth factor mediated cell proliferation and/or
XX KW inflammation.
XX PS Example 7; Page 50; 201pp; English.
XX CC The present invention relates to a method for ameliorating the effects of
XX CC skin disorders. The method comprises contacting the skin with an
XX CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
XX CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
XX CC inhibiting or reducing growth factor mediated cell proliferation,
XX CC inflammation and/or other disorders. The present sequence is an
XX CC oligonucleotide which can be used to design the antisense
XX CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
XX CC F45161). The method is useful for ameliorating the effects of psoriasis,
XX CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
XX CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
XX CC hyperneovascular condition such as a neovascular condition of the retina,
XX CC brain or skin, growth factor-mediated malignancies, other sclerotic
XX CC disease, kidney disease, hyperproliferation of the inside of blood
XX CC vessels or any other hyperplasia
XX SQ Sequence 15 BP; 5 A; 4 C; 4 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 1.2%; Score 12.4; DB 1; Length 15;
XX Best Local Similarity 92.9%; Pred. No. 3.5e+02;
XX Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 2045 TGTCCTGGCAGGC 2058
XX DB |||||
XX 14 TGTCCTGGCAGTC 1
XX
XX RESULT 518
XX AAF46654/c
XX ID AAF46654 standard; DNA; 15 BP.
XX AC
XX AC AAF46654;
XX DT
XX DT 30-MAR-2001 (first entry)

```

XX IGFBP3 oligonucleotide #74.  
DE  
XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;  
KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;  
KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;  
KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;  
KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;  
KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;  
KW hyperneovascular condition; hyperplasia; kidney disease;  
KW neovascular condition of the retina; ss.  
XX  
XX Homo sapiens.  
XX WO200078341-A1.  
XX 28-DEC-2000.  
XX 21-JUN-2000; 2000WO-AU000693.  
XX 21-JUN-1999; 99US-0140345P.  
XX (MURD-) MURDOCH CHILDRENS RES INST.  
XX Wright CJ, Werther GA, Edmondson SR;  
XX WPI; 2001-041421/05.  
XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering  
PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that  
PT inhibits or reduces growth factor mediated cell proliferation and/or  
PT inflammation.  
XX  
XX Example 7; Page 44; 201pp; English.  
XX The present invention relates to a method for ameliorating the effects of  
CC skin disorders. The method comprises contacting the skin with an  
CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1  
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of  
CC inhibiting or reducing growth factor mediated cell proliferation,  
CC inflammation and/or other disorders. The present sequence is an  
CC oligonucleotide which can be used to design the antisense  
CC oligonucleotides of the present invention (see AAF45151 and AAF45153-  
CC F45161). The method is useful for ameliorating the effects of psoriasis,  
CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,  
CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a  
CC hyperneovascular condition such as a neovascular condition of the retina,  
CC brain or skin, growth factor-mediated malignancies, other sclerotic  
CC disease, kidney disease, hyperproliferation of the inside of blood  
CC vessels or any other hyperplasia  
XX  
XX Sequence 15 BP; 4 A; 6 C; 4 G; 1 T; 0 U; 0 Other;  
SQ  
Query Match 1.2%; Score 12.4; DB 1; Length 15;  
Best Local Similarity 92.9%; Pred. No. 3.5e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2047 TCCTTGGCAGGCTG 2060  
Db 14 TCCTTGGCAGGCTG 1  
RESULT 519  
AAF50117  
ID AAF50117 standard; DNA; 15 BP.  
XX  
XX AAF50117;  
AC  
XX 30-MAR-2001 (first entry)  
DT  
XX IGF-I oligonucleotide #1077.  
DE  
XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;  
KW

KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;  
KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;  
KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;  
KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;  
KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;  
KW hyperneovascular condition; hyperplasia; kidney disease;  
KW neovascular condition of the retina; ss.  
XX  
XX Homo sapiens.  
XX WO200078341-A1.  
XX 28-DEC-2000.  
XX 21-JUN-2000; 2000WO-AU000693.  
XX 21-JUN-1999; 99US-0140345P.  
XX (MURD-) MURDOCH CHILDRENS RES INST.  
XX Wright CJ, Werther GA, Edmondson SR;  
XX WPI; 2001-041421/05.  
XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering  
PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that  
PT inhibits or reduces growth factor mediated cell proliferation and/or  
PT inflammation.  
XX  
XX Example 8; Page 67; 201pp; English.  
XX The present invention relates to a method for ameliorating the effects of  
CC skin disorders. The method comprises contacting the skin with an  
CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1  
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of  
CC inhibiting or reducing growth factor mediated cell proliferation,  
CC inflammation and/or other disorders. The present sequence is an  
CC oligonucleotide which can be used to design the antisense  
CC oligonucleotides of the present invention (see AAF45151 and AAF45153-  
CC F45161). The method is useful for ameliorating the effects of psoriasis,  
CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,  
CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a  
CC hyperneovascular condition such as a neovascular condition of the retina,  
CC brain or skin, growth factor-mediated malignancies, other sclerotic  
CC disease, kidney disease, hyperproliferation of the inside of blood  
CC vessels or any other hyperplasia  
XX  
XX Sequence 15 BP; 3 A; 4 C; 2 G; 6 T; 0 U; 0 Other;  
SQ  
Query Match 1.2%; Score 12.4; DB 1; Length 15;  
Best Local Similarity 92.9%; Pred. No. 3.5e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1983 AATCTCTCTCAGAT 1996  
Db 2 ACTTCTCTCAGAT 15  
RESULT 520  
AAF53695  
ID AAF53695 standard; DNA; 15 BP.  
XX  
XX AAF53695;  
AC  
XX 30-MAR-2001 (first entry)  
DT  
XX IGF-I oligonucleotide #4655.  
DE  
XX  
XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;  
KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;  
KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;  
KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;  
KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;  
KW





PD 28-DEC-2000.  
 XX  
 XX  
 PF 21-JUN-2000; 2000WO-AU000693.  
 XX  
 XX 21-JUN-1999; 99US-0140345P.  
 PR  
 XX (MURD-) MURDOCH CHILDRENS RES INST.  
 XX  
 PA Wraight CJ, Werther GA, Edmondson SR;  
 XX WPI; 2001-041421/05.  
 XX  
 XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering  
 PT UV (ultra-violet) treatment (optional) and an antisenese nucleic acid that  
 PT inhibits or reduces growth factor mediated cell proliferation and/or  
 PT inflammation.  
 XX  
 XX Example 7; Page 56; 201pp; English.  
 PS  
 CC The present invention relates to a method for ameliorating the effects of  
 CC skin disorders. The method comprises contacting the skin with an  
 CC antisenese oligonucleotide, (for Insulin-like Growth Factor [IGF]-1  
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of  
 CC inhibiting or reducing growth factor mediated cell proliferation,  
 CC inflammation and/or other disorders. The present sequence is an  
 CC oligonucleotide which can be used to design the antisenese  
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-  
 CC F45161). The method is useful for ameliorating the effects of psoriasis,  
 CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,  
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a  
 CC hyperneovascular condition such as a neovascular condition of the retina,  
 CC brain or skin, growth factor-mediated malignancies, other sclerotic  
 CC disease, kidney disease, hyperproliferation of the inside of blood  
 CC vessels or any other hyperplasia  
 XX  
 XX Sequence 15 BP; 2 A; 3 C; 1 G; 9 T; 0 U; 0 Other;  
 SQ  
 Query Match 1.2%; Score 12.4; DB 1; Length 15;  
 Best Local Similarity 92.9%; Pred. No. 3.5e+02;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2248 AGTTGAATAAAG 2261  
 DB 15 AGATGAATAAAG 2  
 RESULT 523  
 AAF48748/C  
 ID AAF48748 standard; DNA; 15 BP.  
 XX  
 XX AAF48748;  
 XX  
 XX 30-MAR-2001 (first entry)  
 XX  
 XX IGFBP3 oligonucleotide #2168.  
 XX  
 KW Antisenese therapy; antiproliferative; antiinflammatory; antipsoriatic;  
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;  
 KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;  
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;  
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;  
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;  
 KW hyperneovascular condition; hyperplasia; kidney disease;  
 KW neovascular condition of the retina; ss.  
 XX  
 XX Homo sapiens.  
 XX  
 XX WO200078341-A1.  
 XX  
 XX 28-DEC-2000.  
 XX  
 XX 21-JUN-2000; 2000WO-AU000693.  
 XX  
 XX 28-DEC-2000.  
 XX  
 XX 21-JUN-2000; 2000WO-AU000693.  
 XX  
 XX

PR 21-JUN-1999; 99US-0140345P.  
 XX  
 XX (MURD-) MURDOCH CHILDRENS RES INST.  
 XX  
 XX Wraight CJ, Werther GA, Edmondson SR;  
 XX WPI; 2001-041421/05.  
 XX  
 XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering  
 PT UV (ultra-violet) treatment (optional) and an antisenese nucleic acid that  
 PT inhibits or reduces growth factor mediated cell proliferation and/or  
 PT inflammation.  
 XX  
 XX Example 7; Page 58; 201pp; English.  
 PS  
 CC The present invention relates to a method for ameliorating the effects of  
 CC skin disorders. The method comprises contacting the skin with an  
 CC antisenese oligonucleotide, (for Insulin-like Growth Factor [IGF]-1  
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of  
 CC inhibiting or reducing growth factor mediated cell proliferation,  
 CC inflammation and/or other disorders. The present sequence is an  
 CC oligonucleotide which can be used to design the antisenese  
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-  
 CC F45161). The method is useful for ameliorating the effects of psoriasis,  
 CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,  
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a  
 CC hyperneovascular condition such as a neovascular condition of the retina,  
 CC brain or skin, growth factor-mediated malignancies, other sclerotic  
 CC disease, kidney disease, hyperproliferation of the inside of blood  
 CC vessels or any other hyperplasia  
 XX  
 XX Sequence 15 BP; 5 A; 1 C; 4 G; 5 T; 0 U; 0 Other;  
 SQ  
 Query Match 1.2%; Score 12.4; DB 1; Length 15;  
 Best Local Similarity 92.9%; Pred. No. 3.5e+02;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1495 ATCAGATAGCATCT 1508  
 DB 15 ATCATATAGCATCT 2  
 RESULT 524  
 AAF48472/C  
 ID AAF48472 standard; DNA; 15 BP.  
 XX  
 XX AAF48472;  
 XX  
 XX 30-MAR-2001 (first entry)  
 XX  
 XX IGFBP3 oligonucleotide #1892.  
 XX  
 KW Antisenese therapy; antiproliferative; antiinflammatory; antipsoriatic;  
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;  
 KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;  
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;  
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;  
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;  
 KW hyperneovascular condition; hyperplasia; kidney disease;  
 KW neovascular condition of the retina; ss.  
 XX  
 XX Homo sapiens.  
 XX  
 XX WO200078341-A1.  
 XX  
 XX 28-DEC-2000.  
 XX  
 XX 21-JUN-2000; 2000WO-AU000693.  
 XX  
 XX 21-JUN-1999; 99US-0140345P.  
 XX  
 XX (MURD-) MURDOCH CHILDRENS RES INST.  
 XX

PI Wright CJ, Werther GA, Edmondson SR;  
 DR WPI; 2001-041421/05.  
 XX  
 PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering  
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that  
 PT inhibits or reduces growth factor mediated cell proliferation and/or  
 PT inflammation.  
 XX  
 XX Example 7; Page 56; 201pp; English.  
 PS  
 XX The present invention relates to a method for ameliorating the effects of  
 CC skin disorders. The method comprises contacting the skin with an  
 CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1  
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of  
 CC inhibiting or reducing growth factor mediated cell proliferation,  
 CC inflammation and/or other disorders. The present sequence is an  
 CC oligonucleotide which can be used to design the antisense  
 CC oligonucleotides of the present invention (see AAP45151 and AAP45153-  
 CC F45161). The method is useful for ameliorating the effects of psoriasis,  
 CC ichthyosis, pityriasis, ruba, pilaris, seborrheoa, keloids, keratosis,  
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a  
 CC hyperneovascular condition such as a neovascular condition of the retina,  
 CC brain or skin, growth factor-mediated malignancies, other sclerotic  
 CC disease, kidney disease, hyperproliferation of the inside of blood  
 CC vessels or any other hyperplasia  
 XX  
 SQ Sequence 15 BP; 2 A; 4 C; 0 G; 9 T; 0 U; 0 Other;  
 Query Match 1.2%; Score 12.4; DB 1; Length 15;  
 Best Local Similarity 92.9%; Pred. No. 3.5e+02;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2248 AGTTGAAATAAAG 2261  
 DB 14 AGATGAAATAAAG 1  
 RESULT 525  
 ABX03996/C  
 ID ABX03996 standard; DNA; 15 BP.  
 AC ABX03996;  
 XX  
 XX 09-JAN-2003 (first entry)  
 DT  
 DE Resistance gene carb-4 DNA fragment.  
 XX  
 KW Detection; probe; diagnosis; oral disease; parodontitis; caries; therapy;  
 KW polymorphism; virulence factor; antibiotic resistance gene; prognosis;  
 KW oral infection; detection; pathogen; coronary heart disease;  
 KW diabetic symptom; ss.  
 XX  
 OS Unidentified.  
 XX  
 XX DB20110013-UI.  
 XX  
 XX 18-OCT-2001.  
 XX  
 XX 13-MAR-2001; 2001DE-02010013.  
 XX  
 XX 13-MAR-2001; 2001DE-01012348.  
 PR 13-MAR-2001; 2001DE-02010013.  
 XX  
 XX (ROET/) ROETGER A.  
 PA  
 XX WPI; 2001-657777/76.  
 DR  
 XX Oligonucleotide array, useful for diagnosing oral diseases, particularly  
 PT parodontitis, carries human or microbial reference sequences.  
 PT  
 XX Claim 10; Page 27; 58pp; German.  
 PS  
 XX  
 CC This invention describes a novel nucleotide carrier with probes used for  
 CC diagnosis of oral diseases, particularly parodontitis, but also caries,  
 CC especially to identify genetic predisposition (as indicated by  
 CC polymorphisms) to disease and to identify causative microorganisms or  
 CC their associated virulence factors and antibiotic resistance genes, e.g.  
 CC for selection of therapy and for prognosis. They are also useful for  
 CC research into oral infections. The carriers allow simultaneous detection  
 CC of both host and pathogen parameters, providing quickly and simply an  
 CC individual's parodontitis profile, including detection of pathogens that  
 CC are associated with increased risk of coronary heart diseases and/or  
 CC aggravation of diabetic symptoms, and of opportunistic pathogens.  
 CC AX03870-ABX04044 represent DNA fragments used to illustrate the method  
 CC of the invention  
 XX  
 SQ Sequence 15 BP; 4 A; 3 C; 3 G; 5 T; 0 U; 0 Other;  
 Query Match 1.2%; Score 12.4; DB 1; Length 15;  
 Best Local Similarity 92.9%; Pred. No. 3.5e+02;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1275 TAGCACAAAGTTATT 1288  
 DB 15 TAGCACAAAGTTATT 2  
 RESULT 526  
 AAH18788  
 ID AAH18788 standard; DNA; 15 BP.  
 XX  
 AC AAH18788;  
 XX  
 XX 25-JUN-2001 (first entry)  
 DT  
 XX Human IL4 allele-specific primer SEQ ID NO: 47.  
 DE  
 XX Human; interleukin-4; IL4; single nucleotide polymorphism; SNP; atopy;  
 KW inflammatory disorder; immune disorder; population diversity;  
 KW paternity test; forensic test; cytokine; chromosome 5q31.1; probe;  
 KW PCR primer; ss.  
 XX  
 XX Homo sapiens.  
 OS  
 XX WO200123404-A1.  
 PN  
 XX 05-APR-2001.  
 PD  
 XX 28-SEP-2000; 2000WO-USQ26608.  
 PF  
 XX 30-SEP-1999; 99US-0156825P.  
 PR  
 XX (GENA-) GENAISSANCE PHARM INC.  
 PA  
 XX Chew A, Choi JY, Denton RR, Nandabalan K, Stephens JC;  
 PI WPI; 2001-316132/33.  
 XX  
 XX Polynucleotide comprising novel single nucleotide polymorphisms in human  
 PT interleukin-4 gene for use in studying expression, function of  
 PT interleukin-4, in developing drugs, diagnosis and treatment of immune  
 PT disorders.  
 XX  
 XX Claim 12; Page 16; 71pp; English.  
 PS  
 XX The present invention provides the protein, cDNA and gene of human  
 CC interleukin-4 (IL4). The coding sequences for this protein contain single  
 CC nucleotide polymorphisms (SNPs) which may be associated with differences  
 CC in susceptibility to atopy, inflammatory and immune diseases and  
 CC different drug responses. They may also be used in applications such as  
 CC forensic and paternity testing and studying population diversity and  
 CC anthropological lineage. The IL4 gene is found on human chromosome 5q31.1  
 CC  
 XX Sequence 15 BP; 3 A; 1 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 1.2%; Score 12.4; DB 1; Length 15;  
Best Local Similarity 92.9%; Pred. No. 3.5e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2158 GGAGCATTGTTT 2171  
DB 2 GGAGCATTGTTT 15

RESULT 527  
ABX79833  
ID ABX79833 standard; cDNA; 15 BP.  
XX AC ABX79833;  
XX DT 17-APR-2003 (first entry)  
XX DE EST polymorphic DNA repeat polynucleotide #158.  
XX KW EST; expressed sequence tag; ss; polymorphic repeat; tandem repeat;  
KW polymorphic marker prediction of ubiquitous simple sequences; POMPOUS;  
KW Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;  
KW Haw River syndrome; Huntington's disease; fragile-X syndrome;  
KW Friedrich's ataxia; myotonic dystrophy; hyperandrogenaemia;  
KW spinal atrophy; bulbar atrophy; spinocerebellar ataxia.  
XX KW Homo sapiens.  
XX OS  
XX PN US6472154-B1.  
XX PD 29-OCT-2002.  
XX PP 31-DEC-1999; 99US-00475947.  
XX PR 31-DEC-1999; 99US-00475947.  
XX PS (TEXA) UNIV TEXAS SYSTEM.  
XX PI Garner HR, Wren JD, Minna JD, Fondon JW;  
XX WPI; 2003-208818/20.  
XX PT Identifying a candidate polymorphic repeat within a coding sequence, for  
PT understanding or treating genetic disease, comprises detecting tandem  
PT repeats in a target coding sequence and scoring the repeats for  
PT polymorphic probability.  
XX Example; Col 747; 588pp; English.

CC The invention discloses a method for identifying a candidate polymorphic  
CC repeat within a coding sequence (expressed sequence tag, EST), which  
CC comprises detecting tandem repeats in a target coding sequence, scoring  
CC the repeats for polymorphic probability and generating a dataset  
CC correlating the repeats with polymorphic probability to identify a  
CC candidate polymorphic repeat. The computational methods (polymorphic  
CC marker prediction of ubiquitous simple sequences, POMPOUS, and Rep-X) are  
CC useful for identifying and detecting candidate polymorphic repeats in  
CC human genes, which can be used to understand, treat or eliminate genetic  
CC diseases, predispositions or adverse drug-treatment reactions. Examples  
CC of diseases linked to nucleotide repeats are Machado-Joseph, Haw River  
CC syndrome, Huntington's disease, fragile-X syndrome, Friedrich's ataxia,  
CC myotonic dystrophy, hyperandrogenaemia, spinal and bulbar atrophy and  
CC spinocerebellar ataxia. The sequences presented in ABX79676-ABX80022 are  
CC the polymorphic repeats identified for a search of human ESTs

SQ Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 1 Other;  
Query Match 1.2%; Score 12.4; DB 1; Length 15;  
Best Local Similarity 86.7%; Pred. No. 3.5e+02;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1865 TTTTATTTTGTGTT 1879  
DB TTTTATTTTGTGTT 15

Db 1 TTTTATTTTGTGTT 15  
RESULT 528  
ACD56418/c  
ID ACD56418 standard; RNA; 15 BP.  
XX AC ACD56418;  
XX DT 24-SEP-2003 (first entry)  
XX DE HBV enzymatic nucleic acid substrate sequence #143.  
XX KW Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;  
KW RNA stability; RNA expression; RNA synthesis; antisense;  
KW enzymatic nucleic acid; hammerhead ribozyme; DNazyme; inozyme; zinzyme;  
KW amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;  
KW HBV reverse transcriptase; Enhancer I region; viral replication;  
KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;  
KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;  
KW virucide; antiinflammatory; substrate; ss.  
XX Hepatitis B virus.  
XX OS WO200281494-A1.  
XX PN 17-OCT-2002.  
XX PD 26-MAR-2002; 2002WO-US009187.  
XX PF 26-MAR-2001; 2001US-00817879.  
XX PR 08-JUN-2001; 2001US-00877478.  
XX PR 08-JUN-2001; 2001US-0296876P.  
XX PR 24-OCT-2001; 2001US-0335059P.  
XX PR 05-DEC-2001; 2001US-0337055P.  
XX PS (RIBO-) RIBOZYME PHARM INC.  
XX PA (BLAT) BLATT L.  
XX PA (MACE) MACEJAK D.  
XX PA (MCSW) MCSWIGGEN J.  
XX PA (MORR) MORRISSEY D.  
XX PA (PAVC) PAVCO P.  
XX PA (LEEP) LEE P.  
XX PA (DRAP) DRAPER K.  
XX PA (ROBE) ROBERTS E.  
XX PI Blatt I, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;  
PI Draper K, Roberts E;  
XX WPI; 2003-229207/22.  
XX PT Novel compound useful for treating cirrhosis, liver failure,  
XX hepatocellular carcinoma, or condition associated with hepatitis C virus  
XX infection.  
XX Example 1; Page 219; 387pp; English.  
XX The present invention relates to nucleic acid molecules which modulate  
XX the synthesis, expression and/or stability of Hepatitis C virus (HCV) or  
XX Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense  
XX and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,  
XX inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed  
XX are nucleic acid decoy molecules and aptamers that bind to HBV reverse  
XX transcriptase and/or HBV reverse transcriptase primer sequences, as well  
XX as oligonucleotides that specifically bind the Enhancer I region of HBV  
XX DNA. The nucleic acids may be used to modulate the expression of HBV  
XX genes and HBV viral replication. Also disclosed is a method for screening  
XX compounds and/or potential therapies directed against HBV, and compounds  
XX that modulate the expression and/or replication of HCV. The compounds and  
XX methods of the invention are useful for the treatment of degenerative and  
XX disease states related to HBV and HCV infection, replication and gene  
XX expression such as cirrhosis, liver failure, and hepatocellular  
XX carcinoma. The present sequence represents a substrate for one of the HBV

CC enzymatic nucleic acid sequences disclosed in the present invention  
 XX Sequence 15 BP; 2 A; 3 C; 4 G; 0 T; 6 U; 0 Other;  
 SQ

Query Match 1.2%; Score 12.4; DB 1; Length 15;  
 Best Local Similarity 92.9%; Pred. No. 3.5e+02;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2095 AATGAACAAATGGC 2108  
 Db 14 ACTGAACAAATGGC 1

RESULT 529  
 ACD56180/c  
 ID ACD56180 standard; RNA; 15 BP.

XX AC ACD56180;

DT 23-SEP-2003 (first entry)

DE HBV enzymatic nucleic acid substrate sequence #69.

XX Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;  
 KW RNA stability; RNA expression; RNA synthesis; antisense;  
 KW enzymatic nucleic acid; hammerhead ribozyme; DNazyme; inozyme; zinzyme;  
 KW amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;  
 KW HBV reverse transcriptase; Enhancer I region; viral replication;  
 KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;  
 KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;  
 KW viricide; antiinflammatory; substrate; ss.

OS Hepatitis B virus.

XX WO200281494-A1.

PN 17-OCT-2002.

XX 26-MAR-2002; 2002WO-US009187.

XX 26-MAR-2001; 2001US-00817879.

PR 08-JUN-2001; 2001US-00877478.

PR 08-JUN-2001; 2001US-0296876P.

PR 24-OCT-2001; 2001US-0335059P.

PR 05-DEC-2001; 2001US-0337055P.

XX (RIBO-) RIBOZYME PHARM INC.

PA (BLAT/) BLATT L.

PA (MACE/) MACEJAK D.

PA (MCSW/) MCSWIGGEN J.

PA (MORR/) MORRISSEY D.

PA (PAVC/) PAVCO P.

PA (LEEF/) LEE P.

PA (DRAP/) DRAPER K.

PA (ROBE/) ROBERTS E.

XX Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;

PI Draper K, Roberts E;

XX WPI; 2003-229207/22.

XX Novel compound useful for treating cirrhosis, liver failure,

PT hepatocellular carcinoma, or condition associated with hepatitis C virus

PT infection.

XX Example 1; Page 214; 387pp; English.

CC as oligonucleotides that specifically bind the Enhancer I region of HBV  
 CC DNA. The nucleic acids may be used to modulate the expression of HBV  
 CC genes and HBV viral replication. Also disclosed is a method for screening  
 CC compounds and/or potential therapies directed against HBV, and compounds  
 CC that modulate the expression and/or replication of HCV. The compounds and  
 CC methods of the invention are useful for the treatment of degenerative and  
 CC disease states related to HBV and HCV infection, replication and gene  
 CC expression such as cirrhosis, liver failure, and hepatocellular  
 CC carcinoma. The present sequence represents a substrate for one of the HBV  
 CC enzymatic nucleic acid sequences disclosed in the present invention  
 XX  
 SQ Sequence 15 BP; 2 A; 3 C; 3 G; 0 T; 7 U; 0 Other;

Query Match 1.2%; Score 12.4; DB 1; Length 15;  
 Best Local Similarity 92.9%; Pred. No. 3.5e+02;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2095 AATGAACAAATGGC 2108  
 Db 15 ACTGAACAAATGGC 2

RESULT 530

ADEI3970/c

XX ID ADEI3970 standard; DNA; 15 BP.

XX AC ADEI3970;

XX 29-JAN-2004 (first entry)

DE Optineurin promoter motif, repeat element or regulatory region #79.

XX Human; optineurin; ds; ophthalmological; single nucleotide polymorphism;

KW SNP; glaucoma; progressive ocular hypertensive disorder;

KW glaucoma related disorder; motif; repeat element; regulatory region.

XX Homo sapiens.

OS US2003190617-A1.

XX 09-OCT-2003.

XX 06-MAR-2002; 2002US-00091281.

XX 06-MAR-2002; 2002US-00091281.

XX (SIEE/) SI E.

PA (RAYM/) RAYMOND V.

PA (MORI/) MORISSETTE J.

XX Raymond V, Morissette J, Si E;

XX WPI; 2003-864169/80.

XX New nucleic acid sequences of the optineurin gene are useful to detect

PT polymorphisms particularly single nucleotide polymorphisms in the

PT optineurin promoter to diagnose, prognose and treat glaucoma and related

PT disorders.

XX Claim 11; SEQ ID NO 81; 159pp; English.

XX The invention relates to an isolated nucleic acid (N1) comprising at

CC least 20 but not more than 1500 consecutive nucleotides of the optineurin

CC promoter appearing as ADEI3890. Also included are the optineurin promoter

CC operably linked to a heterologous nucleic acid, a nucleic acid capable of

CC detecting a single nucleotide polymorphism (SNP) in the optineurin

CC promoter, a host cell comprising the promoter operably linked to a

CC The present invention relates to nucleic acid molecules which modulate

CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or

CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense

CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,

CC inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed

CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse

CC in a sample containing DNA, determining the presence or increased  
 CC susceptibility to glaucoma or to a progressive ocular hypertensive  
 CC disorder resulting in loss of visual field in a patient (or the severity  
 CC or progression of glaucoma in a patient, comprising providing  
 CC amplification reaction primers that direct amplification of a selected  
 CC nucleic acid region containing the variation within the optineurin  
 CC promoter and amplifying the DNA) and detecting a polymorphism (comprising  
 CC obtaining a sample containing human genomic DNA, providing a nucleic acid  
 CC capable of detecting a SNP located within an optineurin promoter, and  
 CC detecting the polymorphism). The invention is used to diagnose and  
 CC prognose glaucoma, and also to treat glaucoma related disorders. The  
 CC present sequence is an optineurin promoter motif, repeat element or  
 CC putative regulatory region.

XX SQ Sequence 15 BP; 5 A; 3 C; 0 G; 7 T; 0 U; 0 Other;  
 Query Match 1.2%; Score 12.4; DB 1; Length 15;  
 Best Local Similarity 92.9%; Pred. No. 3.5e+02;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1535 AAGTGTAAATGAGA 1548  
 Db 14 AAGTGTAAATGAAA 1

RESULT 531  
 ABC12933  
 ID ABC12933 standard; DNA; 13 BP.  
 XX AC ABC12933;  
 XX DT 20-FEB-2002 (first entry)  
 XX DE Oligonucleotide SEQ ID NO 12940 for detecting SNP TSC0003018.  
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.  
 XX PN WO200177384-A2.  
 XX PD 18-OCT-2001.  
 XX PF 06-APR-2001; 2001WO-IB0000713.  
 XX PR 07-APR-2000; 2000DE-01019173.  
 XX PA (EPIC-) EPIGENOMICS AG.  
 XX PI Olek A, Piepenbrock C, Berlin K;  
 XX WPI; 2001-657177/75.  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.

XX PS Claim 1; SEQ ID NO 12940; 29pp + Sequence Listing; German.  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 13 BP; 6 A; 1 C; 0 G; 6 T; 0 U; 0 Other;  
 Query Match 1.1%; Score 12; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1813 TATATATATATA 1824  
 Db 1 TATATATATATA 12

RESULT 532  
 ABF19131  
 ID ABF19131 standard; DNA; 13 BP.  
 XX AC ABF19131;  
 XX DT 21-FEB-2002 (first entry)  
 XX DE Oligonucleotide SEQ ID NO 119128 for detecting SNP TSC0029746.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB0000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIC-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.

XX PS Claim 1; SEQ ID NO 119128; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 13 BP; 6 A; 1 C; 0 G; 6 T; 0 U; 0 Other;

Query Match 1.1%; Score 12; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1814 ATATATATATAT 1825  
 Db 2 ATATATATATAT 13

RESULT 533

```

ABCL12932/c
ID ABC12932 standard; DNA; 13 BP.
XX
XX AC ABC12932;
XX
XX DT 20-FEB-2002 (first entry)
XX
XX DE Oligonucleotide SEQ ID NO 12939 for detecting SNP TSC0003018.
XX
XX SN; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX PN WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX
XX PR 07-APR-2000; 2000DE-01019173.
XX
XX PA (EPIG-) EPIGENOMICS AG.
XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX PS Claim 1; SEQ ID NO 12939; 29pp + Sequence Listing; German.
XX
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 13 BP; 6 A; 0 C; 1 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 12; DB 1; Length 13;
XX Best Local Similarity 100.0%; Pred. No. 3.5e+02;
XX Mismatches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1813 TATATATATATA 1824
XX
XX DB 13 TATATATATATA 2
XX
XX RESULT 534
XX ABF19130/c
XX ID ABF19130 standard; DNA; 13 BP.
XX
XX AC ABF19130;
XX
XX XX 21-FEB-2002 (first entry)
XX
XX DE Oligonucleotide SEQ ID NO 119127 for detecting SNP TSC0029746.
XX
XX SN; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX

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OS Homo sapiens.
XX
XX PN WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX
XX PR 07-APR-2000; 2000DE-01019173.
XX
XX PA (EPIG-) EPIGENOMICS AG.
XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX PS Claim 1; SEQ ID NO 119127; 29pp + Sequence Listing; German.
XX
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 13 BP; 6 A; 0 C; 1 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 12; DB 1; Length 13;
XX Best Local Similarity 100.0%; Pred. No. 3.5e+02;
XX Mismatches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1814 ATATATATATAT 1825
XX
XX DB 12 ATATATATATAT 1
XX
XX RESULT 535
XX AAT30426
XX ID AAT30426 standard; DNA; 22 BP.
XX
XX AC AAT30426;
XX
XX DT 28-JAN-1997 (first entry)
XX
XX DE Compound simple sequence repeat primer (CA)6.5(TA)4.5.
XX
XX KW Detection; polymorphism; perfect compound simple sequence repeat;
XX adaptor directed primer; genome; genetic; fingerprinting;
XX amplified fragment length polymorphism assay; microsatellite region;
XX genetic trait marking; germplasm comparisons; compound; ss.
XX
XX OS Synthetic.
XX
XX PN WO9617082-A2.
XX
XX PD 06-JUN-1996.
XX
XX PF 21-NOV-1995; 95WO-US015150.
XX
XX PR 28-NOV-1994; 94US-00346456.
XX
XX PA (DUPO ) DU PONT DE NEMOURS & CO E I.
XX

```

PI Morgante M, Vogel JM;  
 DR WPI; 1996-277795/28.  
 XX  
 PT Modified amplified fragment length polymorphism assay - for detection of  
 PT polymorphism esp. in microsatellite regions.  
 XX  
 PS Disclosure; Fig 1c; 173pp; English.  
 XX  
 CC Detecting polymorphisms between 2 nucleic acid samples, esp. in  
 CC microsatellite regions, comprises digesting the nucleic acid to generate  
 CC fragments, ligating adaptor segments to their ends, amplifying them using  
 CC primer directed amplification and comparing the prods. to detect  
 CC differences. The primers used in the amplification comprise a primer  
 CC consisting of a perfect cpd. simple sequence repeat (SSR), and an adaptor  
 CC directed primer, comprising a sequence complementary to an adaptor  
 CC segment. The present sequence is an example of a compound SSR primer. The  
 CC method represents a modified amplified fragment length polymorphism  
 CC assay, which is partic. useful for genome fingerprinting, i.e. for  
 CC genetic trait marking and germplasm comparisons  
 XX  
 SQ Sequence 22 BP; 11 A; 6 C; 0 G; 5 T; 0 U; 0 Other;  
 Query Match 1.1%; Score 12; DB 1; Length 22;  
 Best Local Similarity 75.0%; Pred. No. 4.4e+02;  
 Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 QY 1813 TATATATATATATATGTACA 1832  
 DB 1 TATATATATACACACACA 20  
 RESULT 536  
 AAH91159  
 ID AAH91159 standard; DNA; 19 BP.  
 XX  
 AC AAH91159;  
 XX  
 XX 09-OCT-2001 (first entry)  
 DT  
 DE Human inflammatory bowel disease associated polymorphic site #234.  
 XX  
 KW Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis;  
 KW single nucleotide polymorphism; SNP; chromosome 19p13; paternity test;  
 KW chromosome 5q31-33; forensic test; gene therapy; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 FH misc\_feature 9  
 FT /\*tag= a  
 FT /note= "SNP, optional deletion at this position"  
 XX  
 XX WO200148511-A2.  
 XX  
 XX 14-JUN-2001.  
 XX  
 XX 11-DEC-2000; 2000WO-US033632.  
 XX  
 XX 10-DEC-1999; 99US-0170257P.  
 PR 10-APR-2000; 2000US-0196046P.  
 XX  
 XX (WHEED ) WHITEHEAD INST BIOMEDICAL RES.  
 PA (ELLI-) ELLIPSIS BIOTHERAPEUTICS CORP.  
 PA  
 PI Daly M, Hudson TJ, Lander ES, Rioux J, Saminovitich K;  
 XX WPI; 2001-367874/38.  
 DR  
 XX Testing for the presence of polymorphisms associated with inflammatory  
 PT bowel disease, using a hybridization assay.  
 PT  
 XX Claim 1; Page 48; 463pp; English.  
 PS

XX The present invention describes a method for detecting the presence of  
 CC polymorphisms associated with inflammatory bowel diseases such as  
 CC ulcerative colitis and Crohn's disease. The methods can be used to detect  
 CC the presence of genetic polymorphisms associated with inflammatory bowel  
 CC disease and correlating their occurrence with disease states. They may be  
 CC used in this way for phenotypic correlations, forensics, paternity  
 CC testing, medicine and genetic analysis. The present sequence is a  
 CC polymorphic site described in the exemplification of the invention  
 XX  
 SQ Sequence 19 BP; 9 A; 4 C; 0 G; 5 T; 0 U; 1 Other;  
 Query Match 1.1%; Score 11.6; DB 1; Length 19;  
 Best Local Similarity 73.7%; Pred. No. 4.6e+02;  
 Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 QY 1813 TATATATATATATATGTAC 1831  
 DB 1 TATATATANACACATAC 19  
 RESULT 537  
 ABC98272/c  
 ID ABC98272 standard; DNA; 13 BP.  
 XX  
 AC ABC98272;  
 XX  
 XX 21-FEB-2002 (first entry)  
 DT  
 DE Oligonucleotide SEQ ID NO 98289 for detecting SNP TSC0024420.  
 XX  
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200177384-A2.  
 XX  
 XX 18-OCT-2001.  
 PD  
 XX 06-APR-2001; 2001WO-IB000713.  
 PF  
 XX 07-APR-2000; 2000DE-01019173.  
 PR  
 XX (EPIG-) EPIGENOMICS AG.  
 PA  
 XX Olek A, Piepenbrock C, Berlin K;  
 PI WPI; 2001-657177/75.  
 XX  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX  
 PS Claim 1; SEQ ID NO 98289; 29pp + Sequence Listing; German.  
 XX  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pdt\_sequences  
 XX  
 SQ Sequence 13 BP; 5 A; 0 C; 1 G; 7 T; 0 U; 0 Other;  
 Query Match 1.1%; Score 11.4; DB 1; Length 13;



Best Local Similarity 92.3%; Pred. No. 4e+02; Mismatches 0; Indels 1; Gaps 0;

QY 1814 ATATATATATATA 1826  
 Db 13 ATATATATATACA 1

RESULT 538  
 ABC98273  
 ID ABC98273 standard; DNA; 13 BP.  
 XX  
 AC ABC98273;  
 XX  
 DT 21-FEB-2002 (first entry)  
 XX  
 DE Oligonucleotide SEQ ID NO 98290 for detecting SNP TSC0024420.  
 XX  
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200177384-A2.  
 XX  
 PD 18-OCT-2001.  
 XX  
 PF 06-APR-2001; 2001WO-IB000713.  
 XX  
 PR 07-APR-2000; 2000DE-01019173.  
 XX  
 PA (EPIG-) EPIGENOMICS AG.  
 XX  
 PI Olek A, Piepenbrock C, Berlin K;  
 XX  
 DR WPI; 2001-657177/75.  
 XX  
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX  
 PS Claim 1; SEQ ID NO 98290; 29pp + Sequence Listing; German.  
 XX  
 CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 13 BP; 7 A; 1 C; 0 G; 5 T; 0 U; 0 Other;

Query Match 1.1%; Score 11.4; DB 1; Length 13;  
 Best Local Similarity 92.3%; Pred. No. 4e+02;  
 Mismatches 0; Mismatches 1; Indels 0; Gaps 0;

QY 1814 ATATATATATATA 1826  
 Db 1 ATATATATATACA 1

RESULT 539  
 ABF38750/C  
 ID ABF38750 standard; DNA; 13 BP.  
 XX  
 AC ABF38750;  
 XX

XX 21-FEB-2002 (first entry)  
 XX Oligonucleotide SEQ ID NO 138747 for detecting SNP TSC0034761.  
 XX  
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200177384-A2.  
 XX  
 PD 18-OCT-2001.  
 XX  
 PF 06-APR-2001; 2001WO-IB000713.  
 XX  
 PR 07-APR-2000; 2000DE-01019173.  
 XX  
 PA (EPIG-) EPIGENOMICS AG.  
 XX  
 PI Olek A, Piepenbrock C, Berlin K;  
 XX  
 DR WPI; 2001-657177/75.  
 XX  
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX  
 PS Claim 1; SEQ ID NO 138747; 29pp + Sequence Listing; German.  
 XX  
 CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 13 BP; 5 A; 0 C; 1 G; 7 T; 0 U; 0 Other;

Query Match 1.1%; Score 11.4; DB 1; Length 13;  
 Best Local Similarity 92.3%; Pred. No. 4e+02;  
 Mismatches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1814 ATATATATATATA 1826  
 Db 13 ACATATATATATA 1

RESULT 540  
 ABC28589  
 ID ABC28589 standard; DNA; 13 BP.  
 XX  
 AC ABC28589;  
 XX  
 DT 20-FEB-2002 (first entry)  
 XX  
 DE Oligonucleotide SEQ ID NO 28606 for detecting SNP TSC0008245.  
 XX  
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200177384-A2.  
 XX

PD 18-OCT-2001.  
 XX  
 PF 06-APR-2001; 2001WO-IB000713.  
 XX  
 PR 07-APR-2000; 2000DE-01019173.  
 XX  
 PA (EPIG-) EPIGENOMICS AG.  
 XX  
 PI Olek A, Piepenbrock C, Berlin K;  
 XX  
 DR WPI; 2001-657177/75.  
 XX  
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX  
 PS Claim 1; SEQ ID NO 28606; 29pp + Sequence Listing; German.  
 XX  
 CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 13 BP; 6 A; 1 C; 0 G; 6 T; 0 U; 0 Other;  
 XX  
 Query Match 1.1%; Score 11.4; DB 1; Length 13;  
 Best Local Similarity 92.3%; Pred. No. 4e+02; 1; Indels 0; Gaps 0;  
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1813 TATATATATATAT 1825  
 DB 1 TACATATATATAT 13  
 RESULT 541  
 ABC28588/C  
 ID ABC28588 standard; DNA; 13 BP.  
 XX  
 AC ABC28588;  
 XX  
 DT 20-FEB-2002 (first entry)  
 XX  
 DE Oligonucleotide SEQ ID NO 28605 for detecting SNP TSC0008245.  
 XX  
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200177384-A2.  
 XX  
 PD 18-OCT-2001.  
 XX  
 PF 06-APR-2001; 2001WO-IB000713.  
 XX  
 PR 07-APR-2000; 2000DE-01019173.  
 XX  
 PA (EPIG-) EPIGENOMICS AG.  
 XX  
 PI Olek A, Piepenbrock C, Berlin K;  
 XX  
 DR WPI; 2001-657177/75.  
 XX  
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX  
 PS Claim 1; SEQ ID NO 28606; 29pp + Sequence Listing; German.  
 XX  
 CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
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 Best Local Similarity 92.3%; Pred. No. 4e+02; 1; Indels 0; Gaps 0;  
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 QY 1813 TATATATATATAT 1825  
 DB 1 TACATATATATAT 13  
 RESULT 541  
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 ID ABC28588 standard; DNA; 13 BP.  
 XX  
 AC ABC28588;  
 XX  
 DT 20-FEB-2002 (first entry)  
 XX  
 DE Oligonucleotide SEQ ID NO 28605 for detecting SNP TSC0008245.  
 XX  
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200177384-A2.  
 XX  
 PD 18-OCT-2001.  
 XX  
 PF 06-APR-2001; 2001WO-IB000713.  
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 PR 07-APR-2000; 2000DE-01019173.  
 XX  
 PA (EPIG-) EPIGENOMICS AG.  
 XX  
 PI Olek A, Piepenbrock C, Berlin K;  
 XX  
 DR WPI; 2001-657177/75.  
 XX  
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is

PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX  
 PS Claim 1; SEQ ID NO 28605; 29pp + Sequence Listing; German.  
 XX  
 CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
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 SQ Sequence 13 BP; 6 A; 0 C; 1 G; 6 T; 0 U; 0 Other;  
 XX  
 Query Match 1.1%; Score 11.4; DB 1; Length 13;  
 Best Local Similarity 92.3%; Pred. No. 4e+02; 1; Indels 0; Gaps 0;  
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 DB 13 TACATATATATAT 1  
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 AC ABF38751;  
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 DT 21-FEB-2002 (first entry)  
 XX  
 DE Oligonucleotide SEQ ID NO 138748 for detecting SNP TSC0034761.  
 XX  
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200177384-A2.  
 XX  
 PD 18-OCT-2001.  
 XX  
 PF 06-APR-2001; 2001WO-IB000713.  
 XX  
 PR 07-APR-2000; 2000DE-01019173.  
 XX  
 PA (EPIG-) EPIGENOMICS AG.  
 XX  
 PI Olek A, Piepenbrock C, Berlin K;  
 XX  
 DR WPI; 2001-657177/75.  
 XX  
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX  
 PS Claim 1; SEQ ID NO 138748; 29pp + Sequence Listing; German.  
 XX  
 CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073.

CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC [http://wipo.int/pub/publ/published\\_pct\\_sequences](http://wipo.int/pub/publ/published_pct_sequences)

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SQ Sequence 13 BP; 7 A; 1 C; 0 G; 5 T; 0 U; 0 Other;
      Query Match      1.1%; Score 11.4; DB 1; Length 13;
      Best Local Similarity 92.3%; Pred.No. 4e+02;
      Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 1 ACATATATATATA 13

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91	91	91
92	92	92
93	93	93
94	94	94
95	95	95
96	96	96
97	97	97
98	98	98
99	99	99
100	100	100

XX DE Human connective tissue growth factor, RT-PCR primer #2.

Human; endothelial cell-specific molecule 4; EC5M4; neovasculature; imaging vascular endothelium; proliferative disease; cancer; psoriasis; diabetic retinopathy; atherosclerosis; hemorrhagia; endothelial damage; tumour neovasculature; cardiac disease; endometriosis; hypoxic condition; angiogenesis; cytostatic; RT-PCR; connective tissue growth factor; reverse transcription-PCR; primer: ss.

XX  
OS  
Homo sapiens.

XX PN WO200236771-A2.

XX  
PD  
10-MAY-2002.

XX PF 06~NOV-2001; 2001WO-GB004906.

XX  
PR 06-NOV-2000: 2000US-0245566P.

PR 06-NOV-2000; 2000US-0245566P;  
PR 07-MAR-2001; 2001US-0273662P;

XX PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.

XX PI Bicknell R. Huminiacki L:

XX  
DR WPI: 2002-508120/54.

XX Novel endothelial cell-specific molecule polypeptide 1 or 4, useful for PT imaging, diagnosing and treating a condition involving vascular PT endothelium e.g. cancer, cardiac disease, endometrios, diabetes.

XX PS Example 1: Page 165: 248pp: English.

The present invention relates to endothelial cell-specific molecule 4 (ECSM4), and the polynucleotide sequences encoding it. The ECSM4 proteins are useful for imaging vascular endothelium in the body of an individual, and for diagnosing and treating a proliferative disease or condition involving the vascular endothelium (preferably, neovasculation), such as cancer, psoriasis, diabetic retinopathy, atherosclerosis or hemorrhagia. The ECSM4 proteins are also useful in the manufacture of diagnostic or prognostic agent for such conditions. The proteins are also useful for detecting endothelial damage or activation, detecting a tumour or tumour neovasculation, cardiac disease, or endometriosis by detecting the amount of ECSM4 present in a sample. The polynucleotide sequences encoding ECSM4 are useful in gene therapy for treating a hypoxic condition such as cancer, cardiac disease, endometriosis or atherosclerosis and in the manufacture of medicaments for treating the above disease. The sequences are useful for modulating angiogenesis in an individual. The present sequence represents a RT-PCR primer for RNA encoding human connective tissue growth factor

RESULT 545

XX  
SQ Sequence 20 BP; 8 A; 3 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 1.1%; Score 11.4; DB 1; Length 20;  
Best Local Similarity 92.3%; Pred. No. 4.8e+02;  
Matches 12; Conservative 0; Mismatches 1; Indels

Qy 1879 TTTAATGCTTGA 1891  
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Db 16 TTTCATGCTTGA 4

RESULTS 344  
ABC89602/C

ID ABC8960Z Standard; DNA; 13 BF.  
XX  
XX

AC	ABC9902;		
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XX	21-FEB-2002 (first entry)		
XX			
XX			
XX	Oligonucleotide SEQ ID NO 89619 for detecting SNP TSC0022467.		
XX			
XX	SNP: single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;		
XX	peptide nucleic acid; cytosine methylation; cardiovascular; primes; ss;		
KW	central nervous system; gastrointestinal; respiratory; immune; metabolic		

XX Homo sapiens.

XX  
PN  
WO200277384-A218-OCT-2001  
PD  
XXXX  
PF  
06-APR-2001: 2001WO-TB0000713XX  
PR 07-APR-2000: 2000DE-01019173.XX  
DA (EPTG-) EPTGENOMICS AG

XX  
Dr. Oleg A. Pionerbrock  
Berlin K.

XX  
WPT: 2001-657177/75

XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
PT

XX  
pg  
Claim 1: SEQ ID NO 89619: 29np + Sequence Listing: German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -AB09989, ABP0010-ABF9989, ABH0010-ABH9999 and AB10010-AB182073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at [www.int.pat/public/patseq](http://www.int.pat/public/patseq)

XX  
SQ  
Sequence 13 BP. 5 A. 0 C. 1 G. 6 T. 0 U. 1 Other.

Quorum: Met 4/10

Best Local Similarity 1

Search completed: April 2, 2004, 14:31:05  
Job time : 9 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 2, 2004, 14:35:20 ; Search time 4 Seconds  
(without alignments)

2.749 Million cell updates/sec

Title: us-10-006-191-19

Perfect score: 1049

Sequence: 1 ttgaactgattcacatctca.....gtgtatatattttctataaa 1049

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 0.5

Searched: 296 seqs, 5242 residues

Total number of hits satisfying chosen parameters: 592

Minimum DB seq length: 8

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 316 summaries

Database : rge.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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6	25	2.4	25	1	AR201291
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12	22.2	2.1	27	1	I31231
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15	21.8	2.1	25	1	I31234
16	21.8	2.1	27	1	AR051255
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29	21.4	2.0	25	1	AX115976
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31	21	2.0	21	1	I31248
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92	16.4	1.6	18	1	AR071779
93	16.4	1.6	18	1	AR071800
94	16.4	1.6	18	1	AR071804
95	16.4	1.6	18	1	AR071806
96	16.4	1.6	18	1	AR071808
97	16.4	1.6	18	1	AR071809
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121	15	1.4	15	1	AR074711	ACCESSION:AR074711	C 194	13.8	1.3	17	1	BD241082	ACCESSION:BD241082
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132	15	1.4	18	1	AX599902	ACCESSION:AX599902	C 205	13.8	1.3	17	1	AR236087	ACCESSION:AR236087
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137	15	1.4	32	1	AR259469	ACCESSION:AR259469	C 210	13.8	1.3	17	1	AR433962	ACCESSION:AR433962
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148	14.4	1.4	17	1	IS5317	ACCESSION:IS5317	C 221	13.4	1.3	15	1	IS1784	ACCESSION:IS1784
149	14.4	1.4	17	1	AR188671	ACCESSION:AR188671	C 222	13.4	1.3	15	1	I84393	ACCESSION:I84393
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151	14.4	1.4	17	1	AR324524	ACCESSION:AR324524	C 224	13.4	1.3	15	1	AR241795	ACCESSION:AR241795
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170	14	1.3	14	1	AX175251	ACCESSION:AX175251	C 243	13	1.2	15	1	AR242246	ACCESSION:AR242246
171	14	1.3	14	1	BD084125	ACCESSION:BD084125	C 244	13	1.2	15	1	AR242247	ACCESSION:AR242247
172	14	1.3	14	1	BD084125	ACCESSION:BD084125	C 245	13	1.2	15	1	AX635886	ACCESSION:AX635886
173	14	1.3	14	1	BD084125	ACCESSION:BD084125	C 246	13	1.2	15	1	AX636032	ACCESSION:AX636032
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179	14	1.3	17	1	AR047068	ACCESSION:AR047068	C 252	12.8	1.2	16	1	AR175845	ACCESSION:AR175845

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315 12.4 1.2 15 1 AX638069
316 12.4 1.2 15 1 AX638071
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## ALIGNMENTS

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RESULT 1
AR090280/c 32 bp DNA
LOCUS AR090280 400 from patent US 5994076.
DEFINITION Sequence 400 from patent US 5994076.
linear PAT 07-SEP-2000
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ACCESSION E32226
VERSION AR090280.1 GI:10017035
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 32)
AUTHORS Chenchik, A., Jokhadze, G. and Bibilashvili, R.
TITLE Methods of assaying differential expression
JOURNAL Patent: US 5994076-A 400 30-NOV-1999;
FEATURES
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RESULT 2
AR197315/c 32 bp DNA
LOCUS AR197315 400 from patent US 6352829.
DEFINITION Sequence 400 from patent US 6352829.
AUTHORS Chenchik, A., Jokhadze, G. and Bibilashvili, R.
TITLE Methods of assaying differential expression
JOURNAL Patent: US 6352829-A 400 05-MAR-2002;
FEATURES
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RESULT 3
AR259469/c 32 bp DNA
LOCUS AR259469 400 from patent US 6489455.
DEFINITION Sequence 400 from patent US 6489455.
AUTHORS Chenchik, A., Jokhadze, G. and Bibilashvili, R.
TITLE Methods of assaying differential expression
JOURNAL Patent: US 6489455-A 400 03-DEC-2002;
FEATURES
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Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4
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LOCUS E32218 30 bp DNA linear PAT 18-JUN-2001
DEFINITION Method for isolating satellite sequence.
ACCESSION E32218
VERSION E32218.1 GI:13021838
KEYWORDS JP 2000060559-A/20.
SOURCE Haliotis discus discus
ORGANISM Haliotis discus discus
Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
Vetigastropoda; Haliotidae; Haliotidae; Haliotis.
1 (bases 1 to 30)
HIDEAKI, T. and Masashi, S.
Method for isolating satellite sequence
Patent: JP 2000060559-A 20 29-FEB-2000;
NATL INST OF AGROBIOLOGICAL RESOURCES
OS Haliotis discus discus
PN JP 2000060559-A/20
PD 29-FEB-2000
PF 18-AUG-1998 JP 1998232153
PR HIDEAKI TAKAHASHI, MASASHI SEXINO
PI C12N15/09, C12Q1/68, C12N15/00
PC C12N15/09, C12Q1/68, C12N15/00
CC C12N15/09, C12Q1/68, C12N15/00
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RESULT 5
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LOCUS BD242741 25 bp DNA linear PAT 17-JUL-2003
DEFINITION Connective tissue growth factor (CTGF) and methods of use.
ACCESSION BD242741
VERSION BD242741.1 GI:133052511
KEYWORDS JP 2002529066-A/6.
SOURCE synthetic construct
ORGANISM artificial sequences.
1 (bases 1 to 25)
Schmidt, B.F., Allen, M.L., Sverdrup, F. and Carmichael, D.F.
Connective tissue growth factor (CTGF) and methods of use
Patent: JP 2002529066-A 6 10-SEP-2002;
FIBROGEN INC
OS Artificial Sequence
PN JP 2002529066-A/6
PD 10-SEP-2002
PF 05-NOV-1999 JP 2000581045
PR 06-NOV-1998 US 09/187478, 14-APR-1999 US 09/292036 PI
BRIAN FREDERICK SCHMIDT, MARGARET LEAH ALLEN, FRAN SVERDRUP, PI
DAVID F CARMICHAEL
PC C12N15/09, A61K31/711, A61K48/00, A61P1/16, A61P9/00, A61P9/10, PC

Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 32 CTTGTGGCAAGTGAATTGCTGTAAAGCC 1

RESULT 4
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LOCUS E32218 30 bp DNA linear PAT 18-JUN-2001
DEFINITION Method for isolating satellite sequence.
ACCESSION E32218
VERSION E32218.1 GI:13021838
KEYWORDS JP 2000060559-A/20.
SOURCE Haliotis discus discus
ORGANISM Haliotis discus discus
Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
Vetigastropoda; Haliotidae; Haliotidae; Haliotis.
1 (bases 1 to 30)
HIDEAKI, T. and Masashi, S.
Method for isolating satellite sequence
Patent: JP 2000060559-A 20 29-FEB-2000;
NATL INST OF AGROBIOLOGICAL RESOURCES
OS Haliotis discus discus
PN JP 2000060559-A/20
PD 29-FEB-2000
PF 18-AUG-1998 JP 1998232153
PR HIDEAKI TAKAHASHI, MASASHI SEXINO
PI C12N15/09, C12Q1/68, C12N15/00
PC C12N15/09, C12Q1/68, C12N15/00
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RESULT 5
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LOCUS BD242741 25 bp DNA linear PAT 17-JUL-2003
DEFINITION Connective tissue growth factor (CTGF) and methods of use.
ACCESSION BD242741
VERSION BD242741.1 GI:133052511
KEYWORDS JP 2002529066-A/6.
SOURCE synthetic construct
ORGANISM artificial sequences.
1 (bases 1 to 25)
Schmidt, B.F., Allen, M.L., Sverdrup, F. and Carmichael, D.F.
Connective tissue growth factor (CTGF) and methods of use
Patent: JP 2002529066-A 6 10-SEP-2002;
FIBROGEN INC
OS Artificial Sequence
PN JP 2002529066-A/6
PD 10-SEP-2002
PF 05-NOV-1999 JP 2000581045
PR 06-NOV-1998 US 09/187478, 14-APR-1999 US 09/292036 PI
BRIAN FREDERICK SCHMIDT, MARGARET LEAH ALLEN, FRAN SVERDRUP, PI
DAVID F CARMICHAEL
PC C12N15/09, A61K31/711, A61K48/00, A61P1/16, A61P9/00, A61P9/10, PC

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A61P13/12,
PC A61P17/00, A61P19/02, A61P41/00, A61P43/00, C07K14/475, C07K16/22,
PC C12N1/15,
PC C12N1/19, C12N1/21, C12N5/10, C12P21/02, C12Q1/68, A61K35/74, PC
A61K35/76,
PC C12P21/08, C12N15/00, C12N5/00
CC Antisense CTGF oligonucleotide
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Db 25 ATTAGACTGGACAGCTTGTGGCAAG 1

RESULT 6
AR201291/c
LOCUS AR201291 25 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 9 from patent US 6358741.
ACCESSION AR201291
VERSION AR201291.1 GI:20252179
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 25)
AUTHORS Schmidt, B. Frederick., Allen, M. Leah., Sverdrup, F. and Carmichael, D. F.
TITLE Connective tissue growth factor (CTGF) and methods of use
JOURNAL Patent: US 6358741-A 9 19-MAR-2002;
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Query Match 2.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 12;
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Db 25 ATTAGACTGGACAGCTTGTGGCAAG 1

RESULT 7
BD242742/c
LOCUS BD242742 25 bp DNA linear PAT 17-JUL-2003
DEFINITION Connective tissue growth factor (CTGF) and methods of use.
ACCESSION BD242742
VERSION BD242742.1 GI:133052512
KEYWORDS JP 2002529066-A/7.
SOURCE synthetic construct
ORGANISM artificial sequences.
1 (bases 1 to 25)
Schmidt, B.F., Allen, M.L., Sverdrup, F. and Carmichael, D.F.
Connective tissue growth factor (CTGF) and methods of use
Patent: JP 2002529066-A 7 10-SEP-2002;
FIBROGEN INC
OS Artificial Sequence
PN JP 2002529066-A/7
PD 10-SEP-2002
PF 05-NOV-1999 JP 2000581045

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PR 06-NOV-1998 US 09/187478.14-APR-1999 US 09/292036 PI  
BRIAN FREDERICK SCHMIDT, MARGARET LEAH ALLEN, FRAN SVERDRUP, PI  
DAVID F CARMICHAEL  
PC C12N15/09, A61K31/711, A61K48/00, A61P1/16, A61P9/00, A61P9/10, PC  
A61P13/12, A61P17/00, A61P19/02, A61P41/00, A61P43/00, C07K14/475, C07K16/22,  
PC C12N1/15,  
PC C12N1/19, C12N1/21, C12N5/10, C12P21/02, C12Q1/68, A61K35/74, PC  
A61K35/76,  
PC C12P21/08, C12N15/00, C12N5/00  
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QY 1742 GTGAATTCGCTGTAACAAGCCAGA 1766  
Db 25 GTGAATTCGCTGTAACAAGCCAGA 1

RESULT 8  
AR201292/c  
LOCUS AR201292 25 bp DNA linear PAT 20-APR-2002  
DEFINITION Sequence 10 from patent US 6358741.  
ACCESSION AR201292  
VERSION AR201292.1 GI:20252180  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 25)  
AUTHORS Schmidt, B. Frederick., Allen, M. Leah., Sverdrup, F. and Carmichael, D. F.  
TITLE Connective tissue growth factor (CTGF) and methods of use  
JOURNAL Patent: US 6358741-A 10 19-MAR-2002;  
FEATURES  
source Location/Qualifiers  
1..25  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 2.2%; Score 23.4; DB 1; Length 25;  
Best Local Similarity 96.0%; Pred. No. 19;  
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1742 GTGAATTCGCTGTAACAAGCCAGA 1766  
Db 25 GTGAATTCGCTGTAACAAGCCAGA 1

RESULT 9  
AX196894/c  
LOCUS AX196894 27 bp DNA linear PAT 07-SEP-2001  
DEFINITION Sequence 601 from Patent WO0151627.  
ACCESSION AX196894  
VERSION AX196894.1 GI:15387100  
KEYWORDS  
SOURCE Glycine max (soybean)  
ORGANISM Glycine max  
REFERENCE 1  
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.  
Query Match 2.3%; Score 23; DB 1; Length 24;  
Best Local Similarity 100.0%; Pred. No. 20;

TITLE Nucleic acid molecules and other molecules associated with soybean cyst nematode resistance  
JOURNAL Patent: WO 0151627-A 601 19-JUL-2001;  
MONSANTO COMPANY (US)  
FEATURES  
source Location/Qualifiers  
1..27  
/organism="Glycine max"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:3847"  
/note="Seq ID: 240017\_region\_G3\_11301\_29\_Forward\_Primer"

Query Match 2.2%; Score 23.4; DB 1; Length 27;  
Best Local Similarity 96.0%; Pred. No. 21;  
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1795 TGTGTGTGTGTGTGTGTATATAT 1819  
Db 27 TGTGTGTGTGTGTGTGTATATAT 3

RESULT 10  
AR074790/c  
LOCUS AR074790 24 bp DNA linear PAT 28-AUG-2000  
DEFINITION Sequence 87 from patent US 5955276.  
ACCESSION AR074790  
VERSION AR074790.1 GI:10001543  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 24)  
AUTHORS Morgante, M. and Vogel, J. Marie.  
TITLE Compound microsatellite primers for the detection of genetic polymorphisms  
JOURNAL Patent: US 5955276-A 87 21-SEP-1999;  
FEATURES  
source Location/Qualifiers  
1..24  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 2.2%; Score 23; DB 1; Length 24;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1805 TGTGTGTGTATATATATATATAT 1827  
Db 24 TGTGTGTGTATATATATATATAT 2

RESULT 11  
AX116747/c  
LOCUS AX116747 24 bp DNA linear PAT 11-MAY-2001  
DEFINITION Sequence 1870 from Patent WO0129262.  
ACCESSION AX116747  
VERSION AX116747.1 GI:14033689  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Picoult-Newburg, L. and Pohl, M.  
TITLE Genotyping reagents, kits and methods of use thereof  
JOURNAL Patent: WO 0129262-A 1870 26-APR-2001;  
ORCHID Biosciences, Inc. (US)  
FEATURES  
source Location/Qualifiers  
1..24  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Primer"

Query Match 2.3%; Score 23; DB 1; Length 24;  
Best Local Similarity 100.0%; Pred. No. 20;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1791 ATTGTGTGTGTGTGTGTGTGTGT 1813  
Db 23 ATTGTGTGTGTGTGTGTGTGTGT 1

RESULT 12  
I31231/c 131231 27 bp DNA linear PAT 06-FEB-1997  
LOCUS Sequence 143 from patent US 5582979.  
DEFINITION I31231  
ACCESSION I31231  
VERSION I31231.1 GI:1822022  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 27)  
AUTHORS Weber, J.L.  
TITLE Length polymorphisms in (dC-dA).sub.n.(dG-dT).sub.n sequences and method of using the same  
JOURNAL Patent: US 5582979-A 143 10-DEC-1996;  
FEATURES Location/Qualifiers  
source 1..27  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 2.1%; Score 22.2; DB 1; Length 27;  
Best Local Similarity 88.9%; Pred. No. 30;  
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTATAT 1819  
Db 27 TGTGTGTGTGTGTGTGTGTGTGT 1

RESULT 13  
AX175241 AX175241 27 bp DNA linear PAT 03-JUL-2001  
LOCUS Sequence 5 from Patent WO0144465.  
DEFINITION AX175241  
ACCESSION AX175241  
VERSION AX175241.1 GI:14598609  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.

REFERENCE 1  
AUTHORS Phillips, N.C. and Filion, M.C.  
TITLE Therapeutically useful synthetic oligonucleotides  
JOURNAL Patent: WO 0144465-A 5 21-JUN-2001;  
Bioniche Life Sciences Inc. (CA)  
FEATURES Location/Qualifiers  
source 1..27  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"

Query Match 2.1%; Score 22.2; DB 1; Length 27;  
Best Local Similarity 88.9%; Pred. No. 30;  
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTATAT 1819  
Db 1 TGTGTGTGTGTGTGTGTGTGTGT 27

RESULT 14  
AR074791/c AR074791 22 bp DNA linear PAT 28-AUG-2000  
LOCUS Sequence 88 from patent US 5955276.  
DEFINITION AR074791  
ACCESSION AR074791  
VERSION AR074791.1 GI:10001544  
KEYWORDS

Unknown.  
ORGANISM Unknown.  
Unclassified.

REFERENCE 1 (bases 1 to 22)  
AUTHORS Morgante, M. and Vogel, J. Marie.  
TITLE Compound microsatellite primers for the detection of genetic polymorphisms  
JOURNAL Patent: US 5955276-A 88 21-SEP-1999;  
FEATURES Location/Qualifiers  
source 1..22  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 2.1%; Score 22; DB 1; Length 22;  
Best Local Similarity 100.0%; Pred. No. 23;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1801 TGTGTGTGTGTATATATATA 1822  
Db 22 TGTGTGTGTGTATATATA 1

RESULT 15  
I31234/c I31234 25 bp DNA linear PAT 06-FEB-1997  
LOCUS Sequence 146 from patent US 5582979.  
DEFINITION I31234  
ACCESSION I31234  
VERSION I31234.1 GI:1822025  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 25)  
AUTHORS Weber, J.L.  
TITLE Length polymorphisms in (dC-dA).sub.n.(dG-dT).sub.n sequences and method of using the same  
JOURNAL Patent: US 5582979-A 146 10-DEC-1996;  
FEATURES Location/Qualifiers  
source 1..25  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 2.1%; Score 21.8; DB 1; Length 25;  
Best Local Similarity 92.0%; Pred. No. 30;  
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTATAT 1817  
Db 25 TGTGTGTGTGTGTGTGTGTGTGT 1

RESULT 16  
AR051255/c AR051255 27 bp DNA linear PAT 29-SEP-1999  
LOCUS Sequence 23 from patent US 5830658.  
DEFINITION AR051255  
ACCESSION AR051255  
VERSION AR051255.1 GI:5974619  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 27)  
AUTHORS Gryaznov, S.M.  
TITLE Convergent synthesis of branched and multiply connected macromolecular structures  
JOURNAL Patent: US 5830658-A 23 03-NOV-1998;  
FEATURES Location/Qualifiers  
source 1..27  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 2.1%; Score 21.8; DB 1; Length 27;  
Best Local Similarity 92.0%; Pred. No. 33;

Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTAT 1817  
Db 26 TGTGTGTGTGTGTGTGTGTGT 2

RESULT 17  
AX127802/c  
LOCUS  
DEFINITION Sequence 23 from patent US 6180777.  
ACCESSION AR127802  
VERSION AR127802.1 GI:14114397  
KEYWORDS  
SOURCE Unknown.  
ORGANISM  
REFERENCE 1 (bases 1 to 27)  
AUTHORS Horn, T.  
TITLE Synthesis of branched nucleic acids  
JOURNAL Patent: US 6180777-A 23 30-JAN-2001;  
FEATURES  
source  
1. .27  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 2.1%; Score 21.8; DB 1; Length 27;  
Best Local Similarity 92.0%; Pred. No. 33;  
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTAT 1817  
Db 26 TGTGTGTGTGTGTGTGTGTGT 2

RESULT 18  
I28384/c  
LOCUS  
DEFINITION Sequence 23 from patent US 5571677.  
ACCESSION I28384  
VERSION I28384.1 GI:1819160  
KEYWORDS  
SOURCE Unknown.  
ORGANISM  
REFERENCE 1 (bases 1 to 27)  
AUTHORS Gvaznov, S.M.  
TITLE Convergent synthesis of branched and multiply connected  
JOURNAL macromolecular structures  
FEATURES  
source  
1. .27  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 2.1%; Score 21.8; DB 1; Length 27;  
Best Local Similarity 92.0%; Pred. No. 33;  
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTAT 1817  
Db 26 TGTGTGTGTGTGTGTGTGTGT 2

RESULT 19  
AX175237  
LOCUS  
DEFINITION Sequence 1 from Patent WO0144465.  
ACCESSION AX175237  
VERSION AX175237.1 GI:14598605  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct

artificial sequences.

REFERENCE 1  
AUTHORS Phillips, N.C. and Filion, M.C.  
TITLE Therapeutically useful synthetic oligonucleotides  
JOURNAL Patent: WO 0144465-A 1 21-JUN-2001;  
Bioniche Life Sciences Inc. (CA)

FEATURES  
source  
1. .27  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"

Query Match 2.1%; Score 21.8; DB 1; Length 27;  
Best Local Similarity 92.0%; Pred. No. 33;  
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTAT 1817  
Db 2 TGTGTGTGTGTGTGTGTGTGT 26

RESULT 20  
AX175302  
LOCUS  
DEFINITION Sequence 66 from Patent WO0144465.  
ACCESSION AX175302  
VERSION AX175302.1 GI:14598670  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.

REFERENCE 1  
AUTHORS Phillips, N.C. and Filion, M.C.  
TITLE Therapeutically useful synthetic oligonucleotides  
JOURNAL Patent: WO 0144465-A 66 21-JUN-2001;  
Bioniche Life Sciences Inc. (CA)

FEATURES  
source  
1. .27  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"

Query Match 2.1%; Score 21.8; DB 1; Length 27;  
Best Local Similarity 92.0%; Pred. No. 33;  
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTAT 1817  
Db 2 TGTGTGTGTGTGTGTGTGTGT 26

RESULT 21  
AX189457  
LOCUS  
DEFINITION Sequence 2 from Patent WO0147561.  
ACCESSION AX189457  
VERSION AX189457.1 GI:15142969  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.

REFERENCE 1  
AUTHORS Phillips, N.C. and Filion, M.C.  
TITLE Hyaluronic acid in the treatment of cancer  
JOURNAL Patent: WO 0147561-A 2 05-JUL-2001;  
Bioniche Life Sciences Inc. (CA)

FEATURES  
source  
1. .27  
/organism="synthetic construct"  
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/db\_xref="taxon:32630"  
/note="Synthetic Oligonucleotide"

Query Match 2.1%; Score 21.8; DB 1; Length 27;  
Best Local Similarity 92.0%; Pred. No. 33;  
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTAT 1817  
DB 2 TGTGTGTGTGTGTGTGTGTGT 26

RESULT 22  
I31542/c  
LOCUS I31542 23 bp DNA linear PAT 06-FEB-1997  
DEFINITION Sequence 454 from patent US 5582979.  
ACCESSION I31542  
VERSION I31542.1 GI:1822333  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 23)  
AUTHORS Weber, J.L.  
TITLE Length polymorphisms in (dC-dA).sub.n.(dG-dT).sub.n sequences and method of using the same  
JOURNAL Patent: US 5582979-A 454 10-DEC-1996;  
FEATURES Location/Qualifiers  
source 1..23  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 2.0%; Score 21.4; DB 1; Length 23;  
Best Local Similarity 95.7%; Pred. No. 29;  
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTAT 1815  
DB 23 TGTGTGTGTGTGTGTGTGT 1

RESULT 23  
AX116678  
LOCUS AX116678 23 bp DNA linear PAT 11-MAY-2001  
DEFINITION Sequence 1801 from Patent WO0129262.  
ACCESSION AX116678  
VERSION AX116678.1 GI:14033620  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Picoult-Newburg, L. and Pohl, M.  
TITLE Genotyping reagents, kits and methods of use thereof  
JOURNAL Patent: WO 0129262-A 1801 26-APR-2001;  
Orchid Biosciences, Inc. (US)  
FEATURES Location/Qualifiers  
source 1..23  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/notes="Primer"

Query Match 2.0%; Score 21.4; DB 1; Length 23;  
Best Local Similarity 95.7%; Pred. No. 29;  
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1790 TATTGTGTGTGTGTGTGTG 1812  
DB 1 TTTTGTGTGTGTGTGTGTG 23

RESULT 24  
I31533/c  
LOCUS I31533 24 bp DNA linear PAT 06-FEB-1997  
DEFINITION Sequence 445 from patent US 5582979.

ACCESSION I31533  
VERSION I31533.1 GI:1822324  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 24)  
AUTHORS Weber, J.L.  
TITLE Length polymorphisms in (dC-dA).sub.n.(dG-dT).sub.n sequences and method of using the same  
JOURNAL Patent: US 5582979-A 445 10-DEC-1996;  
FEATURES Location/Qualifiers  
source 1..24  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 2.0%; Score 21.4; DB 1; Length 24;  
Best Local Similarity 95.7%; Pred. No. 31;  
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTAT 1815  
DB 24 TGTGTGTGTGTGTGTGTGT 2

RESULT 25  
AX104876  
LOCUS AX104876 24 bp DNA linear PAT 30-APR-2001  
DEFINITION Sequence 1068 from Patent WO0122972.  
ACCESSION AX104876  
VERSION AX104876.1 GI:13921073  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Krieg, A.M., Schetter, C. and Vollmer, J.C.  
TITLE Immotostimulatory nucleic acids  
JOURNAL Patent: WO 0122972-A 1068 05-APR-2001;  
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US); Coley Pharmaceutical GmbH (DE)  
FEATURES Location/Qualifiers  
source 1..24  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"

Query Match 2.0%; Score 21.4; DB 1; Length 24;  
Best Local Similarity 95.7%; Pred. No. 31;  
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTAT 1815  
DB 1 TGTGTGTGTGTGTGTGTGT 23

RESULT 26  
AX175257  
LOCUS AX175257 24 bp DNA linear PAT 03-JUL-2001  
DEFINITION Sequence 21 from Patent WO0144465.  
ACCESSION AX175257  
VERSION AX175257.1 GI:14598625  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Phillips, N.C. and Filion, M.C.  
TITLE Therapeutically useful synthetic oligonucleotides  
JOURNAL Patent: WO 0144465-A 21 21-JUN-2001;  
Bioniche Life Sciences Inc. (CA)  
FEATURES Location/Qualifiers  
source 1..24

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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match      2.0%; Score 21.4; DB 1; Length 24;
Best Local Similarity 95.7%; Pred. No. 31;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTGTGTGTGTAT 1815
Db 1 TGTGTGTGTGTGTGTGTGTGTGT 23

RESULT 27
AX175258
LOCUS AX175258 24 bp DNA linear PAT 03-JUL-2001
DEFINITION Sequence 22 from Patent WO0144465.
ACCESSION AX175258
VERSION AX175258.1 GI:14598626
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Phillips,N.C. and Fillion,M.C.
TITLE Therapeutically useful synthetic oligonucleotides
JOURNAL Patent: WO 0144465-A 22 21-JUN-2001;
Bioniche Life Sciences, Inc. (CA)
FEATURES
source
Location/Qualifiers
1..24
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match      2.0%; Score 21.4; DB 1; Length 24;
Best Local Similarity 95.7%; Pred. No. 31;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTGTGTGTGTAT 1815
Db 2 TGTGTGTGTGTGTGTGTGTGTGT 24

RESULT 28
AX547929
LOCUS AX547929 24 bp DNA linear PAT 01-MAR-2003
DEFINITION Sequence 1068 from Patent WO02053141.
ACCESSION AX547929
VERSION AX547929.1 GI:25813073
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Bratzler,R.L.
TITLE Inhibition of angiogenesis by nucleic acids
JOURNAL Patent: WO 02053141-A 1068 11-JUL-2002;
Coley Pharmaceutical Group, Inc. (US)
FEATURES
source
Location/Qualifiers
1..24
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic Sequence"

Query Match      2.0%; Score 21.4; DB 1; Length 24;
Best Local Similarity 95.7%; Pred. No. 31;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTGTGTGTGTAT 1815
Db 1 TGTGTGTGTGTGTGTGTGTGTGT 23

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RESULT 29
AX115976
LOCUS AX115976 25 bp DNA linear PAT 11-MAY-2001
DEFINITION Sequence 1099 from Patent WO0129262.
ACCESSION AX115976
VERSION AX115976.1 GI:14032918
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Picoult-Newburg,L. and Pohl,M.
TITLE Genotyping reagents, kits and methods of use thereof
JOURNAL Patent: WO 0129262-A 1099 26-APR-2001;
Orchid BioSciences, Inc. (US)
FEATURES
source
Location/Qualifiers
1..25
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

Query Match      2.0%; Score 21.4; DB 1; Length 25;
Best Local Similarity 95.7%; Pred. No. 33;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTGTGTGTGTAT 1815
Db 2 TGTGTGTGTGTGTGTGTGTGTGT 24

RESULT 30
AX117836/c
LOCUS AX117836 25 bp DNA linear PAT 11-MAY-2001
DEFINITION Sequence 2959 from Patent WO0129262.
ACCESSION AX117836
VERSION AX117836.1 GI:14034787
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Picoult-Newburg,L. and Pohl,M.
TITLE Genotyping reagents, kits and methods of use thereof
JOURNAL Patent: WO 0129262-A 2959 26-APR-2001;
Orchid BioSciences, Inc. (US)
FEATURES
source
Location/Qualifiers
1..25
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

Query Match      2.0%; Score 21.4; DB 1; Length 25;
Best Local Similarity 95.7%; Pred. No. 33;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTGTGTGTGTAT 1815
Db 23 TGTGTGTGTGTGTGTGTGTGTGT 1

RESULT 31
I31248/c
LOCUS I31248 21 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 160 from patent US 5582979.
ACCESSION I31248
VERSION I31248.1 GI:1822039
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.

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REFERENCE 1 (bases 1 to 21)
AUTHORS Weber,J.L.
TITLE Length polymorphisms in (dC-dA).sub.n.(dG-dT).sub.n sequences and
method of using the same
JOURNAL Patent: US 5582979-A 160 10-DEC-1996;
FEATURES
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        1..21
        /organism="unknown"
        /mol_type="unassigned DNA"
Query Match
    2.0%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred.No. 29;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTGTGTGTGT 1813
Db 21 TGTGTGTGTGTGTGTGTGT 1

RESULT 32
AX104715 AX104715 21 bp DNA linear PAT 30-APR-2001
LOCUS
DEFINITION Sequence 907 from Patent WO0122972.
ACCESSION AX104715
VERSION AX104715.1 GI:13920912
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
        artificial sequences.
REFERENCE 1
AUTHORS Kriegl,A.M., Schetter,C. and Vollmer,J.C.
TITLE Immunostimulatory nucleic acids
JOURNAL Patent: WO 0122972-A 907 05-APR-2001;
        UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
        GmbH (DE)
FEATURES
    source
        1..21
        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
Query Match
    2.0%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred.No. 29;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTGTGTGTGT 1813
Db 1 TGTGTGTGTGTGTGTGTGT 21

RESULT 33
AX175255 AX175255 21 bp DNA linear PAT 03-JUL-2001
LOCUS
DEFINITION Sequence 19 from Patent WO0144465.
ACCESSION AX175255
VERSION AX175255.1 GI:14598623
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
        artificial sequences.
REFERENCE 1
AUTHORS Phillips,N.C. and Fillion,M.C.
TITLE Therapeutically useful synthetic oligonucleotides
JOURNAL Patent: WO 0144465-A 19 21-JUN-2001;
        Bioniche Life Sciences Inc. (CA)
FEATURES
    source
        1..21
        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
Query Match
    2.0%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred.No. 29;

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Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTGTGTGTGT 1813
Db 1 TGTGTGTGTGTGTGTGTGT 21

RESULT 34
AX547768 AX547768 21 bp DNA linear PAT 01-MAR-2003
LOCUS
DEFINITION Sequence 907 from Patent WO02053141.
ACCESSION AX547768
VERSION AX547768.1 GI:25812912
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
        artificial sequences.
REFERENCE 1
AUTHORS Bratzler,R.L.
TITLE Inhibition of angiogenesis by nucleic acids
JOURNAL Patent: WO 02053141-A 907 11-JUL-2002;
        Coley Pharmaceutical Group, Inc. (US)
FEATURES
    source
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        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
        /note="Synthetic Sequence"
Query Match
    2.0%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred.No. 29;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTGTGTGTGT 1813
Db 1 TGTGTGTGTGTGTGTGTGT 21

RESULT 35
I31213/c I31213 22 bp DNA linear PAT 06-FEB-1997
LOCUS
DEFINITION Sequence 125 from patent US 5582979.
ACCESSION I31213
VERSION I31213.1 GI:1822004
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 22)
AUTHORS Weber,J.L.
TITLE Length polymorphisms in (dC-dA).sub.n.(dG-dT).sub.n sequences and
method of using the same
JOURNAL Patent: US 5582979-A 125 10-DEC-1996;
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        /mol_type="unassigned DNA"
Query Match
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Best Local Similarity 100.0%; Pred.No. 31;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTGTGTGTGT 1813
Db 21 TGTGTGTGTGTGTGTGTGT 1

RESULT 36
AR127801/c AR127801 23 bp DNA linear PAT 16-MAY-2001
LOCUS
DEFINITION Sequence 22 from patent US 6180777.
ACCESSION AR127801
VERSION AR127801.1 GI:14114396

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KEYWORDS	Unknown.
SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1 (bases 1 to 23)
AUTHORS	Horn,T.
TITLE	Synthesis of branched nucleic acids
JOURNAL	Patent: US 6180777-A 22 30-JAN-2001;
FEATURES	Location/Qualifiers
source	1..23 /organism="unknown" /mol_type="unassigned DNA"
Query Match	2.0%; Score 21; DB 1; Length 23;
Best Local Similarity	100.0%; Pred.No. 33;
Matches	21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1793 TGTGTCGTGTCGTGTCGTGTCGT 1813
Db	22 TGTGTCGTGTCGTGTCGTGTCGT 2
RESULT 37	
AX117828/c	
LOCUS	AX117828 25 bp DNA linear PAT 11-MAY-2001
DEFINITION	Sequence 2951 from Patent WO0129262.
ACCESSION	AX117828
VERSION	AX117828.1 GI:14034779
KEYWORDS	.
SOURCE	synthetic construct
ORGANISM	artificial sequences.
REFERENCE	1
AUTHORS	Picoult-Newburg,L. and Pohl,M.
TITLE	Genotyping reagents, kits and methods of use thereof
JOURNAL	Patent: WO 0129262-A 2951 26-APR-2001;
FEATURES	Orchid Biosciences, Inc. (US) Location/Qualifiers
source	1..25 /organism="synthetic construct" /mol_type="unassigned DNA" /db_xref="taxon:32630" /note="Primer"
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Best Local Similarity	100.0%; Pred.No. 37;
Matches	21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1793 TGTGTCGTGTCGTGTCGTGTCGT 1813
Db	21 TGTGTCGTGTCGTGTCGTGTCGT 1
RESULT 38	
AX117832/c	
LOCUS	AX117832 25 bp DNA linear PAT 11-MAY-2001
DEFINITION	Sequence 2955 from Patent WO0129262.
ACCESSION	AX117832
VERSION	AX117832.1 GI:14034783
KEYWORDS	.
SOURCE	synthetic construct
ORGANISM	artificial sequences.
REFERENCE	1
AUTHORS	Picoult-Newburg,L. and Pohl,M.
TITLE	Genotyping reagents, kits and methods of use thereof
JOURNAL	Patent: WO 0129262-A 2955 26-APR-2001;
FEATURES	Orchid Biosciences, Inc. (US) Location/Qualifiers
source	1..25 /organism="synthetic construct" /mol_type="unassigned DNA" /db_xref="taxon:32630"

KEYWORDS	Unknown.
SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1 (bases 1 to 23)
AUTHORS	Horn,T.
TITLE	Synthesis of branched nucleic acids
JOURNAL	Patent: US 6180777-A 22 30-JAN-2001;
FEATURES	Location/Qualifiers
source	1..23 /organism="unknown" /mol_type="unassigned DNA"
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Matches	21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db	22 TGTGTCGTGTCGTGTCGTGTCGT 2
RESULT 39	
A63570	
LOCUS	A63570 20 bp DNA linear PAT 12-MAR-1998
DEFINITION	Sequence 11 from Patent WO9720924.
ACCESSION	A63570
VERSION	A63570.1 GI:3717225
KEYWORDS	.
SOURCE	unidentified
ORGANISM	unidentified
REFERENCE	1
AUTHORS	Scaggiante,B. and Quadrifoglio,F.
TITLE	A CLASS OF OLIGONUCLEOTIDES, THERAPEUTICALLY USEFUL AS ANTITUMORAL AGENTS
JOURNAL	Patent: WO 9720924-A 11 12-JUN-1997;
COMMENT	SAICOM S R L (IT) Other publication IT MI952539 19970604 Other publication AU 1175497 19970627.
FEATURES	Location/Qualifiers
source	1..20 /organism="unidentified" /mol_type="unassigned DNA" /db_xref="taxon:32644"
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Best Local Similarity	100.0%; Pred.No. 35;
Matches	20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1794 GTGTGTGTGTGTGTGTGTGTGT 1813
Db	1 GTGTGTGTGTGTGTGTGTGTGT 20
RESULT 40	
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LOCUS	AR074792 20 bp DNA linear PAT 28-AUG-2000
DEFINITION	Sequence 89 from patent US 5955276.
ACCESSION	AR074792
VERSION	AR074792.1 GI:10001545
KEYWORDS	.
SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	1 (bases 1 to 20)
AUTHORS	Morgante,M. and Vogel,J.Marie.
TITLE	Compound microsatellite primers for the detection of genetic polymorphisms
JOURNAL	Patent: US 5955276-A 89 21-SEP-1999;
FEATURES	Location/Qualifiers
source	1..20 /organism="unknown" /mol_type="unassigned DNA"
Query Match	1.9%; Score 20; DB 1; Length 20;
Best Local Similarity	100.0%; Pred.No. 35;
Matches	20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1799 TGTGTCGTGTCGTATATA 1818
Db	20 TGTGTCGTGTCGTATATA 1

KEYWORDS	Unknown.
SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1 (bases 1 to 23)
AUTHORS	Horn,T.
TITLE	Synthesis of branched nucleic acids
JOURNAL	Patent: US 6180777-A 22 30-JAN-2001;
FEATURES	Location/Qualifiers
source	1..23 /organism="unknown" /mol_type="unassigned DNA"
Query Match	2.0%; Score 21; DB 1; Length 23;
Best Local Similarity	100.0%; Pred.No. 33;
Matches	21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1793 TGTGTCGTGTCGTGTCGTGTCGT 1813
Db	22 TGTGTCGTGTCGTGTCGTGTCGT 2
RESULT 37	
AX117828/c	
LOCUS	AX117828 25 bp DNA linear PAT 11-MAY-2001
DEFINITION	Sequence 2951 from Patent WO0129262.
ACCESSION	AX117828
VERSION	AX117828.1 GI:14034779
KEYWORDS	.
SOURCE	synthetic construct
ORGANISM	artificial sequences.
REFERENCE	1
AUTHORS	Picolult-Newburg,L. and Pohl,M.
TITLE	Genotyping reagents, kits and methods of use thereof
JOURNAL	Patent: WO 0129262-A 2951 26-APR-2001;
FEATURES	Orchid Biosciences, Inc. (US) Location/Qualifiers
source	1..25 /organism="synthetic construct" /mol_type="unassigned DNA" /db_xref="taxon:32630" /note="Primer"
Query Match	2.0%; Score 21; DB 1; Length 25;
Best Local Similarity	100.0%; Pred.No. 37;
Matches	21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1793 TGTGTCGTGTCGTGTCGTGTCGT 1813
Db	21 TGTGTCGTGTCGTGTCGTGTCGT 1
RESULT 38	
AX117832/c	
LOCUS	AX117832 25 bp DNA linear PAT 11-MAY-2001
DEFINITION	Sequence 2955 from Patent WO0129262.
ACCESSION	AX117832
VERSION	AX117832.1 GI:14034783
KEYWORDS	.
SOURCE	synthetic construct
ORGANISM	artificial sequences.
REFERENCE	1
AUTHORS	Picolult-Newburg,L. and Pohl,M.
TITLE	Genotyping reagents, kits and methods of use thereof
JOURNAL	Patent: WO 0129262-A 2955 26-APR-2001;
FEATURES	Orchid Biosciences, Inc. (US) Location/Qualifiers
source	1..25 /organism="synthetic construct" /mol_type="unassigned DNA" /db_xref="taxon:32630"

KEYWORDS	Unknown.
SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1 (bases 1 to 23)
AUTHORS	Horn,T.
TITLE	Synthesis of branched nucleic acids
JOURNAL	Patent: US 6180777-A 22 30-JAN-2001;
FEATURES	Location/Qualifiers
source	1..23 /organism="unknown" /mol_type="unassigned DNA"
Query Match	2.0%; Score 21; DB 1; Length 23;
Best Local Similarity	100.0%; Pred.No. 33;
Matches	21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1793 TGTGTCGTGTCGTGTCGTGTCGT 1813
Db	22 TGTGTCGTGTCGTGTCGTGTCGT 2
RESULT 39	
A63570	
LOCUS	A63570 20 bp DNA linear PAT 12-MAR-1998
DEFINITION	Sequence 11 from Patent WO9720924.
ACCESSION	A63570
VERSION	A63570.1 GI:3717225
KEYWORDS	.
SOURCE	unidentified
ORGANISM	unidentified
REFERENCE	1
AUTHORS	Scaggiante,B. and Quadrifoglio,F.
TITLE	A CLASS OF OLIGONUCLEOTIDES, THERAPEUTICALLY USEFUL AS ANTITUMORAL AGENTS
JOURNAL	Patent: WO 9720924-A 11 12-JUN-1997;
COMMENT	SAICOM S R L (IT) Other publication IT MI952539 19970604
FEATURES	Other publication AU 1175497 19970627. Location/Qualifiers
source	1..20 /organism="unidentified" /mol_type="unassigned DNA" /db_xref="taxon:32644"
Query Match	1.9%; Score 20; DB 1; Length 20;
Best Local Similarity	100.0%; Pred.No. 35;
Matches	20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1794 GTGTGTGTGTGTGTGTGTGTGT 1813
Db	1 GTGTGTGTGTGTGTGTGTGTGT 20
RESULT 40	
AR074792/c	
LOCUS	AR074792 20 bp DNA linear PAT 28-AUG-2000
DEFINITION	Sequence 89 from patent US 5955276.
ACCESSION	AR074792
VERSION	AR074792.1 GI:10001545
KEYWORDS	.
SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	1 (bases 1 to 20)
AUTHORS	Morgante,M. and Vogel,J.Marie.
TITLE	Compound microsatellite primers for the detection of genetic polymorphisms
JOURNAL	Patent: US 5955276-A 89 21-SEP-1999;
FEATURES	Location/Qualifiers
source	1..20 /organism="unknown" /mol_type="unassigned DNA"
Query Match	1.9%; Score 20; DB 1; Length 20;
Best Local Similarity	100.0%; Pred.No. 35;
Matches	20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1799 TGTGTGTGTGTGTGTATATA 1818
Db	20 TGTGTGTGTGTGTATATA 1

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RESULT 41
AR084543/c
LOCUS AR084543 20 bp DNA linear PAT 01-SEP-2000
DEFINITION Sequence 32 from patent US 5981185.
ACCESSION AR084543
VERSION AR084543.1 GI:10011314
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
TITLE Oligonucleotide repeat arrays
JOURNAL Patent: US 5981185-A 32 09-NOV-1999;
FEATURES
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Location/Qualifiers
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/mol_type="unknown"
/mol_type="unassigned DNA"

Query Match 1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1794 GTGTGTGTGTGTGTGTGT 1813
Db 20 GTGTGTGTGTGTGTGTGT 1

RESULT 42
AR123339/c
LOCUS AR123339 20 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 5 from patent US 6169176.
ACCESSION AR123339
VERSION AR123339.1 GI:14108305
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bruce,T.C. and Dev,A.P.
TITLE Deoxynucleic alkyl thiourea compounds and uses thereof
JOURNAL Patent: US 6169176-A 5 02-JAN-2001;
FEATURES
source
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 35;
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Qy 1794 GTGTGTGTGTGTGTGTGT 1813
Db 20 GTGTGTGTGTGTGTGTGT 1

RESULT 43
AR129684/c
LOCUS AR129684 20 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 88 from patent US 6187545.
ACCESSION AR129684
VERSION AR129684.1 GI:14117581
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS McKay,R., Butler,M.M., Wyatt,J. and Cowsett,L.M.
TITLE Antisense modulation of peptck-cytosolic expression
JOURNAL Patent: US 6187545-A 88 13-FEB-2001;
FEATURES
source
Location/Qualifiers
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Query Match 1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 20 TGTGTGTGTGTGTGTGTGT 1

RESULT 44
AR179298/c
LOCUS AR179298 20 bp DNA linear PAT 03-JUL-2001
DEFINITION Sequence 1 from Patent WO0141813.
ACCESSION AR179298
VERSION AR179298.1 GI:14598969
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Linnik,M.D. and Mcnealy,P.A.
TITLE Methods of treating lupus based on antibody affinity and screening
JOURNAL Patent: WO 0141813-A 1 14-JUN-2001;
FEATURES
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Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 35;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1794 GTGTGTGTGTGTGTGTGT 1813
Db 1 GTGTGTGTGTGTGTGTGT 20

RESULT 45
AR179299/c
LOCUS AR179299 20 bp DNA linear PAT 03-JUL-2001
DEFINITION Sequence 2 from Patent WO0141813.
ACCESSION AR179299
VERSION AR179299.1 GI:14598970
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Linnik,M.D. and Mcnealy,P.A.
TITLE Methods of treating lupus based on antibody affinity and screening
JOURNAL Patent: WO 0141813-A 2 14-JUN-2001;
FEATURES
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Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTGTGTGTGT 1812
Db 20 TGTGTGTGTGTGTGTGTGT 1
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Query Match 1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1794 GTGTGTGTGTGTGTGTGT 1813
Db 20 GTGTGTGTGTGTGTGTGT 1

RESULT 44
AR179298
LOCUS AR179298 20 bp DNA linear PAT 03-JUL-2001
DEFINITION Sequence 1 from Patent WO0141813.
ACCESSION AR179298
VERSION AR179298.1 GI:14598969
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Linnik,M.D. and Mcnealy,P.A.
TITLE Methods of treating lupus based on antibody affinity and screening
JOURNAL Patent: WO 0141813-A 1 14-JUN-2001;
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source
Location/Qualifiers
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Query Match 1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1794 GTGTGTGTGTGTGTGTGT 1813
Db 1 GTGTGTGTGTGTGTGTGT 20

RESULT 45
AR179299/c
LOCUS AR179299 20 bp DNA linear PAT 03-JUL-2001
DEFINITION Sequence 2 from Patent WO0141813.
ACCESSION AR179299
VERSION AR179299.1 GI:14598970
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Linnik,M.D. and Mcnealy,P.A.
TITLE Methods of treating lupus based on antibody affinity and screening
JOURNAL Patent: WO 0141813-A 2 14-JUN-2001;
FEATURES
source
Location/Qualifiers
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/mol_type="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTGTGTGTGT 1812
Db 20 TGTGTGTGTGTGTGTGTGT 1
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RESULT 46
BD016468
LOCUS
DEFINITION Method for regulating telomeric length. linear PAT 27-AUG-2002
ACCESSION BD016468
VERSION BD016468.1 GI:22557644
KEYWORDS JP 2001231567-A/9.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
1 (bases 1 to 20)
REFERENCE
AUTHORS Ota,K. and Shibata,T.
TITLE Method for regulating telomeric length
JOURNAL Patent: JP 2001231567-A 9 28-AUG-2001;
THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, JAPAN SCIENCE AND
TECHNOLOGY CORP
OS Artificial Sequence
PN JP 2001231567-A/9
PD 28-AUG-2001
PF 18-FEB-2000 JP 2000041929
PI KUNIKAZU OTA, TAKEHIKO SHIBATA
PC C12N15/09, A61K35/76, A61K38/00, A61K48/00, A61P43/00,
C07H21/00,
PC C07K14/395, C12N9/16, C12N15/00, A61K37/02
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Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTGT 1813
DB 1 GTGTGTGTGTGTGTGTGT 20

FEATURES
source
1..20
/organism="synthetic construct"

RESULT 47
BD097545
LOCUS
DEFINITION Method for regulating telomeric length. linear PAT 27-AUG-2002
ACCESSION BD097545
VERSION BD097545.1 GI:22643119
KEYWORDS WO 0160996-A/9.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
1 (bases 1 to 20)
REFERENCE
AUTHORS Ota,K. and Shibata,T.
TITLE Method for regulating telomeric length
JOURNAL Patent: WO 0160996-A 9 23-AUG-2001;
THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, JAPAN SCIENCE AND
TECHNOLOGY CORP, KUNIHICO OTA, TAKEHIKO SHIBATA
OS Artificial Sequence
PN WO 0160996-A/9
PD 23-AUG-2001
PF 14-FEB-2001 WO 2001JP001024
PR 18-FEB-2000 JP 00P 41929
PI KUNIHICO OTA, TAKEHIKO SHIBATA
PC C12N15/09, A61K35/76, A61K38/00, A61K48/00, A61P43/00,
C07H21/00,
PC C07K14/395, C12N9/16
CC Description of Artificial Sequence: synthetic DNA FH Key
Location/Qualifiers
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/organism="synthetic construct"

Query Match 1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 GTGTGTGTGTGTGTGTGT 20

FEATURES
source
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/db_xref="taxon:32630"

Query Match 1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTGT 1813
DB 1 GTGTGTGTGTGTGTGTGT 20

FEATURES
source
1..20
/organism="synthetic construct"

RESULT 48
BD105781/c
LOCUS
DEFINITION BD105781 20 bp DNA linear PAT 27-AUG-2002
Conjugates of biologically stable polymers and polynucleotides for
treating systemic lupus erythematosus.
ACCESSION BD105781
VERSION BD105781.1 GI:22651355
KEYWORDS JP 2001354569-A/6.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
1 (bases 1 to 20)
REFERENCE
AUTHORS Conrad,W.J. and Coutts,S.
TITLE Conjugates of biologically stable polymers and polynucleotides for
treating systemic lupus erythematosus
JOURNAL Patent: JP 2001354569-A 6 25-DEC-2001;
LA JOLLA PHARMACEUTICAL CO
COMMENT OS Artificial Sequence
PN JP 2001354569-A/6
PD 25-DEC-2001
PF 04-APR-2001 JP 2001106534
PR 16-JAN-1990 US 466138,13-MAR-1990 US 494118 PI
MICHAEL J CONRAD, STEPHEN COUTTS
PC A61K31/7088, A61K47/48, A61P37/02, C07K14/00, C12N15/00, C12N15/00
CC Synthetic Construct
FH Key Location/Qualifiers
FT source 1..20
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Query Match 1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTGT 1813
DB 20 GTGTGTGTGTGTGTGTGT 1

FEATURES
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Query Match 1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTGT 1813
DB 20 GTGTGTGTGTGTGTGTGT 1

FEATURES
source
1..20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

RESULT 49
AX175256
LOCUS
DEFINITION Sequence 20 from Patent WO0144465. linear PAT 03-JUL-2001
ACCESSION AX175256
VERSION AX175256.1 GI:14598624
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
1
REFERENCE
AUTHORS Phillips,N.C. and Filion,M.C.
TITLE Therapeutically useful synthetic oligonucleotides
JOURNAL Patent: WO 0144465-A 20 21-JUN-2001;
Bioniche Life Sciences Inc. (CA)
FEATURES
source
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/organism="synthetic construct"
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match      1.9%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTGTGT 1813
DB 1 GTGTGTGTGTGTGTGTGTGT 20

RESULT 50
AX398276/c
LOCUS AX398276 21 bp DNA linear PAT 27-MAY-2002
DEFINITION Sequence 1 from Patent WO220543.
ACCESSION AX398276
VERSION AX398276.1 GI:21261077
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Sinha,N.
TITLE Synthesis for oligonucleotide synthesis
JOURNAL Patent: WO 0220543-A 1 14-MAR-2002;
Avecia Biotechnology, Inc. (US)
FEATURES
Source
Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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Query Match      1.9%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTGTGT 1813
DB 20 GTGTGTGTGTGTGTGTGTGT 1

RESULT 51
AX398277
LOCUS AX398277 21 bp DNA linear PAT 27-MAY-2002
DEFINITION Sequence 2 from Patent WO220543.
ACCESSION AX398277
VERSION AX398277.1 GI:21261078
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Sinha,N.
TITLE Synthesis for oligonucleotide synthesis
JOURNAL Patent: WO 0220543-A 2 14-MAR-2002;
Avecia Biotechnology, Inc. (US)
FEATURES
Source
Location/Qualifiers
1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Sequence prepared in Example 4"

Query Match      1.9%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTGTGT 1813
DB 1 GTGTGTGTGTGTGTGTGTGT 20

RESULT 52
AX398277/c
LOCUS AX398277 21 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 10 from patent US 5580969.
ACCESSION AX398277
VERSION AX398277.1 GI:1821338
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
AUTHORS Hoke,G.D., Bradley,M.O., Williams,T.J. and Lee,C.H.
TITLE Antisense oligonucleotides directed against human ICAM-1 RNA
JOURNAL Patent: US 5580969-A 10 03-DEC-1996;
Location/Qualifiers
1..21
/organism="unknown"
/mol_type="unassigned DNA"

Query Match      1.8%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 44;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TCTGTGTGTGTGTGTGTGTGT 1813
DB 21 TCTGTGTGTGTGTGTGTGTGT 1

RESULT 53
AX117030
LOCUS AX117030 24 bp DNA linear PAT 11-MAY-2001
DEFINITION Sequence 2153 from Patent WO0129262.
ACCESSION AX117030
VERSION AX117030.1 GI:14033972
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Picourt-Newburg,L. and Pohl,M.
TITLE Genotyping reagents, kits and methods of use thereof
JOURNAL Patent: WO 0129262-A 2153 26-APR-2001;
Orchid BioSciences, Inc. (US)
FEATURES
Source
Location/Qualifiers
1..24
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

Query Match      1.8%; Score 19.4; DB 1; Length 24;
Best Local Similarity 95.2%; Pred. No. 53;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TCTGTGTGTGTGTGTGTGTGT 1813
DB 1 TCTGTGTGTGTGTGTGTGTGT 21

RESULT 54
AR074777
LOCUS AR074777 19 bp DNA linear PAT 28-AUG-2000
DEFINITION Sequence 74 from patent US 5955276.
ACCESSION AR074777
VERSION AR074777.1 GI:10001530
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Morcante,M. and Vogel,J. Marie.
TITLE Compound microsatellite primers for the detection of genetic
```

polymorphisms  
 JOURNAL Patent: US 595276-A 74 21-SEP-1999;  
 FEATURES Location/Qualifiers  
 source 1..19  
 /organism="unknown"  
 /mol\_type="unassigned DNA"

Query Match 1.8%; Score 19; DB 1; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 43;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1799 TGTGTGTGTGTGTAT 1817  
 Db 1 TGTGTGTGTGTGTAT 19

RESULT 55  
 I31530/c 131530 19 bp DNA linear PAT 06-FEB-1997  
 DEFINITION Sequence 442 from patent US 5582979.  
 ACCESSION I31530  
 VERSION I31530.1 GI:1822321  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 19)  
 AUTHORS Weber, J.L.  
 TITLE Length polymorphisms in (dC-da).sub.n. (dG-dT).sub.n sequences and method of using the same  
 JOURNAL Patent: US 5582979-A 442 10-DEC-1996;  
 FEATURES Location/Qualifiers  
 source 1..19  
 /organism="unknown"  
 /mol\_type="unassigned DNA"

Query Match 1.8%; Score 19; DB 1; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 43;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTGTGT 1811  
 Db 19 TGTGTGTGTGTGTGT 1

RESULT 56  
 AX040467/c 19 bp DNA linear PAT 18-NOV-2000  
 LOCUS AX040467  
 DEFINITION Sequence 7 from Patent WO063365.  
 ACCESSION AX040467  
 VERSION AX040467.1 GI:11230259  
 KEYWORDS  
 SOURCE synthetic construct  
 ORGANISM synthetic construct  
 REFERENCE 1  
 AUTHORS Belotserkovskii, B., Reddy, G. and Zarling, D.  
 TITLE Locked nucleic acid hybrids and methods of use  
 JOURNAL Patent: WO 0063365-A 7 26-OCT-2000;  
 FEATURES Location/Qualifiers  
 source 1..19  
 /organism="synthetic construct"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:32630"  
 /note="Z-DNA"

Query Match 1.8%; Score 19; DB 1; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 43;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTGTGT 1811

Db 19 TGTGTGTGTGTGTGT 1

RESULT 57  
 AX040468 19 bp DNA linear PAT 18-NOV-2000  
 LOCUS AX040468  
 DEFINITION Sequence 8 from Patent WO063365.  
 ACCESSION AX040468  
 VERSION AX040468.1 GI:11230260  
 KEYWORDS  
 SOURCE synthetic construct  
 ORGANISM synthetic construct  
 REFERENCE 1  
 AUTHORS Belotserkovskii, B., Reddy, G. and Zarling, D.  
 TITLE Locked nucleic acid hybrids and methods of use  
 JOURNAL Patent: WO 0063365-A 8 26-OCT-2000;  
 FEATURES Location/Qualifiers  
 source 1..19  
 /organism="synthetic construct"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:32630"  
 /note="Z-DNA"

Query Match 1.8%; Score 19; DB 1; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 43;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTGTGT 1811  
 Db 1 TGTGTGTGTGTGTGT 19

RESULT 58  
 AR126570 21 bp DNA linear PAT 16-MAY-2001  
 LOCUS AR126570  
 DEFINITION Sequence 1 from patent US 6180349.  
 ACCESSION AR126570  
 VERSION AR126570.1 GI:14113163  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 21)  
 AUTHORS Ginzinger, D.G., Godfrey, T.E., Jensen, R.H. and Gray, J.W.  
 TITLE Quantitative PCR method to enumerate DNA copy number  
 JOURNAL Patent: US 6180349-A 1 30-JAN-2001;  
 FEATURES Location/Qualifiers  
 source 1..21  
 /organism="unknown"  
 /mol\_type="unassigned DNA"

Query Match 1.8%; Score 19; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 49;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1794 GTGTGTGTGTGTGTGTG 1812  
 Db 2 GTGTGTGTGTGTGTGTG 20

RESULT 59  
 AR126571 21 bp DNA linear PAT 16-MAY-2001  
 LOCUS AR126571  
 DEFINITION Sequence 2 from patent US 6180349.  
 ACCESSION AR126571  
 VERSION AR126571.1 GI:14113164  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 21)

AUTHORS Ginzinger,D.G., Godfrey,T.E., Jensen,R.H. and Gray,J.W.  
TITLE Quantitative PCR method to enumerate DNA copy number  
JOURNAL Patent: US 6180349-A 2 30-JAN-2001;  
FEATURES Location/Qualifiers  
1. .21  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.8%; Score 19; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 49;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1794 GTGTGTGTGTGTGTGTGTG 1812  
DB 2 GTGTGTGTGTGTGTGTGTG 20

RESULT 60  
BD089174  
LOCUS BD089174 21 bp DNA linear PAT 27-AUG-2002  
DEFINITION A method of arraying genome clone.  
ACCESSION BD089174  
VERSION BD089174.1 GI:22634784  
KEYWORDS JP 2001321190-A/1418.  
SOURCE synthetic construct  
ORGANISM artificial sequences.  
REFERENCE 1 (bases 1 to 21)  
Soeda,E.  
TITLE A method of arraying genome clone  
JOURNAL Patent: JP 2001321190-A 1418 20-NOV-2001;  
THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA  
GENOTECHS

OS Artificial Sequence  
PN JP 2001321190-A/1418  
PD 20-NOV-2001  
PF 12-MAR-2001 JP 2001068285  
PI EIICHI SOEDA  
PC C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N33/53,G01N33/566, PC  
C12N15/09,  
PC C12N15/00  
CC Description of Artificial Sequence:Synthetic DNA FH Key  
Location/Qualifiers  
FT source 1. .21  
FT Location/Qualifiers  
1. .21  
/organism="Artificial Sequence".

FEATURES  
source  
1. .21  
Location/Qualifiers  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"

Query Match 1.8%; Score 19; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 49;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1793 TGTGTGTGTGTGTGTGTGT 1811  
DB 1 TGTGTGTGTGTGTGTGTGT 19

RESULT 61  
AB068223  
LOCUS AB068223 21 bp DNA linear SYN 21-MAY-2003  
DEFINITION Synthetic construct DNA, reverse primer for human STS sts-R12616F  
at 1p36.  
ACCESSION AB068223  
VERSION AB068223.1 GI:15129027  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.  
REFERENCE 1  
Chen,Y.Z., Hayashi,Y., Wu,J.G., Takaoka,E., Maekawa,K.,

Watanabe,N., Inazawa,J., Hosoda,F., Arai,Y., Mizushima,H.,  
Morohashi,A., Ohira,M., Nakagawara,A., Liu,S., Hoshi,M., Horii,A.  
and Soeda,E.  
TITLE A BAC-based STS-content map spanning a 35-Mb region of human  
chromosome 1p35-p36  
JOURNAL Genomics 74 (1), 55-70 (2001)  
MEDLINE 21269192  
PUBMED 11374902  
REFERENCE 2 (bases 1 to 21)  
AUTHORS Horii,A.  
TITLE Direct Submission  
JOURNAL Submitted (04-AUG-2001) Akira Horii, Tohoku University School of  
Medicine, Molecular Pathology; 2-1 Seiryomachi, Aoba-ku, Sendai,  
Miyagi 980-8575 Japan (E-mail:horii@mail.cc.tohoku.ac.jp,  
Tel:81-22-717-8042, Fax:81-22-717-8047)  
FEATURES Location/Qualifiers  
1. .21  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"

misc\_feature 1. .21  
/note="reverse primer for human STS sts-R12616F at 1p36  
sts-R12616F obtained from clones B12616, B156A20,  
B141M15, B137L6, B157P23, Human BAC library  
RPC1-11"

Query Match 1.8%; Score 19; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 49;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1793 TGTGTGTGTGTGTGTGTGT 1811  
DB 1 TGTGTGTGTGTGTGTGTGT 19

RESULT 62  
E32219/c  
LOCUS E32219 20 bp DNA linear PAT 18-JUN-2001  
DEFINITION Method for isolating satellite sequence.  
ACCESSION E32219  
VERSION E32219.1 GI:13021841  
KEYWORDS JP 2000060559-A/21.  
SOURCE Haliotis discus discus  
ORGANISM Haliotis discus discus  
Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;  
Vetigastropoda; Haliotoidea; Haliotidae; Haliotis.

REFERENCE 1 (bases 1 to 20)  
Hideaki,T. and Masashi,S.  
TITLE Method for isolating satellite sequence  
JOURNAL Patent: JP 2000060559-A 21 29-FEB-2000;  
NAIL INST OF AGROBIOLOGICAL RESOURCES  
COMMENT OS Haliotis discus discus  
PN JP 2000060559-A/21  
PD 29-FEB-2000  
PF 18-AUG-1998 JP 1998232153  
PR  
PI HIDEAKI TAKAHASHI,MASASHI SEKINO  
PC C12N15/09,C12Q1/68,C12N15/00  
CC  
FH Key Location/Qualifiers  
FT source 1. .20  
FT Location/Qualifiers  
1. .20  
/organism="Haliotis discus discus"  
/mol\_type="genomic DNA"  
/sub\_species="discus"  
/db\_xref="taxon:91233"

FEATURES  
source  
1. .20  
Location/Qualifiers  
/organism="Haliotis discus discus"  
/mol\_type="genomic DNA"  
/sub\_species="discus"  
/db\_xref="taxon:91233"

Query Match 1.8%; Score 18.4; DB 1; Length 20;  
Best Local Similarity 95.0%; Pred. No. 54;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1793 TGTGTGTGTGTGTGTGTGTG 1812
Db 20 TGTGTGTGTGTGTGTGTGTG 1

RESULT 63
LOCUS AR071775/C 18 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 4 from patent US 5912147.
ACCESSION AR071775
VERSION AR071775.1 GI:7222663
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Stoler,D., Basik,M. and Anderson,G.
TITLE Rapid means of quantitating genomic instability
JOURNAL Patent: US 5912147-A 4 15-JUN-1999;
FEATURES
    source
        Location/Qualifiers
            1..18
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match 1.7%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1791 ATTGTGTGTGTGTGTGTGTG 1808
Db 18 ATTGTGTGTGTGTGTGTGTG 1

RESULT 64
LOCUS AR071776/C 18 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 5 from patent US 5912147.
ACCESSION AR071776
VERSION AR071776.1 GI:7222664
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Stoler,D., Basik,M. and Anderson,G.
TITLE Rapid means of quantitating genomic instability
JOURNAL Patent: US 5912147-A 5 15-JUN-1999;
FEATURES
    source
        Location/Qualifiers
            1..18
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match 1.7%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1799 ATTTGTGTGTGTGTGTGTGTG 1808
Db 18 ATTTGTGTGTGTGTGTGTGTG 1

RESULT 65
LOCUS AR178165/C 18 bp DNA linear PAT 18-DEC-2001
DEFINITION Sequence 1 from patent US 6316186.
ACCESSION AR178165
VERSION AR178165.1 GI:17921058
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Ekins,R.Philip.

TITLE Binding assay using binding agents with tail groups
JOURNAL Patent: US 6316186-A 1 13-NOV-2001;
FEATURES
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        Location/Qualifiers
            1..18
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match 1.7%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTG 1810
Db 18 TGTGTGTGTGTGTGTGTGTG 1

RESULT 66
LOCUS AR178166 18 bp DNA linear PAT 18-DEC-2001
DEFINITION Sequence 2 from patent US 6316186.
ACCESSION AR178166
VERSION AR178166.1 GI:17921059
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Ekins,R.Philip.
TITLE Binding assay using binding agents with tail groups
JOURNAL Patent: US 6316186-A 2 13-NOV-2001;
FEATURES
    source
        Location/Qualifiers
            1..18
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match 1.7%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTGTGT 1811
Db 1 GTGTGTGTGTGTGTGTGTGT 18

RESULT 67
LOCUS AR182079 18 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 28 from patent US 6337188.
ACCESSION AR182079
VERSION AR182079.1 GI:20224995
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Head,S.R., Goelst,P., Karn,J. and Boyce-Jacino,M.
TITLE De novo or 'universal' sequencing array
JOURNAL Patent: US 6337188-A 28 08-JAN-2002;
FEATURES
    source
        Location/Qualifiers
            1..18
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match 1.7%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTG 1810
Db 1 TGTGTGTGTGTGTGTGTGTG 18

RESULT 68
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AR261503
LOCUS AR261503 18 bp DNA linear PAT 29-JAN-2003
DEFINITION Sequence 28 from patent US 6322968.
ACCESSION AR261503
VERSION AR261503.1 GI:28072570
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Head,S.R., Golet,P., Karn,J. and Boyce-Jacino,M.
TITLE De novo or 'universal' sequencing array
JOURNAL Patent: US 6322968-A 28 27-NOV-2001;
FEATURES
    Location/Qualifiers
    source 1..18
        /organism="unknown"
        /mol_type="genomic DNA"

Query Match 1.7%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred.No. 52;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTG 1810
    |||
    |||
    |||
Db 1 TGTGTGTGTGTGTGTGTG 18

RESULT 69
LOCUS AX175253 18 bp DNA linear PAT 03-JUL-2001
DEFINITION Sequence 17 from Patent WO0144465.
ACCESSION AX175253
VERSION AX175253.1 GI:14598621
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Phillips,N.C. and Filion,M.C.
TITLE Therapeutically useful synthetic oligonucleotides
JOURNAL Patent: WO-0144465-A 17 21-JUN-2001;
JOURNAL Bioniche Life Sciences Inc. (CA)
FEATURES
    Location/Qualifiers
    source 1..18
        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"

Query Match 1.7%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred.No. 52;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTG 1810
    |||
    |||
    |||
Db 1 TGTGTGTGTGTGTGTGTG 18

RESULT 70
LOCUS AX175254 18 bp DNA linear PAT 03-JUL-2001
DEFINITION Sequence 18 from Patent WO0144465.
ACCESSION AX175254
VERSION AX175254.1 GI:14598622
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Phillips,N.C. and Filion,M.C.
TITLE Therapeutically useful synthetic oligonucleotides
JOURNAL Patent: WO 0144465-A 18 21-JUN-2001;
JOURNAL Bioniche Life Sciences Inc. (CA)
FEATURES
    Location/Qualifiers

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source 1..18
    /organism="synthetic construct"
    /mol_type="unassigned DNA"
    /db_xref="taxon:32630"

Query Match 1.7%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred.No. 52;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTGTG 1811
    |||
    |||
    |||
Db 1 GTGTGTGTGTGTGTGTGTG 18

RESULT 71
LOCUS BD087486 18 bp DNA linear PAT 27-AUG-2002
DEFINITION De novo or universal sequencing array.
ACCESSION BD087486
VERSION BD087486.1 GI:22633096
KEYWORDS JP 2001524319-A/28.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 18)
AUTHORS Head,S.R., Golet,P., Karn,J. and Jacino,M.B.
TITLE De novo or universal sequencing array
JOURNAL Patent: JP 2001524319-A 28 04-DEC-2001;
JOURNAL ORCHID BIOSCIENCES INC
COMMENT OS Artificial Sequence
PN JP 2001524319-A/28
PD 04-DEC-2001
PF 20-NOV-1998 JP 2000522278
PR 21-NOV-1997 US 08/976427
PI STEVEN R HEAD,PHILIP GOLETT,JONATHAN KARN,MICHAEL BOYCE JACINO
PC C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N33/50,C12N15/00,PC
C12N15/00
CC Synthetic primer
FH Key
FT source 1..18
    Location/Qualifiers
    source 1..18
        /organism="synthetic construct"
        /mol_type="genomic DNA"
        /db_xref="taxon:32630"

Query Match 1.7%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred.No. 52;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTG 1810
    |||
    |||
    |||
Db 1 TGTGTGTGTGTGTGTGTG 18

RESULT 72
LOCUS E05497 20 bp DNA linear PAT 29-SEP-1997
DEFINITION PCR primer for detecting polymorphism of Oryza sativa and Zea
maize.
ACCESSION E05497
VERSION E05497.1 GI:12173685
KEYWORDS JP 1993244995-A/7.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 20)
AUTHORS Komatsu,Y. and Kikuchi,Y.
TITLE NEW PRIMER
JOURNAL Patent: JP 1993244995-A 7 24-SEP-1993;
JOURNAL KYOWA HAKKO KOGYO CO LTD
COMMENT OS Artificial gene

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OC Artificial sequence; Genes.
OS Zea maize
PN JP 1993244995-A/7
PD 24-SEP-1993
PF 24-SEP-1991 JP 1991243122
PI KOMATSU YUKI, KIKUCHI YASUHIRO
PC C12Q1/68, C12N15/11;
CC strandedness: Single;
CC topology: linear;
CC hypothetical: No;
CC anti-sense: No;
CC Location/Qualifiers
FEATURES
    source
        1..20
            /organism="synthetic construct"
            /mol_type="genomic DNA"
            /db_xref="taxon:32630"

Query Match
Best Local Similarity 100.0%; Score 18; DB 1; Length 20;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTG 1810
Db 1 TGTGTGTGTGTGTGTG 18

RESULT 73
LOCUS AR129716 20 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 120 from patent US 6187545.
ACCESSION AR129716
VERSION AR129716.1 GI:14117613
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS McKay, R., Butler, M.M., Wyatt, J., and Cowse, L.M.
TITLE Antisense modulation of peck-cytosolic expression
JOURNAL Patent: US 6187545-A 120 13-FEB-2001;
FEATURES
    source
        1..20
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match
Best Local Similarity 94.7%; Score 17.4; DB 1; Length 20;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTG 1812
Db 1 GTGTGTGTGTGTGTG 19

RESULT 74
LOCUS AR181773/20 20 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 235 from patent US 6335194.
ACCESSION AR181773
VERSION AR181773.1 GI:20223987
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bennett, C. Frank., Ackermann, E.J., Swayze, E.E. and Cowse, L.M.
TITLE Antisense modulation of survivin expression
JOURNAL Patent: US 6335194-A 235 01-JAN-2002;
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            /mol_type="unassigned DNA"

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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1795 TGTGTGTGTGTGTGTG 1810
Db 1 TGTGTGTGTGTGTGTG 18

RESULT 75
LOCUS I31536 17 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 448 from patent US 5582979.
ACCESSION I31536
VERSION I31536.1 GI:1822327
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Weber, J.L.
TITLE Length polymorphisms in (dC-dA).sub.n. (dG-dT).sub.n sequences and method of using the same
JOURNAL Patent: US 5582979-A 448 10-DEC-1996;
FEATURES
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Best Local Similarity 100.0%; Score 17; DB 1; Length 17;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1796 TGTGTGTGTGTGTGTG 1809
Db 17 TGTGTGTGTGTGTGTG 1

RESULT 76
LOCUS AX239676 17 bp DNA linear PAT 26-SEP-2001
DEFINITION Sequence 16 from Patent WO0164948.
ACCESSION AX239676
VERSION AX239676.1 GI:15797341
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS van Haeringen, W.A. and van Haeringen, H.
TITLE Universal variable fragments
JOURNAL Patent: WO 0164948-A 16 07-SEP-2001;
FEATURES
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            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="primer"

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Best Local Similarity 100.0%; Score 17; DB 1; Length 17;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1797 TGTGTGTGTGTGTGTG 1808
Db 1 TGTGTGTGTGTGTGTG 17

RESULT 77
LOCUS AX762730 17 bp DNA linear PAT 25-JUN-2003
DEFINITION Sequence 6051 from Patent WO03040369.

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ACCESSION AX762730
VERSION AX762730.1 GI:32257346
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Telleran,A., Anson,R. and Tuijinder,M.
TITLE Sequences involved in tumoral suppression, tumoral reversion,
apoptosis and/or viral resistance phenomena and their use as
medicines
JOURNAL Patent: WO 03040369-A 6051 15-MAY-2003;
Molecular Engines Laboratories (FR)
FEATURES
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 1..6%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2141 GATCAGTTTTTCACT 2157
Db 1 GATCAGTTTTTCACT 17
RESULT 78
AR071772/c
LOCUS AR071772 18 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 1 from patent US 5912147.
ACCESSION AR071772
VERSION AR071772.1 GI:7222660
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Stoler,D., Basik,M. and Anderson,G.
TITLE Rapid means of quantitating genomic instability
JOURNAL Patent: US 5912147-A 1 15-JUN-1999;
FEATURES
Location/Qualifiers
source
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/organism="unknown"
/mol_type="unassigned DNA"
Query Match 1..6%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1792 TTGTGTGTGTGTGTGTG 1808
Db 17 TTGTGTGTGTGTGTGTG 1
RESULT 79
AR071774/c
LOCUS AR071774 18 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 3 from patent US 5912147.
ACCESSION AR071774
VERSION AR071774.1 GI:7222662
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Stoler,D., Basik,M. and Anderson,G.
TITLE Rapid means of quantitating genomic instability
JOURNAL Patent: US 5912147-A 3 15-JUN-1999;
FEATURES
Location/Qualifiers
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Query Match 1..6%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1792 TTGTGTGTGTGTGTGTG 1808
Db 17 TTGTGTGTGTGTGTGTG 1
RESULT 80
AR071799/c
LOCUS AR071799 18 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 28 from patent US 5912147.
ACCESSION AR071799
VERSION AR071799.1 GI:7222687
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Stoler,D., Basik,M. and Anderson,G.
TITLE Rapid means of quantitating genomic instability
JOURNAL Patent: US 5912147-A 28 15-JUN-1999;
FEATURES
Location/Qualifiers
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Db 17 TTGTGTGTGTGTGTGTG 1
RESULT 81
AR071801/c
LOCUS AR071801 18 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 30 from patent US 5912147.
ACCESSION AR071801
VERSION AR071801.1 GI:7222689
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Stoler,D., Basik,M. and Anderson,G.
TITLE Rapid means of quantitating genomic instability
JOURNAL Patent: US 5912147-A 30 15-JUN-1999;
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Best Local Similarity 100.0%; Pred. No. 68;
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QY 1794 GTGTGTGTGTGTGTGTG 1810
Db 17 GTGTGTGTGTGTGTGTG 1
RESULT 82
AR071802/c
LOCUS AR071802 18 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 31 from patent US 5912147.
ACCESSION AR071802
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Query Match 1..6%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1792 TTGTGTGTGTGTGTGTG 1808
Db 17 TTGTGTGTGTGTGTGTG 1
RESULT 80
AR071799/c
LOCUS AR071799 18 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 28 from patent US 5912147.
ACCESSION AR071799
VERSION AR071799.1 GI:7222687
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Stoler,D., Basik,M. and Anderson,G.
TITLE Rapid means of quantitating genomic instability
JOURNAL Patent: US 5912147-A 28 15-JUN-1999;
FEATURES
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 68;
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QY 1792 TTGTGTGTGTGTGTGTG 1808
Db 17 TTGTGTGTGTGTGTGTG 1
RESULT 81
AR071801/c
LOCUS AR071801 18 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 30 from patent US 5912147.
ACCESSION AR071801
VERSION AR071801.1 GI:7222689
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Stoler,D., Basik,M. and Anderson,G.
TITLE Rapid means of quantitating genomic instability
JOURNAL Patent: US 5912147-A 30 15-JUN-1999;
FEATURES
Location/Qualifiers
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Query Match 1..6%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1794 GTGTGTGTGTGTGTGTG 1810
Db 17 GTGTGTGTGTGTGTGTG 1
RESULT 82
AR071802/c
LOCUS AR071802 18 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 31 from patent US 5912147.
ACCESSION AR071802
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VERSION AR071802.1 GI:7222690  
 KEYWORDS Unknown.  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 18)  
 AUTHORS Stoler,D., Basik,M. and Anderson,G.  
 TITLE Rapid means of quantitating genomic instability  
 JOURNAL Patent: US 5912147-A 31-15-JUN-1999;  
 FEATURES Location/Qualifiers  
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Query Match 1.6%; Score 17; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 68;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 17 GTGTGTGTGTGTGTG 1

RESULT 83  
 E36173/c  
 LOCUS AR071803 18 bp DNA linear PAT 18-FEB-2000  
 DEFINITION Sequence 32 from patent US 5912147.  
 ACCESSION AR071803  
 VERSION AR071803.1 GI:7222691  
 KEYWORDS Unknown.  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 18)  
 AUTHORS Stoler,D., Basik,M. and Anderson,G.  
 TITLE Rapid means of quantitating genomic instability  
 JOURNAL Patent: US 5912147-A 32-15-JUN-1999;  
 FEATURES Location/Qualifiers  
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 /mol\_type="unassigned DNA"

Query Match 1.6%; Score 17; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 68;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTG 1810  
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 Db 17 GTGTGTGTGTGTGTG 1

RESULT 84  
 E36173  
 LOCUS E36173 20 bp DNA linear PAT 31-JAN-2002  
 DEFINITION Upstream regulatory sequence of melanocortin-1 receptor gene and utilization thereof.  
 ACCESSION E36173  
 VERSION E36173.1 GI:18626400  
 KEYWORDS JP 2000166563-A/15.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 20)  
 AUTHORS Moro,O., Ifuku,O. and Ideta,T.  
 TITLE Upstream regulatory sequence of melanocortin-1 receptor gene and utilization thereof  
 JOURNAL Patent: JP 2000166563-A 15 20-JUN-2000;  
 SHISEIDO CO LTD  
 COMMENT OS Homo sapiens (human)  
 PN JP 2000166563-A/15  
 PD 20-JUN-2000  
 PF 04-DEC-1998 JP 1998345881

PR OSAMU MORO,OJI IFUKU,TATSURO IDETA  
 PI C12N15/09,C12N5/10,C12Q1/68//C07K14/705,(C12N15/09,  
 PC C12R1:91),  
 PC C12N15/00,C12N5/00,(C12N15/00,C12R1:91)  
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 FT source 1..20  
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 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"

Query Match 1.6%; Score 16.8; DB 1; Length 20;  
 Best Local Similarity 90.0%; Pred. No. 82;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1811 TGTATATATATATATGTA 1830  
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 Db 1 TATATATATATATATATA 20

RESULT 85  
 E36173/c  
 LOCUS E36173 20 bp DNA linear PAT 31-JAN-2002  
 DEFINITION Upstream regulatory sequence of melanocortin-1 receptor gene and utilization thereof.  
 ACCESSION E36173  
 VERSION E36173.1 GI:18626400  
 KEYWORDS JP 2000166563-A/15.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 20)  
 AUTHORS Moro,O., Ifuku,O. and Ideta,T.  
 TITLE Upstream regulatory sequence of melanocortin-1 receptor gene and utilization thereof  
 JOURNAL Patent: JP 2000166563-A 15 20-JUN-2000;  
 SHISEIDO CO LTD  
 COMMENT OS Homo sapiens (human)  
 PN JP 2000166563-A/15  
 PD 20-JUN-2000  
 PF 04-DEC-1998 JP 1998345881

PR OSAMU MORO,OJI IFUKU,TATSURO IDETA  
 PI C12N15/09,C12N5/10,C12Q1/66,C12Q1/68//C07K14/705,(C12N15/09,  
 PC C12R1:91),  
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QY 1811 TGTATATATATATATGTA 1830  
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 Db 20 TATATATATATATATATA 1

RESULT 86  
 AR242049/c  
 LOCUS AR242049 20 bp DNA linear PAT 20-DEC-2002

DEFINITION Sequence 337 from patent US 6472154.

ACCESSION AR242049

VERSION AR242049.1 GI:27287861

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

UNCLASSIFIED.

REFERENCE 1 (bases 1 to 20)

AUTHORS Garner,H.R., Wren,J.D., Minna,J.D. and Fondon,J.W. III.

TITLE Polymorphic repeats in human genes

JOURNAL Patent: US 6472154-A 337 29-OCT-2002;

FEATURES Location/Qualifiers

source 1..20

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/mol\_type="genomic DNA"

Query Match 1..6%; Score 16.8; DB 1; Length 20;

Best Local Similarity 90.0%; Pred.No.82;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1792 TTGTGTGTGTGTGTGTGTGT 1811

Db 20 TGGGGTGTGTGTGTGTGT 1

RESULT 87

AX556883/c

LOCUS AX556883

DEFINITION Sequence 10 from Patent WO02058723.

ACCESSION AX556883

VERSION AX556883.1 GI:25899981

KEYWORDS synthetic construct

SOURCE synthetic construct

ORGANISM artificial sequences.

REFERENCE 1

AUTHORS Vicari,A.P., Caux,C. and Laface,D.

TITLE Chemokines as adjuvants of immune response

JOURNAL Patent: WO 02058723-A 10 01-AUG-2002;

FEATURES Schering Corporation (US)

source Location/Qualifiers

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/organism="synthetic construct"

/mol\_type="unassigned DNA"

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/note="primer"

Query Match 1..6%; Score 16.8; DB 1; Length 21;

Best Local Similarity 90.0%; Pred.No.88;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTGT 1813

Db 21 GTGTGTGTGTGTGTGTGT 2

RESULT 88

AX825106

LOCUS AX825106

DEFINITION Sequence 4 from Patent WO03072818.

ACCESSION AX825106

VERSION AX825106.1 GI:39750835

KEYWORDS synthetic construct

SOURCE synthetic construct

ORGANISM artificial sequences.

REFERENCE 1

AUTHORS Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.

TITLE Method for sorting single-stranded nucleic acids

JOURNAL Patent: WO 03072818-A 4 04-SEP-2003;

FEATURES Degussa Bioactives GmbH (DE)

source Location/Qualifiers

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/organism="synthetic construct"

/mol\_type="unassigned DNA"

/db\_xref="taxon:32630"

/note="primer"

Query Match 1..6%; Score 16.8; DB 1; Length 21;

Best Local Similarity 90.0%; Pred.No.88;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTGT 1813

Db 21 GTGTGTGTGTGTGTGTGT 2

RESULT 89

AX074790

LOCUS AR074790

DEFINITION Sequence 87 from patent US 5955276.

ACCESSION AR074790

VERSION AR074790.1 GI:10001543

KEYWORDS Unknown.

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 24)

AUTHORS Morgante,M. and Vogel,J.Marie.

TITLE Compound microsatellite primers for the detection of genetic

JOURNAL polymorphisms

FEATURES Patent: US 5955276-A 87 21-SEP-1999;

source Location/Qualifiers

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/organism="unknown"

/mol\_type="unassigned DNA"

Query Match 1..6%; Score 16.8; DB 1; Length 24;

Best Local Similarity 90.0%; Pred.No.1e+02;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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/db\_xref="taxon:32630"

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/note="LNA-T (Locked Nucleic Acid)"

/mod\_base=OTHER

modified\_base 6

/note="LNA-T (Locked Nucleic Acid)"

/mod\_base=OTHER

modified\_base 9

/note="LNA-T (Locked Nucleic Acid)"

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/note="LNA-T (Locked Nucleic Acid)"

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modified\_base 15

/note="LNA-T (Locked Nucleic Acid)"

/mod\_base=OTHER

modified\_base 18

/note="LNA-T (Locked Nucleic Acid)"

/mod\_base=OTHER

Query Match 1..6%; Score 16.8; DB 1; Length 21;

Best Local Similarity 90.0%; Pred.No.88;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTTAAAT 1884

Db 2 TTTTATTTTGTGTTTAAAT 21

RESULT 89

AR074790

LOCUS AR074790

DEFINITION Sequence 87 from patent US 5955276.

ACCESSION AR074790

VERSION AR074790.1 GI:10001543

KEYWORDS Unknown.

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 24)

AUTHORS Morgante,M. and Vogel,J.Marie.

TITLE Compound microsatellite primers for the detection of genetic

JOURNAL polymorphisms

FEATURES Patent: US 5955276-A 87 21-SEP-1999;

source Location/Qualifiers

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/mol\_type="unassigned DNA"

Query Match 1..6%; Score 16.8; DB 1; Length 24;

Best Local Similarity 90.0%; Pred.No.1e+02;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1813 TATATATATATATATGAC 1832

Db 1 TATATATATATATATACACA 20

RESULT 90

AR071778/c

LOCUS AR071778

DEFINITION Sequence 7 from patent US 5912147.

ACCESSION AR071778

VERSION AR071778.1 GI:7222666

KEYWORDS Unknown.

SOURCE Unknown.

ORGANISM Unknown.

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Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Stoler,D., Basik,M. and Anderson,G.
TITLE Rapid means of quantitating genomic instability
JOURNAL Patent: US 5912147-A 7 15-JUN-1999;
FEATURES Location/Qualifiers
source
1..18
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Query Match 1.6%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 79;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1791 ATTGTGTGTGTGTGTGTG 1808
Db 18 ACTGTGTGTGTGTGTGTG 1

RESULT 91
AR071779/c
LOCUS AR071779 18 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 8 from patent US 5912147.
ACCESSION AR071779
VERSION AR071779.1 GI:7222667
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Stoler,D., Basik,M. and Anderson,G.
TITLE Rapid means of quantitating genomic instability
JOURNAL Patent: US 5912147-A 8 15-JUN-1999;
FEATURES Location/Qualifiers
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/mol_type="unassigned DNA"
Query Match 1.6%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 79;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1791 ATTGTGTGTGTGTGTGTG 1808
Db 18 ACTGTGTGTGTGTGTGTG 1

RESULT 92
AR071800/c
LOCUS AR071800 18 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 29 from patent US 5912147.
ACCESSION AR071800
VERSION AR071800.1 GI:7222688
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Stoler,D., Basik,M. and Anderson,G.
TITLE Rapid means of quantitating genomic instability
JOURNAL Patent: US 5912147-A 29 15-JUN-1999;
FEATURES Location/Qualifiers
source
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/mol_type="unassigned DNA"
Query Match 1.6%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 79;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1793 TCTGTGTGTGTGTGTGTG 1810
Db 18 TCTGTGTGTGTGTGTGTG 1

Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Stoler,D., Basik,M. and Anderson,G.
TITLE Rapid means of quantitating genomic instability
JOURNAL Patent: US 5912147-A 7 15-JUN-1999;
FEATURES Location/Qualifiers
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/mol_type="unassigned DNA"
Query Match 1.6%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 79;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1791 ATTGTGTGTGTGTGTGTG 1808
Db 18 ACTGTGTGTGTGTGTGTG 1

RESULT 93
AR071804/c
LOCUS AR071804 18 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 33 from patent US 5912147.
ACCESSION AR071804
VERSION AR071804.1 GI:7222692
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Stoler,D., Basik,M. and Anderson,G.
TITLE Rapid means of quantitating genomic instability
JOURNAL Patent: US 5912147-A 33 15-JUN-1999;
FEATURES Location/Qualifiers
source
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/mol_type="unassigned DNA"
Query Match 1.6%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 79;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1791 ATTGTGTGTGTGTGTGTG 1808
Db 18 AATGTGTGTGTGTGTGTG 1

RESULT 94
AR071806/c
LOCUS AR071806 18 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 35 from patent US 5912147.
ACCESSION AR071806
VERSION AR071806.1 GI:7222694
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Stoler,D., Basik,M. and Anderson,G.
TITLE Rapid means of quantitating genomic instability
JOURNAL Patent: US 5912147-A 35 15-JUN-1999;
FEATURES Location/Qualifiers
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/mol_type="unassigned DNA"
Query Match 1.6%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 79;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1791 ATTGTGTGTGTGTGTGTG 1808
Db 18 AATGTGTGTGTGTGTGTG 1

RESULT 95
AR071808/c
LOCUS AR071808 18 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 37 from patent US 5912147.
ACCESSION AR071808
VERSION AR071808.1 GI:7222696
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Stoler,D., Basik,M. and Anderson,G.
TITLE Rapid means of quantitating genomic instability
JOURNAL Patent: US 5912147-A 37 15-JUN-1999;
FEATURES Location/Qualifiers
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source
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/organism="unknown"
/mol_type="unassigned DNA"

Query Match      1.6%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 79;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1791 ATTGTGTGTGTGTGTGTG 1808
DB 18 AATGTGTGTGTGTGTGTG 1

RESULT 96
AR071809/c
LOCUS          18 bp      DNA      linear      PAT 18-FEB-2000
DEFINITION    Sequence 38 from patent US 5912147.
ACCESSION     AR071809
VERSION       AR071809.1 GI:7222697
KEYWORDS      UNCLASSIFIED
ORGANISM      Unknown.
REFERENCE     1 (bases 1 to 18)
AUTHORS      Stoler,D., Basik,M. and Anderson,G.
TITLE        Rapid means of quantitating genomic instability
JOURNAL      Patent: US 5912147-A 38 15-JUN-1999;
FEATURES     Location/Qualifiers
source       1..18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match      1.6%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 79;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1791 ATTGTGTGTGTGTGTGTG 1808
DB 18 AATGTGTGTGTGTGTGTG 1

RESULT 97
E28534
LOCUS          18 bp      DNA      linear      PAT 18-JUN-2001
DEFINITION    Method for labeling oligonucleotide and utilization thereof.
ACCESSION     E28534
VERSION       E28534.1 GI:13025386
KEYWORDS      UNCLASSIFIED
SOURCE        Unidentified
ORGANISM      Unclassified.
REFERENCE     1 (bases 1 to 18)
AUTHORS      Kenichi,H., Hiroshi,Y. and Masahide,N.
TITLE        Method for labeling oligonucleotide and utilization thereof
JOURNAL      Patent: JP 199075880-A 1 23-MAR-1999;
COMMENT      CEMO SERO THERAPEUT RES INST
PN          JP 199075880-A/1
PD          23-MAR-1999
PF          10-JUL-1998 JP 1998195719
PR          PI KENICHI HANAKI,HIROSHI YOSHIKURA,MASAHIDE NOZAKI PC
C12N15/09,C12Q1/68,G01N33/58,C12N15/00
CC          Strandedness: Single;
FH          Key
FT          Location/Qualifiers
source       1..18
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match      1.6%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 79;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1791 ATTGTGTGTGTGTGTGTG 1808
DB 18 AATGTGTGTGTGTGTGTG 1

RESULT 97
E28534
LOCUS          18 bp      DNA      linear      PAT 18-JUN-2001
DEFINITION    Method for labeling oligonucleotide and utilization thereof.
ACCESSION     E28534
VERSION       E28534.1 GI:13025386
KEYWORDS      UNCLASSIFIED
SOURCE        Unidentified
ORGANISM      Unclassified.
REFERENCE     1 (bases 1 to 18)
AUTHORS      Kenichi,H., Hiroshi,Y. and Masahide,N.
TITLE        Method for labeling oligonucleotide and utilization thereof
JOURNAL      Patent: JP 199075880-A 1 23-MAR-1999;
COMMENT      CEMO SERO THERAPEUT RES INST
PN          JP 199075880-A/1
PD          23-MAR-1999
PF          10-JUL-1998 JP 1998195719
PR          PI KENICHI HANAKI,HIROSHI YOSHIKURA,MASAHIDE NOZAKI PC
C12N15/09,C12Q1/68,G01N33/58,C12N15/00
CC          Strandedness: Single;
FH          Key
FT          Location/Qualifiers
source       1..18
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
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Query Match      1.6%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 79;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1813 TATATATATATATATGTA 1830
DB 1 TATATATATATATATATA 18

RESULT 98
E28534/c
LOCUS          18 bp      DNA      linear      PAT 18-JUN-2001
DEFINITION    Method for labeling oligonucleotide and utilization thereof.
ACCESSION     E28534
VERSION       E28534.1 GI:13025386
KEYWORDS      UNCLASSIFIED
SOURCE        Unidentified
ORGANISM      Unclassified.
REFERENCE     1 (bases 1 to 18)
AUTHORS      Kenichi,H., Hiroshi,Y. and Masahide,N.
TITLE        Method for labeling oligonucleotide and utilization thereof
JOURNAL      Patent: JP 199075880-A 1 23-MAR-1999;
COMMENT      CEMO SERO THERAPEUT RES INST
PN          JP 199075880-A/1
PD          23-MAR-1999
PF          10-JUL-1998 JP 1998195719
PR          PI KENICHI HANAKI,HIROSHI YOSHIKURA,MASAHIDE NOZAKI PC
C12N15/09,C12Q1/68,G01N33/58,C12N15/00
CC          Strandedness: Single;
FH          Key
FT          Location/Qualifiers
source       1..18
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match      1.6%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 79;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1813 TATATATATATATATGTA 1830
DB 18 TATATATATATATATATA 1

RESULT 99
AR241816
LOCUS          18 bp      DNA      linear      PAT 20-DEC-2002
DEFINITION    Sequence 104 from patent US 6472154.
ACCESSION     AR241816
VERSION       AR241816.1 GI:27287628
KEYWORDS      UNCLASSIFIED
SOURCE        Unknown.
ORGANISM      Unclassified.
REFERENCE     1 (bases 1 to 18)
AUTHORS      Garner,H.R., Wren,J.D., Minna,J.D. and Fondon,J.W. III.
TITLE        Polymorphic repeats in human genes
JOURNAL      Patent: US 6472154-A 104 29-OCT-2002;
FEATURES     Location/Qualifiers
source       1..18
/organism="unknown"
/mol_type="genomic DNA"

Query Match      1.6%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 79;
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Best Local Similarity 94.4%; Pred.No. 91;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1813 TATATATATATATATGTA 1830
DB 2 TATATATATATATATATA 19

RESULT 102
BD084130/c
LOCUS
DEFINITION Polymorphisms and new genes in the region of the human
hemochromatosis gene.
ACCESSION BD084130
VERSION BD084130.1 GI:22629740
KEYWORDS JP 2001525663-A/18.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 20)
REFERENCE Pedar,J.N. Kronmal,G.S., Lauer,P.M., Ruddy,D.A., Thomas,W.J.,
AUTHORS Tsuchinashi,Z. and Wolff,R.K.
TITLE Polymorphisms and new genes in the region of the human
hemochromatosis gene
JOURNAL Patent: JP 2001525663-A 18 11-DEC-2001;
PROGENITOR INC
COMMENT OS Homo sapiens (human)
PN JP 2001525663-A/18
PD 11-DEC-2001
PF 30-SEP-1997 JP 1998516815
PR 01-OCT-1996 US 08/724394,07-MAY-1997 US 08/852495 PI
JOHN N FEDEr,GREGORY S KEONVAL,PETER M LAUER,DAVID A RUDDY, PI
WINSTON J THOMAS,ZENTA TSUCHIHASHI,ROGER K WOLFF PC
C07H21/04,C12Q1/68,C12N15/63,C12N15/85,C12P21/02 CC
and new genes in the region of the human CC hemochromatosis gene
FH Key Location/Qualifiers
FT source 1..20
FT Location/Qualifiers
1..20
/organism='Homo sapiens (human)'

FEATURES
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1..20
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/mol_type='genomic DNA'
/db_xref='taxon:9606'

Query Match 1.6%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred.No. 91;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1813 TATATATATATATGTA 1830
DB 19 TATATATATATATATATA 2

RESULT 103
AL2053
LOCUS
DEFINITION Oligonucleotide.
ACCESSION AL2053
VERSION AL2053.1 GI:491255
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
1 (bases 1 to 16)
REFERENCE Eppien,J.F.
AUTHORS Process for the detection of restriction fragment length
TITLE polymorphisms in eukaryotic genomes
JOURNAL Patent: EP 0266787-A 13 11-MAY-1986;
Max-Planck-Gesellschaft zur Foerderung der Wissenschaften
FEATURES
Location/Qualifiers
1..16
/organism="synthetic construct"

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/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"

Query Match 1.5%; Score 16; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 75;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGT 1809  
DB 1 GTGTGTGTGTGTGTGT 16

RESULT 104  
LOCUS A12054 16 bp DNA linear PAT 09-DEC-1993  
DEFINITION Oligonucleotide.  
ACCESSION A12054  
VERSION A12054.1 GI:489449  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM artificial sequences.  
REFERENCE 1 (bases 1 to 16)  
AUTHORS Eppelen,J.T.  
TITLE Process for the detection of restriction fragment length polymorphisms in eukaryotic genomes  
JOURNAL Patent: EP 0266787-A 14 11-MAY-1988;  
Max-Planck-Gesellschaft zur Foerderung der Wissenschaften  
FEATURES  
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/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"

Query Match 1.5%; Score 16; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 75;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGT 1809  
DB 16 GTGTGTGTGTGTGTGT 1

RESULT 105  
LOCUS E32224/c 16 bp DNA linear PAT 18-JUN-2001  
DEFINITION Method for isolating satellite sequence.  
ACCESSION E32224  
VERSION E32224.1 GI:13021854  
KEYWORDS JP 2000060559-A/26.  
SOURCE Haliotis discus discus  
ORGANISM Haliotis discus discus  
REFERENCE 1 (bases 1 to 16)  
AUTHORS Hideaki,T. and Masashi,S.  
TITLE Method for isolating satellite sequence  
JOURNAL Patent: JP 2000060559-A 26 29-FEB-2000;  
NATL INST OF AGROBIOLOGICAL RESOURCES  
COMMENT OS Haliotis discus discus  
PN JP 2000060559-A/26  
PD 29-FEB-2000  
PF 18-AUG-1998 JP 1998232153  
PR HIDEAKI TAKAHASHI,MASASHI SEKINO  
PC C12N15/09,C12Q1/68,C12N15/00  
CC  
FH Key Location/Qualifiers  
FT source  
1..16  
/organism="Haliotis discus discus".  
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source  
1..16  
/organism="Haliotis discus discus"

/mol\_type="genomic DNA"  
/sub\_species="discus"  
/db\_xref="taxon:91233"

Query Match 1.5%; Score 16; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 75;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGT 1808  
DB 16 TGTGTGTGTGTGTGTGT 1

RESULT 106  
LOCUS I31527/c 16 bp DNA linear PAT 06-FEB-1997  
DEFINITION Sequence 439 from patent US 5582979.  
ACCESSION I31527  
VERSION I31527.1 GI:1822318  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 16)  
AUTHORS Weber,J.L.  
TITLE Length polymorphisms in (dC-dA).sub.n.(dG-dT).sub.n sequences and method of using the same  
JOURNAL Patent: US 5582979-A 439 10-DEC-1996;  
FEATURES  
Location/Qualifiers  
1..16  
source  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.5%; Score 16; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 75;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGT 1808  
DB 16 TGTGTGTGTGTGTGTGT 1

RESULT 107  
LOCUS AR328667 16 bp RNA linear PAT 17-AUG-2003  
DEFINITION Sequence 6069 from patent US 6566127.  
ACCESSION AR328667  
VERSION AR328667.1 GI:33714475  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 16)  
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.  
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor  
JOURNAL Patent: US 6566127-A 6069 20-MAY-2003;  
FEATURES  
Location/Qualifiers  
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source  
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/mol\_type="unassigned RNA"

Query Match 1.5%; Score 16; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 75;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGT 1809  
DB 1 GTGTGTGTGTGTGTGT 16

RESULT 108  
AX239677

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LOCUS AX239677 17 bp DNA linear PAT 26-SEP-2001
DEFINITION Sequence 17 from Patent WO0164948.
ACCESSION AX239677
VERSION AX239677.1 GI:15797342
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS van Haeringen,W.A. and van Haeringen,H.
TITLE Universal variable fragments
JOURNAL Patent: WO 0164948-A 17 07-SEP-2001;
Dr. van Haeringen Laboratorium B.V. (NL)
FEATURES
source
1. .17
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="primer"
Query Match 1.5%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred.No. 81;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1793 TGTGTGTGTGTGTGTG 1808
Db 2 TGTGTGTGTGTGTGTG 17
RESULT 109
AX239678
LOCUS AX239678 17 bp DNA linear PAT 26-SEP-2001
DEFINITION Sequence 18 from Patent WO0164948.
ACCESSION AX239678
VERSION AX239678.1 GI:15797343
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS van Haeringen,W.A. and van Haeringen,H.
TITLE Universal variable fragments
JOURNAL Patent: WO 0164948-A 18 07-SEP-2001;
Dr. van Haeringen Laboratorium B.V. (NL)
FEATURES
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="primer"
Query Match 1.5%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred.No. 81;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1793 TGTGTGTGTGTGTGTG 1808
Db 2 TGTGTGTGTGTGTGTG 17
RESULT 110
AX239679/c
LOCUS AX239679/c 17 bp DNA linear PAT 26-SEP-2001
DEFINITION Sequence 19 from Patent WO0164948.
ACCESSION AX239679
VERSION AX239679.1 GI:15797344
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS van Haeringen,W.A. and van Haeringen,H.
TITLE Universal variable fragments
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JOURNAL Patent: WO 0164948-A 19 07-SEP-2001;
Dr. van Haeringen Laboratorium B.V. (NL)
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1. .17
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="primer"
Query Match 1.5%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred.No. 81;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1793 TGTGTGTGTGTGTGTG 1808
Db 17 TGTGTGTGTGTGTGTG 2
RESULT 111
AX239680/c
LOCUS AX239680 17 bp DNA linear PAT 26-SEP-2001
DEFINITION Sequence 20 from Patent WO0164948.
ACCESSION AX239680
VERSION AX239680.1 GI:15797345
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS van Haeringen,W.A. and van Haeringen,H.
TITLE Universal variable fragments
JOURNAL Patent: WO 0164948-A 20 07-SEP-2001;
Dr. van Haeringen Laboratorium B.V. (NL)
FEATURES
source
1. .17
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="primer"
Query Match 1.5%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred.No. 81;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1793 TGTGTGTGTGTGTGTG 1808
Db 17 TGTGTGTGTGTGTGTG 2
RESULT 112
AX239681/c
LOCUS AX239681 17 bp DNA linear PAT 26-SEP-2001
DEFINITION Sequence 21 from Patent WO0164948.
ACCESSION AX239681
VERSION AX239681.1 GI:15797346
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS van Haeringen,W.A. and van Haeringen,H.
TITLE Universal variable fragments
JOURNAL Patent: WO 0164948-A 21 07-SEP-2001;
Dr. van Haeringen Laboratorium B.V. (NL)
FEATURES
source
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/db_xref="taxon:32630"
/note="primer"
Query Match 1.5%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred.No. 81;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1793 TGTGTGTGTGTGTGTG 1808
Db 17 TGTGTGTGTGTGTGTG 2
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Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTGTG 1808
Db 17 TGTGTGTGTGTGTG 2

RESULT 113
LOCUS AR071773 18 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 2 from patent US 5912147.
ACCESSION AR071773
VERSION AR071773.1 GI:7222661
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Stoler,D., Basik,M. and Anderson,G.
TITLE Rapid means of quantitating genomic instability
JOURNAL Patent: US 5912147-A 2 15-JUN-1999;
FEATURES Location/Qualifiers
source
1..18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.5%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTGTG 1808
Db 16 TGTGTGTGTGTGTG 1

RESULT 114
LOCUS AR071777 18 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 6 from patent US 5912147.
ACCESSION AR071777
VERSION AR071777.1 GI:7222665
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Stoler,D., Basik,M. and Anderson,G.
TITLE Rapid means of quantitating genomic instability
JOURNAL Patent: US 5912147-A 6 15-JUN-1999;
FEATURES Location/Qualifiers
source
1..18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.5%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTGTG 1808
Db 16 TGTGTGTGTGTGTG 1

RESULT 115
LOCUS AR071805 18 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 34 from patent US 5912147.
ACCESSION AR071805
VERSION AR071805.1 GI:7222693
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Stoler,D., Basik,M. and Anderson,G.
TITLE Rapid means of quantitating genomic instability
JOURNAL Patent: US 5912147-A 6 15-JUN-1999;
FEATURES Location/Qualifiers
source
1..18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.5%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTGTG 1808
Db 16 TGTGTGTGTGTGTG 1

RESULT 116
LOCUS AR071807 18 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 36 from patent US 5912147.
ACCESSION AR071807
VERSION AR071807.1 GI:7222695
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Stoler,D., Basik,M. and Anderson,G.
TITLE Rapid means of quantitating genomic instability
JOURNAL Patent: US 5912147-A 36 15-JUN-1999;
FEATURES Location/Qualifiers
source
1..18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.5%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTGTG 1808
Db 16 TGTGTGTGTGTGTG 1

RESULT 117
LOCUS AX115187 18 bp DNA linear PAT 11-MAY-2001
DEFINITION Sequence 310 from Patent WO0123262.
ACCESSION AX115187
VERSION AX115187.1 GI:14032129
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Picoult-Newburg,L. and Pohl,M.
TITLE Genotyping reagents, kits and methods of use thereof
JOURNAL Patent: WO 0123262-A 310 26-APR-2001;
FEATURES Location/Qualifiers
source
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Primer"

Query Match 1.5%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1794 GTGTGTGTGTGTGTG 1810
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REFERENCE 1 (bases 1 to 18)
AUTHORS Stoler,D., Basik,M. and Anderson,G.
TITLE Rapid means of quantitating genomic instability
JOURNAL Patent: US 5912147-A 34 15-JUN-1999;
FEATURES Location/Qualifiers
source
1..18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.5%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTGTG 1808
Db 16 TGTGTGTGTGTGTG 1

RESULT 116
LOCUS AR071807/c 18 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 36 from patent US 5912147.
ACCESSION AR071807
VERSION AR071807.1 GI:7222695
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Stoler,D., Basik,M. and Anderson,G.
TITLE Rapid means of quantitating genomic instability
JOURNAL Patent: US 5912147-A 36 15-JUN-1999;
FEATURES Location/Qualifiers
source
1..18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.5%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTGTG 1808
Db 16 TGTGTGTGTGTGTG 1

RESULT 117
LOCUS AX115187 18 bp DNA linear PAT 11-MAY-2001
DEFINITION Sequence 310 from Patent WO0123262.
ACCESSION AX115187
VERSION AX115187.1 GI:14032129
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Picoult-Newburg,L. and Pohl,M.
TITLE Genotyping reagents, kits and methods of use thereof
JOURNAL Patent: WO 0123262-A 310 26-APR-2001;
FEATURES Location/Qualifiers
source
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Primer"

Query Match 1.5%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1794 GTGTGTGTGTGTGTG 1810
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Db 1 GTGTGTGTGTGTGTGCG 17
|||||
RESULT 118
AX355057 18 bp DNA linear PAT 06-FEB-2002
LOCUS
DEFINITION Sequence 85 from Patent WO0197843.
ACCESSION AX355057
VERSION AX355057.1 GI:18619724
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 artificial sequences.
AUTHORS Weiner, G. and Hartmann, G.
TITLE Methods for enhancing antibody-induced cell lysis and treating
JOURNAL cancer
FEATURES
source
Location/Qualifiers
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide-phosphorothioate backbone"

Query Match 1.5%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1814 ATATATATATATATGTA 1830
|||||
Db 1 ATATATATATATATA 17

RESULT 119
AX355057/c
LOCUS
DEFINITION Sequence 85 from Patent WO0197843.
ACCESSION AX355057
VERSION AX355057.1 GI:18619724
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 artificial sequences.
AUTHORS Weiner, G. and Hartmann, G.
TITLE Methods for enhancing antibody-induced cell lysis and treating
JOURNAL cancer
FEATURES
source
Location/Qualifiers
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide-phosphorothioate backbone"

Query Match 1.5%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1814 ATATATATATATGTA 1830
|||||
Db 18 ATATATATATATATA 2

RESULT 120
AX355057/c
LOCUS
DEFINITION Sequence 85 from Patent WO0197843.
ACCESSION AX355057
VERSION AX355057.1 GI:18619724
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 artificial sequences.
AUTHORS Weiner, G. and Hartmann, G.
TITLE Methods for enhancing antibody-induced cell lysis and treating
JOURNAL cancer
FEATURES
source
Location/Qualifiers
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide-phosphorothioate backbone"

Query Match 1.5%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1814 ATATATATATATGTA 1830
|||||
Db 18 ATATATATATATATA 2

RESULT 121
AX355057/c
LOCUS
DEFINITION Sequence 8 from Patent US 5955276.
ACCESSION AR074711
VERSION AR074711.1 GI:10001464
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Morgante, M. and Vogel, J. Marie.
TITLE Compound microsatellite primers for the detection of genetic
JOURNAL polymorphisms
FEATURES
source
Location/Qualifiers
1..15
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTGTGT 1807
|||||
Db 15 TGTGTGTGTGTGTGT 1

RESULT 122
AX355057/c
LOCUS
DEFINITION Sequence 9 from Patent US 5955276.
ACCESSION AR074712
VERSION AR074712.1 GI:10001465
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Morgante, M. and Vogel, J. Marie.
TITLE Compound microsatellite primers for the detection of genetic
JOURNAL polymorphisms
FEATURES
source
Location/Qualifiers
1..15
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1794 GTGTGTGTGTGTGTG 1808
|||||
Db 15 GTGTGTGTGTGTGTG 1

RESULT 123
AX355057/c
LOCUS
DEFINITION Sequence 7 from Patent US 5955276.
ACCESSION AR074710
VERSION AR074710.1 GI:10001463
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Morgante, M. and Vogel, J. Marie.
TITLE Compound microsatellite primers for the detection of genetic
JOURNAL polymorphisms
FEATURES
source
Location/Qualifiers
1..15
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1794 GTGTGTGTGTGTGTG 1808
|||||
Db 15 GTGTGTGTGTGTGTG 1

RESULT 124
AX355057/c
LOCUS
DEFINITION Sequence 8 from Patent US 5955276.
ACCESSION AR074711
VERSION AR074711.1 GI:10001464
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Morgante, M. and Vogel, J. Marie.
TITLE Compound microsatellite primers for the detection of genetic
JOURNAL polymorphisms
FEATURES
source
Location/Qualifiers
1..15
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTGTGT 1807
|||||
Db 15 TGTGTGTGTGTGTGT 1

RESULT 125
AX355057/c
LOCUS
DEFINITION Sequence 9 from Patent US 5955276.
ACCESSION AR074712
VERSION AR074712.1 GI:10001465
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Morgante, M. and Vogel, J. Marie.
TITLE Compound microsatellite primers for the detection of genetic
JOURNAL polymorphisms
FEATURES
source
Location/Qualifiers
1..15
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1794 GTGTGTGTGTGTGTG 1808
|||||
Db 15 GTGTGTGTGTGTGTG 1
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Query Match      1.4%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1813 TATATATATATAT 1827
Db 2 TATATATATATAT 16

RESULT 128
LOCUS I38642 16 bp DNA linear PAT 13-MAY-1997
DEFINITION Sequence 2 from patent US 5614617.
ACCESSION I38642
VERSION I38642.1 GI:2084696
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Cook, P.D. and Sanghvi, Y.S.
TITLE Nuclease resistant, pyrimidine modified oligonucleotides that
detect and modulate gene expression
JOURNAL Patent: US 5614617-A 2 25-MAR-1997;
FEATURES
source
Location/Qualifiers
1..16
/organism="unknown"
/mol_type="unassigned DNA"

Query Match      1.4%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1813 TATATATATATAT 1827
Db 15 TATATATATATAT 1

RESULT 129
LOCUS AR328666 16 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 6068 from patent US 5566127.
ACCESSION AR328666
VERSION AR328666.1 GI:33714474
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 5566127-A 6068 20-MAY-2003;
FEATURES
source
Location/Qualifiers
1..16
/organism="unknown"
/mol_type="unassigned RNA"

Query Match      1.4%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGT 1807
Db 2 TGTGTGTGTGTGTGT 16

RESULT 130
LOCUS AR328668 16 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 6070 from patent US 5566127.
ACCESSION AR328668
VERSION AR328668.1 GI:33714476

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KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 5566127-A 6070 20-MAY-2003;
FEATURES
source
Location/Qualifiers
1..16
/organism="unknown"
/mol_type="unassigned RNA"

Query Match      1.4%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGT 1808
Db 1 GTGTGTGTGTGTGTGT 15

RESULT 131
LOCUS AX599310 18 bp DNA linear PAT 14-FEB-2003
DEFINITION Sequence 650 from Patent WO02077272.
ACCESSION AX599310
VERSION AX599310.1 GI:28399452
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Berlin, K., Braun, A., Distler, J., Guetig, D., Howe, A., Mueller, J.,
Olek, A., Piepenbrock, C., Adorjan, P., Grabs, G., Lesche, R., Leu, E.,
Lewin, A., Lipscher, E., Maier, S., Model, F., Mueller, V., Otto, T.,
Pelet, C. and Ziebarth, H.
TITLE Methods and nucleic acids for the analysis of hematopoietic cell
proliferative disorders
JOURNAL Patent: WO 02077272-A 650 03-OCT-2002;
FEATURES
source
Location/Qualifiers
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Detection oligonucleotide for ELK1"

Query Match      1.4%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e-02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1867 TTTATTTTGTGTGT 1881
Db 1 TTTATTTTGTGTGT 15

RESULT 132
LOCUS AX599902 18 bp DNA linear PAT 14-FEB-2003
DEFINITION Sequence 1242 from Patent WO02077272.
ACCESSION AX599902
VERSION AX599902.1 GI:28400052
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Berlin, K., Braun, A., Distler, J., Guetig, D., Howe, A., Mueller, J.,
Olek, A., Piepenbrock, C., Adorjan, P., Grabs, G., Lesche, R., Leu, E.,
Lewin, A., Lipscher, E., Maier, S., Model, F., Mueller, V., Otto, T.,
Pelet, C. and Ziebarth, H.

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TITLE Methods and nucleic acids for the analysis of hematopoietic cell  
proliferative disorders  
JOURNAL Patent: WO 03077272-A 1242 03-OCT-2002;  
Epigenomics AG (DE)  
FEATURES  
source  
Location/Qualifiers  
1..18  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Detection oligonucleotide for ELK1"

Query Match 1.4%; Score 15; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1867 TTTATTTTGTGTTT 1881  
|||||  
Db 1 TTTATTTTGTGTTT 15

RESULT 133  
AX767726 18 bp DNA linear PAT 02-JUL-2003  
LOCUS  
DEFINITION Sequence 374 from Patent WO03044226.  
ACCESSION AX767726  
VERSION AX767726.1 GI:32436331  
KEYWORDS  
synthetic construct  
artificial sequences.  
ORGANISM  
source  
Burger,M., Caldwell,C., Genc,B., Becker,E., Maier,S. and  
Nimmrich,I.  
AUTHORS  
TITLE Method and nucleic acids for the analysis of a lymphoid cell  
proliferative disorder  
JOURNAL Patent: WO 03044226-A 374 30-MAY-2003;  
Epigenomics AG (DE)  
FEATURES  
source  
Location/Qualifiers  
1..18  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Detection oligonucleotide for ELK1"

Query Match 1.4%; Score 15; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1867 TTTATTTTGTGTTT 1881  
|||||  
Db 1 TTTATTTTGTGTTT 15

RESULT 134  
AX796164 18 bp DNA linear PAT 04-OCT-2003  
LOCUS  
DEFINITION Sequence 507 from Patent WO03052135.  
ACCESSION AX796164  
VERSION AX796164.1 GI:37516830  
KEYWORDS  
synthetic construct  
artificial sequences.  
ORGANISM  
source  
Burger,M., Field,J.K., Genc,B., Liloglou,T., Lipscher,E., Maier,S.  
and Nimmrich,I.  
AUTHORS  
TITLE Method and nucleic acids for the analysis of a lung cell  
proliferative disorder  
JOURNAL Patent: WO 03052135-A 507 26-JUN-2003;  
Epigenomics AG (DE)  
FEATURES  
source  
Location/Qualifiers  
1..18  
/organism="synthetic construct"

/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Detection oligonucleotide for ELK1"

Query Match 1.4%; Score 15; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1867 TTTATTTTGTGTTT 1881  
|||||  
Db 1 TTTATTTTGTGTTT 15

RESULT 135  
AR090280 32 bp DNA linear PAT 07-SEP-2000  
LOCUS  
DEFINITION Sequence 400 from patent US 5994076.  
ACCESSION AR090280  
VERSION AR090280.1 GI:10017035  
KEYWORDS  
Unknown.  
ORGANISM  
source  
Unclassified.  
REFERENCE 1 (bases 1 to 32)  
AUTHORS Chenchik,A., Jekhadze,G. and Bibilashvili,R.  
TITLE Methods of assaying differential expression  
JOURNAL Patent: US 5994076-A 400 30-NOV-1999;  
FEATURES  
source  
Location/Qualifiers  
1..32  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.4%; Score 15; DB 1; Length 32;  
Best Local Similarity 67.7%; Pred. No. 2e+02;  
Matches 21; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1731 GCTTGTGGCAAGTGAATTCCTGTAAACAAG 1761  
|||||  
Db 2 GCTTGTACAGGCAATTCACCTGCCACAAG 32

RESULT 136  
AR197315 32 bp DNA linear PAT 20-APR-2002  
LOCUS  
DEFINITION Sequence 400 from patent US 6352829.  
ACCESSION AR197315  
VERSION AR197315.1 GI:20247164  
KEYWORDS  
Unknown.  
ORGANISM  
source  
Unclassified.  
REFERENCE 1 (bases 1 to 32)  
AUTHORS Chenchik,A., Jekhadze,G. and Bibilashvili,R.  
TITLE Methods of assaying differential expression  
JOURNAL Patent: US 6352829-A 400 05-MAR-2002;  
FEATURES  
source  
Location/Qualifiers  
1..32  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.4%; Score 15; DB 1; Length 32;  
Best Local Similarity 67.7%; Pred. No. 2e+02;  
Matches 21; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1731 GCTTGTGGCAAGTGAATTCCTGTAAACAAG 1761  
|||||  
Db 2 GCTTGTACAGGCAATTCACCTGCCACAAG 32

RESULT 137  
AR259469 32 bp DNA linear PAT 20-DEC-2002  
LOCUS  
DEFINITION Sequence 400 from patent US 6489455.

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ACCESSION AR259469
VERSION AR259469.1 GI:27309980
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 32)
AUTHORS Chenchik,A., Jakhadze,G. and Bibilashvili,R.
TITLE Methods of assaying differential expression
JOURNAL Patent: US 6489455-A 400 03-DEC-2002;
FEATURES
    source
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            /organism="unknown"
            /mol_type="genomic DNA"
Query Match 1.4%; Score 15; DB 1; Length 32;
Best Local Similarity 67.7%; Pred. No. 2e+02;
Matches 21; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 1731 GCTTGTGCAGTGAATTGCTGTAAACAAG 1761
    |||||
Db 2 GCTTGTACAGCAAAATTCATTGCCACAAG 32

RESULT 138
LOCUS AX028843 18 bp DNA linear PAT 24-NOV-2000
DEFINITION Sequence 27 from Patent WO9732023.
ACCESSION AX028843
VERSION AX028843.1 GI:10189946
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Brugliera,F., Holton,T.A. and Michael,M.Z.
TITLE Genetic sequences encoding flavonoid pathway enzymes and uses
JOURNAL Patent: WO 9732023-A 27 04-SEP-1997;
FLORENE LIMITED (AU); BRUGLIERA FILIPPA (AU); HOLTON TIMOTHY
ALBERT (AU); MICHAEL MICHAEL ZENON (AU)
FEATURES
    source
        1..18
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Oligonucleotide"
Query Match 1.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1865 TTTTATTTTGTGTTTA 1882
    |||||
Db 1 TTTTATTTTGTGTTTA 18

RESULT 139
LOCUS AR050989 16 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 58 from patent US 5830644.
ACCESSION AR050989
VERSION AR050989.1 GI:5974353
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS West,M.D., Shay,J. and Wright,W.E.
TITLE Method for screening for agents which increase telomerase activity
JOURNAL Patent: US 5830644-A 58 03-NOV-1998;
FEATURES
    Location/Qualifiers

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source
    1..16
        /organism="unknown"
        /mol_type="unassigned DNA"
Query Match 1.4%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1793 TGTGTGTGTGTGTGTG 1808
    |||||
Db 1 TGGGTGTGTGTGTGTG 16

RESULT 140
LOCUS I51790 16 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 58 from patent US 5645986.
ACCESSION I51790
VERSION I51790.1 GI:2472991
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS West,M.D., Harley,C.B., Strahl,C.M., McEachern,M.J., Shay,J.,
Wright,W.E., Blackburn,E.H. and Vaziri,H.
TITLE Therapy and diagnosis of conditions related to telomere length
JOURNAL Patent: US 5645986-A 58 08-JUL-1997;
FEATURES
    source
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            /organism="unknown"
            /mol_type="unassigned DNA"
Query Match 1.4%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1793 TGTGTGTGTGTGTGTG 1808
    |||||
Db 1 TGGGTGTGTGTGTGTG 16

RESULT 141
LOCUS I84399 16 bp DNA linear PAT 04-APR-1998
DEFINITION Sequence 57 from patent US 5695932.
ACCESSION I84399
VERSION I84399.1 GI:3021919
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS West,M.D., Shay,J., Wright,W., Blackburn,E.H. and McEachern,M.J.
TITLE Telomerase activity assays for diagnosing pathogenic infections
JOURNAL Patent: US 5695932-A 57 09-DEC-1997;
FEATURES
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            /organism="unknown"
            /mol_type="unassigned DNA"
Query Match 1.4%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1793 TGTGTGTGTGTGTGTG 1808
    |||||
Db 1 TGGGTGTGTGTGTGTG 16

RESULT 142
LOCUS AR204607

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LOCUS AR204607 16 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 57 from patent US 6368789.
ACCESSION AR204607
VERSION AR204607.1 GI:21501976
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 16)
AUTHORS West, M.D., Shay, J., Wright, W. and Blackburn, E.H.
TITLE Screening methods to identify inhibitors of telomerase activity
JOURNAL Patent: US 6368789-A 57 09-APR-2002;
FEATURES
Location/Qualifiers
1..16
/mol_type="unknown"
/mol_type="unassigned DNA"

Query Match 1.4%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTG 1808
Db 1 TGGGTGTGTGTGTGTG 16

RESULT 143
LOCUS AR307317 16 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 80 from patent US 6551774.
ACCESSION AR307317
VERSION AR307317.1 GI:31697844
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 16)
AUTHORS West, M.D., Harley, C.B., Weinrich, S.L., Strahl, C.M., McEachern, M.J.,
Shay, J., Wright, W.E., Blackburn, E.H., Kim, N.W. and Vaziri, H.
TITLE Diagnostic methods for conditions associated with elevated cellular
levels of telomerase activity
JOURNAL Patent: US 6551774-A 80 22-APR-2003;
FEATURES
Location/Qualifiers
1..16
/mol_type="unknown"
/mol_type="genomic DNA"

Query Match 1.4%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 1.1e-02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTG 1808
Db 1 TGGGTGTGTGTGTGTG 16

RESULT 144
LOCUS AR328669 16 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 6071 from patent US 6566127.
ACCESSION AR328669
VERSION AR328669.1 GI:33714477
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 16)
AUTHORS Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Becabedo, J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 6071 20-MAY-2003;
FEATURES
Location/Qualifiers
1..16
source
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/organism="unknown"
/mol_type="unassigned RNA"

Query Match 1.4%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGT 1809
Db 1 GTGTGTGTGTGTGTGTG 16

RESULT 145
LOCUS AR011362 17 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 235 from patent US 5762938.
ACCESSION AR011362
VERSION AR011362.1 GI:3969352
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 17)
AUTHORS Paolletti, E., Perkus, M.E., Taylor, J., Tartaglia, J., Norton, E.K.,
Riviere, M., de Taisne, C., Limbach, K.J., Johnson, G.P., Pincus, S.E.,
Cox, W.I., Audonnet, J.-C., Francis, and Gettig, R. Robert.
TITLE Modified recombinant vaccinia virus and expression vectors thereof
JOURNAL Patent: US 5762938-A 235 03-JUN-1998;
FEATURES
Location/Qualifiers
1..17
/mol_type="unknown"
/mol_type="unassigned DNA"

Query Match 1.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1777 TTTTATTTTCTAATAT 1792
Db 1 TTTTATTTTCTAATAT 16

RESULT 146
LOCUS AR046265 17 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 1058 from patent US 5817796.
ACCESSION AR046265
VERSION AR046265.1 GI:5967730
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 17)
AUTHORS Stinchcomb, D.T., Draper, K., McSwiggen, J. and Jarvis, T.
TITLE C-myc ribozymes having 2'-5'-linked adenylate residues
JOURNAL Patent: US 5817796-A 1058 06-OCT-1998;
FEATURES
Location/Qualifiers
1..17
/mol_type="unknown"
/mol_type="unassigned DNA"

Query Match 1.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1811 TGTATATATATATATA 1826
Db 17 TGTATATATATATAA 2

RESULT 147
LOCUS AR061027 17 bp DNA linear PAT 29-SEP-1999
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DEFINITION Sequence 52 from patent US 5843456.  
ACCESSION AR061027.1 GI:5988718  
VERSION AR061027.1  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
AUTHORS 1 (bases 1 to 17)  
TITLE Paoletti, E. and Maki, J.  
JOURNAL Alvac poxvirus-rabies compositions and combination compositions and uses  
FEATURES Patent: US 5843456-A 52 01-DEC-1998;  
Location/Qualifiers  
1. 17  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.4%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 1.2e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1777 TTTATATTGTAATAT 1792  
Db 1 TTTATATTGTAATAT 16

RESULT 148  
LOCUS I18000 17 bp DNA linear PAT 07-OCT-1996  
DEFINITION Sequence 235 from patent US 5494807.  
ACCESSION I18000  
VERSION I18000.1 GI:1598355  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
AUTHORS 1 (bases 1 to 17)  
TITLE Paoletti, E., Perkus, M.E., Taylor, J., Tartaglia, J., Norton, E.K.,  
Riviere, M., de Taisne, C., Limbach, K.J., Johnson, G.P., Pincus, S.E.,  
Cox, W.I., Audonnet, J.-C.F. and Gettig, R.R.  
JOURNAL NVVAC vaccinia virus recombinants comprising heterologous inserts  
FEATURES Patent: US 5494807-A 235 27-FEB-1996;  
Location/Qualifiers  
1. 17  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.4%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 1.2e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1777 TTTATATTGTAATAT 1792  
Db 1 TTTATATTGTAATAT 16

RESULT 149  
LOCUS I53317/c 17 bp DNA linear PAT 07-OCT-1997  
DEFINITION Sequence 1058 from patent US 5646042.  
ACCESSION I53317  
VERSION I53317.1 GI:2474520  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
AUTHORS 1 (bases 1 to 17)  
TITLE Stinchcomb, D.T., Draper, K., McSwiggen, J. and Jarvis, T.  
JOURNAL C-myb targeted ribozymes  
FEATURES Patent: US 5646042-A 1058 08-JUL-1997;  
Location/Qualifiers  
1. 17  
/organism="unknown"

/mol\_type="unassigned DNA"

Query Match 1.4%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 1.2e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1811 TGTATATATATATATA 1826

Db 17 TGTATATATATATAA 2

RESULT 150  
LOCUS AR188671 17 bp DNA linear PAT 20-APR-2002  
DEFINITION Sequence 4159 from patent US 6346398.  
ACCESSION AR188671  
VERSION AR188671.1 GI:20234636  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
AUTHORS 1 (bases 1 to 17)  
TITLE Pavco, P., McSwiggen, J., Stinchcomb, D. and Escobedo, J.  
JOURNAL Method and reagent for the treatment of diseases or conditions  
FEATURES related to levels of vascular endothelial growth factor receptor  
Patent: US 6346398-A 4159 12-FEB-2002;  
Location/Qualifiers  
1. 17  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.4%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 1.2e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1749 TGCCTGTACACAGCCA 1764

Db 2 TGCCTGTACACAGCCA 17

RESULT 151  
LOCUS AR271518/c 17 bp DNA linear PAT 10-APR-2003  
DEFINITION Sequence 13 from patent US 6503710.  
ACCESSION AR271518  
VERSION AR271518.1 GI:29702938  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
AUTHORS 1 (bases 1 to 17)  
TITLE Gut, I.G., Berlin, K., Lechner, D. and Lebrach, H.  
JOURNAL Mutation analysis using mass spectrometry  
FEATURES Patent: US 6503710-A 13 07-JAN-2003;  
Location/Qualifiers  
1. 17  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 1.4%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 1.2e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1891 ATATTTCATGTTAGC 1906

Db 16 ATATTTCATGTCAGC 1

RESULT 152  
LOCUS AR324524 17 bp RNA linear PAT 17-AUG-2003  
DEFINITION Sequence 1926 from patent US 6566127.  
ACCESSION AR324524

```
VERSION AR324524.1 GI:33710332
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Favco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
JOURNAL related to levels of vascular endothelial growth factor receptor
PATENT Patent: US 6566127-A 1926 20-MAY-2003;
FEATURES Location/Qualifiers
source
1..17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 1.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1749 TGCGTGTACCAAGCCA 1764
Db 2 TGCGTGTACCAAGCCA 17

RESULT 153
LOCUS AR329254 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 6556 from patent US 6566127.
ACCESSION AR329254
VERSION AR329254.1 GI:33715062
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Favco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
JOURNAL related to levels of vascular endothelial growth factor receptor
PATENT Patent: US 6566127-A 6556 20-MAY-2003;
FEATURES Location/Qualifiers
source
1..17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 1.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1750 GCCTGTACCAAGCCAG 1765
Db 1 GCCTGTACCAAGCCAG 16

RESULT 154
LOCUS AX018733 17 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 22 from Patent WO9944633.
ACCESSION AX018733
VERSION AX018733.1 GI:10042955
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Minke,J.M. and Audonnet,J.C.
TITLE Live recombinant vaccines injected with adjuvant
JOURNAL Patent: WO 9944633-A 22 10-SEP-1999;
MINKE JULES MAARTEN (FR); MERIAL SAS (FR); AUDONNET JEAN CHRISTOPHE
FRANC (FR)
FEATURES Location/Qualifiers
source
1..17
/organism="synthetic construct"
/mol_type="unassigned DNA"
```

```
/db_xref="taxon:32630"
/note="Oligonucleotide"

Query Match 1.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1777 TTTATATTGTAATAT 1792
Db 1 TTTATATTGTAATAT 16

RESULT 155
LOCUS AX422370 17 bp RNA linear PAT 18-JUN-2002
DEFINITION Sequence 706 from Patent WO018124.
ACCESSION AX422370
VERSION AX422370.1 GI:21525752
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Jarvis,T., von Carlowitz,I., McSwiggen,J.A., McLaughlin,F.G. and
Randi,A.M.
TITLE Method and reagent for the inhibition of erg
JOURNAL Patent: WO 018124-A 706 22-NOV-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES Location/Qualifiers
source
1..17
/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"

Query Match 1.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1289 TAAATCTGTTTCTA 1304
Db 17 TAAATCTGTTTCTA 2

RESULT 156
LOCUS AX502781 17 bp DNA linear PAT 27-SEP-2002
DEFINITION Sequence 4088 from Patent EP1229046.
ACCESSION AX502781
VERSION AX502781.1 GI:23385074
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Zhan,J.
TITLE Human testis expressed patched like protein
JOURNAL Patent: EP 1229046-A 4088 07-AUG-2002;
Aeomica, Inc. (US)
FEATURES Location/Qualifiers
source
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 1.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2162 GCATTGTTTCTACTT 2177
Db 2 GCATTGTTTCTACTT 17
```



RESULT 157  
AX502782  
LOCUS AX502782 17 bp DNA linear PAT 27-SEP-2002  
DEFINITION Sequence 4089 from Patent EP1229046.  
ACCESSION AX502782  
VERSION AX502782.1 GI:23385075  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Zhan, J.  
TITLE Human testis expressed patched like protein  
JOURNAL Aeonica, Inc. (US)  
FEATURES  
source  
1. 17  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 1.4%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 1.2e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2162 GCATTGTTCTTACTT 2177  
Db 1 GCATTGTTCTTAGTT 16  
RESULT 158  
AX671628/c  
LOCUS AX671628 17 bp DNA linear PAT 27-MAR-2003  
DEFINITION Sequence 73 from Patent WO03004526.  
ACCESSION AX671628  
VERSION AX671628.1 GI:29329976  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Telerman, A., Amson, R. and Tuijinder, M.  
TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses and their use as medicines  
JOURNAL Patent: WO 03004526-A 73 16-JAN-2003;  
Molecular Engines Laboratories (FR)  
FEATURES  
source  
1. 17  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 1.4%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 1.2e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2166 TTGTTTCTTCTTGTAT 2181  
Db 17 TTGTTTCTTCTTGTAT 2  
RESULT 159  
AX723656  
LOCUS AX723656 17 bp DNA linear PAT 08-MAY-2003  
DEFINITION Sequence 1343 from Patent WO03025176.  
ACCESSION AX723656  
VERSION AX723656.1 GI:30502999  
KEYWORDS

SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1  
AUTHORS Telerman, A., Amson, R. and Tuijinder, M.  
TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines  
JOURNAL Patent: WO 03025176-A 1343 27-MAR-2003;  
Molecular Engines Laboratories (FR)  
FEATURES  
source  
1. 17  
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/mol\_type="unassigned DNA"  
/db\_xref="taxon:10090"  
Query Match 1.4%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 1.2e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1292 ATCTGTTTCTTCTACT 1307  
Db 2 ATCTGTTTCTTCTACT 17  
RESULT 160  
AX732198/c  
LOCUS AX732198 17 bp DNA linear PAT 08-MAY-2003  
DEFINITION Sequence 3832 from Patent WO03025175.  
ACCESSION AX732198  
VERSION AX732198.1 GI:30511541  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Telerman, A., Amson, R. and Tuijinder, M.  
TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines  
JOURNAL Patent: WO 03025175-A 3832 27-MAR-2003;  
Molecular Engines Laboratories (FR)  
FEATURES  
source  
1. 17  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 1.4%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 1.2e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1888 TTGATATTTCATGTT 1903  
Db 17 TTGATATTTCATGAT 2  
RESULT 161  
AX736543/c  
LOCUS AX736543 17 bp DNA linear PAT 08-MAY-2003  
DEFINITION Sequence 2133 from Patent WO03025177.  
ACCESSION AX736543  
VERSION AX736543.1 GI:30515831  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Telerman, A., Amson, R. and Tuijinder, M.  
TITLE Sequences involved in phenomena of tumour suppression, tumour

reversion, apoptosis and/or resistance to viruses and the use thereof as medicaments  
 Patent: WO 03025177-A 2133 27-MAR-2003;  
 Molecular Engines Laboratories (FR)  
 FEATURES  
 source

Query Match  
 Best Local Similarity 1.4%; Score 14.4; DB 1; Length 17;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

Query Match  
 Best Local Similarity 1.4%; Score 14.4; DB 1; Length 17;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

QY 1877 TTTTAAATGCTTTGAT 1992  
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 Db 17 TTTTAAATGCTTTGAT 2

RESULT 162  
 AX760931/c  
 LOCUS AX760931 17 bp DNA linear PAT 25-JUN-2003  
 DEFINITION Sequence 4252 from Patent WO03040369.  
 ACCESSION AX760931  
 VERSION AX760931.1 GI:32255547  
 KEYWORDS Homo sapiens (human)  
 SOURCE  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1

REFERENCE  
 AUTHORS Telesman,A., Anson,R. and Tuijnder,M.  
 TITLE Sequences involved in tumoral suppression, tumoral reversion, apoptosis and/or viral resistance phenomena and their use as medicines  
 JOURNAL Patent: WO 03040369-A 4252 15-MAY-2003;  
 Molecular Engines Laboratories (FR)  
 FEATURES  
 source

Query Match  
 Best Local Similarity 1.4%; Score 14.4; DB 1; Length 17;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

Query Match  
 Best Local Similarity 1.4%; Score 14.4; DB 1; Length 17;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

QY 1888 TTGATATTTCAATGTT 1903  
 |||||  
 Db 17 TTGATATTTCAATGAT 2

RESULT 163  
 AX762000/c  
 LOCUS AX762000 17 bp DNA linear PAT 25-JUN-2003  
 DEFINITION Sequence 5321 from Patent WO03040369.  
 ACCESSION AX762000  
 VERSION AX762000.1 GI:32256616  
 KEYWORDS Homo sapiens (human)  
 SOURCE  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1

REFERENCE  
 AUTHORS Telesman,A., Anson,R. and Tuijnder,M.  
 TITLE Sequences involved in tumoral suppression, tumoral reversion, apoptosis and/or viral resistance phenomena and their use as medicines  
 JOURNAL Patent: WO 03040369-A 5321 15-MAY-2003;  
 Molecular Engines Laboratories (FR)  
 FEATURES  
 source

Query Match  
 Best Local Similarity 1.4%; Score 14.4; DB 1; Length 17;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

/mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

Query Match  
 Best Local Similarity 1.4%; Score 14.4; DB 1; Length 17;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

QY 2166 TTGTTTCTACTTTGAT 2181  
 |||||  
 Db 17 TTGTTTCTCTCTTTGAT 2

RESULT 164  
 AX058584  
 LOCUS AX058584 18 bp DNA linear PAT 17-JAN-2001  
 DEFINITION Sequence 36 from Patent WO0077250.  
 ACCESSION AX058584  
 VERSION AX058584.1 GI:12310926  
 KEYWORDS synthetic construct  
 SOURCE synthetic construct  
 ORGANISM synthetic construct  
 artificial sequences.  
 1

REFERENCE  
 AUTHORS Escude,C., Garestier,T., Helene,C. and Roulon,T.  
 TITLE Method for circularizing oligonucleotides around a double stranded nucleic acid, resulting structures and uses thereof  
 JOURNAL Patent: WO 0077250-A 36 21-DEC-2000;  
 INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE (INSERM) (FR) ; CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR)  
 FEATURES  
 source

Query Match  
 Best Local Similarity 1.4%; Score 14.4; DB 1; Length 18;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:32630"  
 /note="Oligonucleotide"

QY 1792 TTGTGTGTGTGTGTGT 1807  
 |||||  
 Db 3 TTGTGTGTGTGTGGT 18

RESULT 165  
 BD104911  
 LOCUS BD104911 18 bp DNA linear PAT 27-AUG-2002  
 DEFINITION Kit and method for determining HLA type.  
 ACCESSION BD104911  
 VERSION BD104911.1 GI:22650485  
 KEYWORDS WO 0192572-A/1015.  
 SOURCE synthetic construct  
 ORGANISM synthetic construct  
 artificial sequences.  
 1 (bases 1 to 18)

REFERENCE  
 AUTHORS Inoko,H., Kagiya,T., Ichihara,T., Matsumura,Y., Moriya,S. and Nishida,M.  
 TITLE Kit and method for determining HLA type  
 JOURNAL Patent: WO 0192572-A 1015 08-DEC-2001;  
 NISSHINBO INDUSTRIES INC.SYTEM RESEARCH INC.HIDETOSHI INOKO, TAEKO KAGIYA, TATSUO ICHIHARA, YOSHIYUKI MATSUMURA,SHOGO MORIYA,MICHIO NISHIDA  
 COMMENT  
 OS Artificial Sequence  
 PN WO 0192572-A/1015  
 PD 06-DEC-2001  
 PF 01-JUN-2001 WO 2001JP004662  
 PI 01-JUN-2000 JP 00P 164798  
 PI HIDETOSHI INOKO, TAEKO KAGIYA, TATSUO ICHIHARA, YOSHIYUKI MATSUMURA, SHOGO MORIYA, MICHIO NISHIDA  
 PI SHOGO MORIYA, MICHIO NISHIDA  
 PC C1201/68, C12M1/00, C12N15/09, G01N33/53  
 CC Description of Artificial Sequence:capture

FEATURES source

Query Match

Best Local Similarity 1.4%; Score 14.4; DB 1; Length 18;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1470 GGGTACCAGCAGAAAG 1485

Db 2 GGGTACCAGCAGACG 17

RESULT 166

LOCUS AR181773

DEFINITION Sequence 235 from patent US 6335194.

ACCESSION AR181773

VERSION AR181773.1 GI:20223987

KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 20)

AUTHORS Bennett,C.Frank., Ackermann,E.J., Swayze,E.B. and Cowser,L.M.

TITLE Antisense modulation of survivin expression

JOURNAL Patent: US 6335194-A 235 01-JAN-2002;

FEATURES

Location/Qualifiers

1. .20

/organism="unknown"

/mol\_type="unassigned DNA"

Query Match

Best Local Similarity 1.4%; Score 14.2; DB 1; Length 20;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1814 ATATATATATATATATGACA 1832

Db 1 ACATATATATATATAACA 19

RESULT 167

E32202/c

LOCUS E32202

DEFINITION Method for isolating satellite sequence.

ACCESSION E32202

VERSION E32202.1 GI:13021735

KEYWORDS

SOURCE JP 2000060559-A/4.

ORGANISM Haliotis discus discus

REFERENCE 1 (bases 1 to 14)

AUTHORS Hideaki,T. and Masashi,S.

TITLE Method for isolating satellite sequence

JOURNAL Patent: JP 2000060559-A 4 29-FEB-2000;

COMMENT NATL INST OF AGROBIOLOGICAL RESOURCES

OS Haliotis discus discus

PN JP 2000060559-A/4

PD 29-FEB-2000

PF 18-AUG-1998 JP 1998232153

PR

PI HIDEAKI TAKAHASHI,MASASHI SEKINO

PC C12N15/09,C12Q1/68,C12N15/00

CC

FT

Key

Location/Qualifiers

1. .14

/organism='Haliotis discus discus'.

FEATURES source

Location/Qualifiers

1. .14

/organism="Haliotis discus discus"

/mol\_type="genomic DNA"

/sub\_species="discus"

/db\_xref="taxon:91233"

Query Match

Best Local Similarity 1.3%; Score 14; DB 1; Length 14;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTG 1806

Db 14 TGTGTGTGTGTGTG 1

RESULT 168

LOCUS I31524/c

DEFINITION Sequence 436 from patent US 5582979.

ACCESSION I31524

VERSION I31524.1 GI:1822315

KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 14)

AUTHORS Weber,J.L.

TITLE Length polymorphisms in (dc-da).sub.n.(dg-dt).sub.n sequences and method of using the same

JOURNAL Patent: US 5582979-A 436 10-DEC-1996;

FEATURES

Location/Qualifiers

1. .14

/organism="unknown"

/mol\_type="unassigned DNA"

Query Match

Best Local Similarity 1.3%; Score 14; DB 1; Length 14;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGT 1807

Db 14 GTGTGTGTGTGTGT 1

RESULT 169

LOCUS AR431517

DEFINITION Sequence 27 from patent US 6653069.

ACCESSION AR431517

VERSION AR431517.1 GI:40193621

KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 14)

AUTHORS Goni,I., Sunamachi,H., Takahashi,M. and Yamanishi,K.

TITLE Method for quality control of an attenuated vericella live vaccine

JOURNAL Patent: US 6653069-A 27 25-NOV-2003;

FEATURES

Location/Qualifiers

1. .14

/organism="unknown"

/mol\_type="genomic DNA"

Query Match

Best Local Similarity 1.3%; Score 14; DB 1; Length 14;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1813 TATATATATATATA 1826

Db 1 TATATATATATATA 14

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RESULT 170
AR431517/c
LOCUS       14 bp      DNA      linear      PAT 18-DEC-2003
DEFINITION  Sequence 27 from patent US 6653069.
ACCESSION  AR431517
VERSION    AR431517.1  GI:40193621
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 14)
AUTHORS   Gomi,Y., Sunamachi,H., Takahashi,M. and Yamanishi,K.
TITLE     Method for quality control of an attenuated varicella live vaccine
JOURNAL   Patent: US 6653069-A 27 25-NOV-2003;
FEATURES   Location/Qualifiers
            source
            1..14
            /organism="unknown"
            /mol_type="genomic DNA"
            Query Match      1.3%; Score 14; DB 1; Length 14;
            Best Local Similarity 100.0%; Pred. No. 1.1e+02;
            Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1813 TATATATATATATA 1826
Db  14 TATATATATATATA 1

RESULT 171
AX175251
LOCUS       14 bp      DNA      linear      PAT 03-JUL-2001
DEFINITION  Sequence 15 from Patent WO0144465.
ACCESSION  AX175251
VERSION    AX175251.1  GI:14598619
KEYWORDS   .
SOURCE     synthetic construct
            synthetic construct
            artificial sequences.
ORGANISM   1
            Phillips,N.C. and Filion,M.C.
REFERENCE  1
AUTHORS   Therapeutically useful synthetic oligonucleotides
TITLE     Patent: WO 0144465-A 15 21-JUN-2001;
JOURNAL   Bioniche Life Sciences Inc. (CA)
FEATURES   Location/Qualifiers
            source
            1..14
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            Query Match      1.3%; Score 14; DB 1; Length 14;
            Best Local Similarity 100.0%; Pred. No. 1.1e+02;
            Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1793 TGTGTGTGTGTGTG 1806
Db  1 TGTGTGTGTGTGTG 14

RESULT 172
BD084125
LOCUS       14 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION  Polymorphisms and new genes in the region of the human
            hemochromatosis gene.
ACCESSION  BD084125
VERSION    BD084125.1  GI:22629735
KEYWORDS   JP 2001525663-A/13.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 14)
AUTHORS   Feder,J.N., Kronmal,G.S., Lauer,P.M., Ruddy,D.A., Thomas,W.J.,
            Tauchihaishi,Z. and Wolff,R.K.
            Polymorphisms and new genes in the region of the human
            hemochromatosis gene
            Patent: JP 2001525663-A 13 11-DEC-2001;
            PROGENITOR INC
            OS Homo sapiens (human)
            PN JP 2001525663-A/13
            PD 11-DEC-2001
            PF 30-SEP-1997 JP 1998516815
            PR 01-OCT-1996 US 08/724394, 07-MAY-1997 US 08/852495 PI
            JOHN N FEDER,GREGORY S KRONMAL,PETER M LAUER,DAVID A RUDDY, PI
            WINSTON J THOMAS,ZENTA TSUCHIHASHI,ROGER K WOLFF PC
            C07H21/04,C12Q1/68,C12N15/63,C12N15/85,C12P21/02 CC Polymorphisms
            and new genes in the region of the human CC hemochromatosis gene
            and new genes in the region of the human CC hemochromatosis gene
            FH Key
            FT source
            1..14
            Location/Qualifiers
            1..14
            /organism="Homo sapiens (human)"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"
            Query Match      1.3%; Score 14; DB 1; Length 14;
            Best Local Similarity 100.0%; Pred. No. 1.1e+02;
            Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1813 TATATATATATATA 1826
Db  1 TATATATATATATA 14

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TITLE      Polymorphisms and new genes in the region of the human
            hemochromatosis gene
JOURNAL    Patent: JP 2001525663-A 13 11-DEC-2001;
            PROGENITOR INC
COMMENT    OS Homo sapiens (human)
            PN JP 2001525663-A/13
            PD 11-DEC-2001
            PF 30-SEP-1997 JP 1998516815
            PR 01-OCT-1996 US 08/724394, 07-MAY-1997 US 08/852495 PI
            JOHN N FEDER,GREGORY S KRONMAL,PETER M LAUER,DAVID A RUDDY, PI
            WINSTON J THOMAS,ZENTA TSUCHIHASHI,ROGER K WOLFF PC
            C07H21/04,C12Q1/68,C12N15/63,C12N15/85,C12P21/02 CC Polymorphisms
            and new genes in the region of the human CC hemochromatosis gene
            and new genes in the region of the human CC hemochromatosis gene
            FH Key
            FT source
            1..14
            Location/Qualifiers
            1..14
            /organism="Homo sapiens (human)"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"
            Query Match      1.3%; Score 14; DB 1; Length 14;
            Best Local Similarity 100.0%; Pred. No. 1.1e+02;
            Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1813 TATATATATATATA 1826
Db  1 TATATATATATATA 14

RESULT 173
BD084125/c
LOCUS       14 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION  Polymorphisms and new genes in the region of the human
            hemochromatosis gene.
ACCESSION  BD084125
VERSION    BD084125.1  GI:22629735
KEYWORDS   JP 2001525663-A/13.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 14)
AUTHORS   Feder,J.N., Kronmal,G.S., Lauer,P.M., Ruddy,D.A., Thomas,W.J.,
            Tauchihaishi,Z. and Wolff,R.K.
            Polymorphisms and new genes in the region of the human
            hemochromatosis gene
            Patent: JP 2001525663-A 13 11-DEC-2001;
            PROGENITOR INC
            OS Homo sapiens (human)
            PN JP 2001525663-A/13
            PD 11-DEC-2001
            PF 30-SEP-1997 JP 1998516815
            PR 01-OCT-1996 US 08/724394, 07-MAY-1997 US 08/852495 PI
            JOHN N FEDER,GREGORY S KRONMAL,PETER M LAUER,DAVID A RUDDY, PI
            WINSTON J THOMAS,ZENTA TSUCHIHASHI,ROGER K WOLFF PC
            C07H21/04,C12Q1/68,C12N15/63,C12N15/85,C12P21/02 CC Polymorphisms
            and new genes in the region of the human CC hemochromatosis gene
            and new genes in the region of the human CC hemochromatosis gene
            FH Key
            FT source
            1..14
            Location/Qualifiers
            1..14
            /organism="Homo sapiens (human)"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"
            Query Match      1.3%; Score 14; DB 1; Length 14;
            Best Local Similarity 100.0%; Pred. No. 1.1e+02;
            Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1813 TATATATATATATA 1826
Db  1 TATATATATATATA 14

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JOURNAL	Patent: US 5817796-A 1855 06-OCT-1998;
FEATURES	
source	1. .17 /organism="unknown" /mol_type="unassigned DNA"
Query Match	1.3%; Score 14; DB 1; Length 17;
Best Local Similarity	100.0%; Pred. No. 1.4e+02;
Matches 14; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	1763 CAGATTTTAAAAA 1776
Db	4 CAGATTTTAAAAA 17
RESULT 177	
AR047064	17 bp DNA linear PAT 29-SEP-1999
LOCUS	
DEFINITION	Sequence 1857 from patent US 5817796.
ACCESSION	AR047064
VERSION	AR047064.1 GI:5968529
KEYWORDS	Unknown.
SOURCE	Unknown.
ORGANISM	Unclassified. 1 (bases 1 to 17) Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T. C-myb ribozymes having 2'-5'-linked adenylylate residues JOURNAL Patent: US 5817796-A 1857 06-OCT-1998; LOCATION/Qualifiers 1. .17 /organism="unknown" /mol_type="unassigned DNA"
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
FEATURES	
source	1.3%; Score 14; DB 1; Length 17; Best Local Similarity 100.0%; Pred. No. 1.4e+02; Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1763 CAGATTTTAAAAA 1776
Db	3 CAGATTTTAAAAA 16
RESULT 178	
AR047066	17 bp DNA linear PAT 29-SEP-1999
LOCUS	
DEFINITION	Sequence 1859 from patent US 5817796.
ACCESSION	AR047066
VERSION	AR047066.1 GI:5968531
KEYWORDS	Unknown.
SOURCE	Unknown.
ORGANISM	Unclassified. 1 (bases 1 to 17) Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T. C-myb ribozymes having 2'-5'-linked adenylylate residues JOURNAL Patent: US 5817796-A 1859 06-OCT-1998; LOCATION/Qualifiers 1. .17 /organism="unknown" /mol_type="unassigned DNA"
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
FEATURES	
source	1.3%; Score 14; DB 1; Length 17; Best Local Similarity 100.0%; Pred. No. 1.4e+02; Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1763 CAGATTTTAAAAA 1776
Db	2 CAGATTTTAAAAA 15
RESULT 179	
AR047068	

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LOCUS AR047068 17 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 1861 from patent US 5817796.
ACCESSION AR047068
VERSION AR047068.1 GI:5968533
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
TITLE C-myb ribozymes having 2'-5'-linked adenylyate residues
JOURNAL Patent: US 5817796-A 1861 06-OCT-1998;
FEATURES
    source
        1..17
            /organism="unknown"
            /mol_type="unassigned DNA"
Query Match 1.3%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1763 CAGATTTTAAAA 1776
Db 1 CAGATTTTAAAA 14

RESULT 180
LOCUS AR074719 17 bp DNA linear PAT 28-AUG-2000
DEFINITION Sequence 16 from patent US 5955276.
ACCESSION AR074719
VERSION AR074719.1 GI:10001472
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Morgante,M. and Vogel,J.Marie.
TITLE Compound microsatellite primers for the detection of genetic
JOURNAL Patent: US 5955276-A 16 21-SEP-1999;
FEATURES
    source
        1..17
            /organism="unknown"
            /mol_type="unassigned DNA"
Query Match 1.3%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTG 1806
Db 17 TGTGTGTGTGTGTG 4

RESULT 181
LOCUS I53319 17 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 1060 from patent US 5646042.
ACCESSION I53319
VERSION I53319.1 GI:2474522
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
TITLE C-myb targeted ribozymes
JOURNAL Patent: US 5646042-A 1060 08-JUL-1997;
FEATURES
    source
        1..17
            /organism="unknown"
            /mol_type="unassigned DNA"
Query Match 1.3%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTG 1806
Db 17 TGTGTGTGTGTGTG 4

RESULT 182
LOCUS I54114 17 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 1855 from patent US 5646042.
ACCESSION I54114
VERSION I54114.1 GI:2475317
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
TITLE C-myb targeted ribozymes
JOURNAL Patent: US 5646042-A 1855 08-JUL-1997;
FEATURES
    source
        1..17
            /organism="unknown"
            /mol_type="unassigned DNA"
Query Match 1.3%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1763 CAGATTTTAAAA 1776
Db 4 CAGATTTTAAAA 17

RESULT 183
LOCUS I54116 17 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 1857 from patent US 5646042.
ACCESSION I54116
VERSION I54116.1 GI:2475319
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
TITLE C-myb targeted ribozymes
JOURNAL Patent: US 5646042-A 1857 08-JUL-1997;
FEATURES
    source
        1..17
            /organism="unknown"
            /mol_type="unassigned DNA"
Query Match 1.3%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1763 CAGATTTTAAAA 1776
Db 3 CAGATTTTAAAA 16

RESULT 184
LOCUS I54118 17 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 1859 from patent US 5646042.
ACCESSION I54118
VERSION I54118.1 GI:2475321
KEYWORDS
```

SOURCE Unknown.  
ORGANISM Unassigned.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.  
TITLE C-myb targeted ribozymes  
JOURNAL Patent: US 5646042-A 1989 08-JUL-1997;  
FEATURES Location/Qualifiers  
1..17  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.3%; Score 14; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1763 CAGATTTTAAAA 1776  
Db 2 CAGATTTTAAAA 15

RESULT 185  
LOCUS I54120 17 bp DNA linear PAT 07-OCT-1997  
DEFINITION Sequence 1861 from patent US 5646042.  
ACCESSION I54120  
VERSION I54120.1 GI:2475323  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unassigned.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.  
TITLE C-myb targeted ribozymes  
JOURNAL Patent: US 5646042-A 1989 08-JUL-1997;  
FEATURES Location/Qualifiers  
1..17  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.3%; Score 14; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1763 CAGATTTTAAAA 1776  
Db 1 CAGATTTTAAAA 14

RESULT 186  
LOCUS AX762502 17 bp DNA linear PAT 25-JUN-2003  
DEFINITION Sequence 5823 from Patent WO03040369.  
ACCESSION AX762502  
VERSION AX762502.1 GI:32257118  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
TITLE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
JOURNAL Telerman,A., Anson,R. and Tuijinder,M.  
FEATURES Sequences involved in tumoral suppression, tumoral reversion,  
apoptosis and/or viral resistance phenomena and their use as  
medicines  
Patent: WO 03040369-A 5823 15-MAY-2003;  
Molecular Engines Laboratories (FR)  
1..17  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 1.3%; Score 14; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1292 ATCTGTTTCTAA 1305  
Db 2 ATCTGTTTCTAA 15

RESULT 187  
LOCUS A28997 17 bp DNA linear PAT 30-JUN-1995  
DEFINITION primer sequence 4 from patent EP0522880.  
ACCESSION A28997  
VERSION A28997.1 GI:1248848  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM artificial construct  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Holton,T.A., Cornish,E.C., Kovacic,F., Tanaka,Y. and Lester,D.R.  
TITLE Genetic sequences encoding flavonoid pathway enzymes and uses  
thereof  
JOURNAL Patent: EP 0522880-A 16 13-JAN-1993;  
INTERNATIONAL FLOWER DEVELOPMENTS Pty. Ltd  
FEATURES Location/Qualifiers  
1..17  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"

Query Match 1.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.4e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTT 1881  
Db 1 TTTTATTTTGTGTTT 17

RESULT 188  
LOCUS AR045081 17 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 874 from patent US 5817796.  
ACCESSION AR045081  
VERSION AR045081.1 GI:5967546  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unassigned.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.  
TITLE C-myb ribozymes having 2'-5'-linked adenylate residues  
JOURNAL Patent: US 5817796-A 874 06-OCT-1998;  
FEATURES Location/Qualifiers  
1..17  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.4e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1765 GATTTTAAAAATTTAT 1781  
Db 17 GATTTTAAAAATATAT 1

RESULT 189  
LOCUS AR057784 17 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 1988 from patent US 5837542.  
ACCESSION AR057784

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VERSION      AR057784.1  GI:5983361
KEYWORDS
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 17)
AUTHORS      Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
              Draper,K.G.
TITLE        Intercellular adhesion molecule-1 (ICAM-1) ribozymes
JOURNAL      Patent: US 5837542-A 1988 17-NOV-1998;
FEATURES     Location/Qualifiers
              1..17
              /organism="unknown"
              /mol_type="unassigned DNA"

Query Match      1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.4e-02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1537 GTGTAATTGAGAAGGAA 1553
Db 17 GGGTAATAGAGAAGGAA 1

RESULT 192
LOCUS      AR141074
DEFINITION Sequence 5 from patent US 6207819.
ACCESSION  AR141074
VERSION     AR141074.1  GI:14483570
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 17)
AUTHORS    Manoharan,M. and Maier,M.A.
TITLE      Compounds, processes and intermediates for synthesis of mixed
              backbone oligomeric compounds
JOURNAL    Patent: US 6207819-A 5 27-MAR-2001;
FEATURES   Location/Qualifiers
              1..17
              /organism="unknown"
              /mol_type="unassigned DNA"

Query Match      1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.4e-02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTTT 1881
Db 1 TTTTATTTTGTGTTTT 17

RESULT 193
LOCUS      AR175846
DEFINITION Sequence 132 from patent US 6309867.
ACCESSION  AR175846
VERSION     AR175846.1  GI:17917145
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 17)
AUTHORS    Cech,T.R. and Nakamura,T.
TITLE      Telomerase
JOURNAL    Patent: US 6309867-A 132 30-OCT-2001;
FEATURES   Location/Qualifiers
              1..17
              /organism="unknown"
              /mol_type="unassigned DNA"

Query Match      1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.4e-02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTTT 1881
Db 1 TTTTATTTTGTGTTTT 17

RESULT 194
LOCUS      BD241082
DEFINITION Methods and products related to genotyping and DNA analysis.
ACCESSION  BD241082
VERSION     BD241082.1  GI:33050852
KEYWORDS   JP 2002525127-A/29.

VERSION      AR115542/c  GI:14095864
KEYWORDS
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 17)
AUTHORS      Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
              Draper,K.G.
TITLE        Ribozyme treatment of diseases or conditions related to levels of
              intercellular adhesion molecule-1 (ICAM-1)
JOURNAL      Patent: US 6132967-A 1988 17-OCT-2000;
FEATURES     Location/Qualifiers
              1..17
              /organism="unknown"
              /mol_type="unassigned DNA"

Query Match      1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.4e-02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTTT 1881
Db 1 TTTTATTTTGTGTTTT 17

RESULT 191
LOCUS      AR115542/c
DEFINITION Sequence 1988 from patent US 6132967.
ACCESSION  AR115542
VERSION     AR115542.1  GI:14095864
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 17)
AUTHORS    Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
              Draper,K.G.
TITLE      Ribozyme treatment of diseases or conditions related to levels of
              intercellular adhesion molecule-1 (ICAM-1)
JOURNAL    Patent: US 6132967-A 1988 17-OCT-2000;
FEATURES   Location/Qualifiers
              1..17
              /organism="unknown"
              /mol_type="unassigned DNA"

Query Match      1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.4e-02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTTT 1881
Db 1 TTTTATTTTGTGTTTT 17

RESULT 190
LOCUS      AR104585
DEFINITION Sequence 132 from patent US 6093809.
ACCESSION  AR104585
VERSION     AR104585.1  GI:12817293
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 17)
AUTHORS    Cech,T.R. and Lingner,J.
TITLE      Telomerase
JOURNAL    Patent: US 6093809-A 132 25-JUL-2000;
FEATURES   Location/Qualifiers
              1..17
              /organism="unknown"
              /mol_type="unassigned DNA"

Query Match      1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.4e-02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTTT 1881
Db 1 TTTTATTTTGTGTTTT 17

RESULT 191
LOCUS      AR115542/c
DEFINITION Sequence 1988 from patent US 6132967.
ACCESSION  AR115542
VERSION     AR115542.1  GI:14095864
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 17)
AUTHORS    Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
              Draper,K.G.
TITLE      Ribozyme treatment of diseases or conditions related to levels of
              intercellular adhesion molecule-1 (ICAM-1)
JOURNAL    Patent: US 6132967-A 1988 17-OCT-2000;
FEATURES   Location/Qualifiers
              1..17
              /organism="unknown"
              /mol_type="unassigned DNA"

Query Match      1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.4e-02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTTT 1881
Db 1 TTTTATTTTGTGTTTT 17

RESULT 190
LOCUS      AR104585
DEFINITION Sequence 132 from patent US 6093809.
ACCESSION  AR104585
VERSION     AR104585.1  GI:12817293
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 17)
AUTHORS    Cech,T.R. and Lingner,J.
TITLE      Telomerase
JOURNAL    Patent: US 6093809-A 132 25-JUL-2000;
FEATURES   Location/Qualifiers
              1..17
              /organism="unknown"
              /mol_type="unassigned DNA"

Query Match      1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.4e-02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTTT 1881
Db 1 TTTTATTTTGTGTTTT 17

RESULT 192
LOCUS      AR141074
DEFINITION Sequence 5 from patent US 6207819.
ACCESSION  AR141074
VERSION     AR141074.1  GI:14483570
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 17)
AUTHORS    Manoharan,M. and Maier,M.A.
TITLE      Compounds, processes and intermediates for synthesis of mixed
              backbone oligomeric compounds
JOURNAL    Patent: US 6207819-A 5 27-MAR-2001;
FEATURES   Location/Qualifiers
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              /organism="unknown"
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Query Match      1.3%; Score 13.8; DB 1; Length 17;
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Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1537 GTGTAATTGAGAAGGAA 1553
Db 17 GGGTAATAGAGAAGGAA 1

RESULT 191
LOCUS      AR115542/c
DEFINITION Sequence 1988 from patent US 6132967.
ACCESSION  AR115542
VERSION     AR115542.1  GI:14095864
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 17)
AUTHORS    Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
              Draper,K.G.
TITLE      Ribozyme treatment of diseases or conditions related to levels of
              intercellular adhesion molecule-1 (ICAM-1)
JOURNAL    Patent: US 6132967-A 1988 17-OCT-2000;
FEATURES   Location/Qualifiers
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              /organism="unknown"
              /mol_type="unassigned DNA"

Query Match      1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.4e-02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTTT 1881
Db 1 TTTTATTTTGTGTTTT 17

RESULT 190
LOCUS      AR104585
DEFINITION Sequence 132 from patent US 6093809.
ACCESSION  AR104585
VERSION     AR104585.1  GI:12817293
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 17)
AUTHORS    Cech,T.R. and Lingner,J.
TITLE      Telomerase
JOURNAL    Patent: US 6093809-A 132 25-JUL-2000;
FEATURES   Location/Qualifiers
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              /organism="unknown"
              /mol_type="unassigned DNA"

Query Match      1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.4e-02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTTT 1881
Db 1 TTTTATTTTGTGTTTT 17

RESULT 191
LOCUS      AR115542/c
DEFINITION Sequence 1988 from patent US 6132967.
ACCESSION  AR115542
VERSION     AR115542.1  GI:14095864
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 17)
AUTHORS    Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
              Draper,K.G.
TITLE      Ribozyme treatment of diseases or conditions related to levels of
              intercellular adhesion molecule-1 (ICAM-1)
JOURNAL    Patent: US 6132967-A 1988 17-OCT-2000;
FEATURES   Location/Qualifiers
              1..17
              /organism="unknown"
              /mol_type="unassigned DNA"

Query Match      1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.4e-02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTTT 1881
Db 1 TTTTATTTTGTGTTTT 17

RESULT 192
LOCUS      AR141074
DEFINITION Sequence 5 from patent US 6207819.
ACCESSION  AR141074
VERSION     AR141074.1  GI:14483570
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 17)
AUTHORS    Manoharan,M. and Maier,M.A.
TITLE      Compounds, processes and intermediates for synthesis of mixed
              backbone oligomeric compounds
JOURNAL    Patent: US 6207819-A 5 27-MAR-2001;
FEATURES   Location/Qualifiers
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              /organism="unknown"
              /mol_type="unassigned DNA"

Query Match      1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.4e-02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1537 GTGTAATTGAGAAGGAA 1553
Db 17 GGGTAATAGAGAAGGAA 1

RESULT 193
LOCUS      AR175846
DEFINITION Sequence 132 from patent US 6309867.
ACCESSION  AR175846
VERSION     AR175846.1  GI:17917145
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 17)
AUTHORS    Cech,T.R. and Nakamura,T.
TITLE      Telomerase
JOURNAL    Patent: US 6309867-A 132 30-OCT-2001;
FEATURES   Location/Qualifiers
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              /organism="unknown"
              /mol_type="unassigned DNA"

Query Match      1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.4e-02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTTT 1881
Db 1 TTTTATTTTGTGTTTT 17

RESULT 194
LOCUS      BD241082
DEFINITION Methods and products related to genotyping and DNA analysis.
ACCESSION  BD241082
VERSION     BD241082.1  GI:33050852
KEYWORDS   JP 2002525127-A/29.


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SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 17)  
 Lenders,J.E., Jordan,B., Housman,D.E. and Charest,A.  
 Methods and products related to genotyping and DNA analysis  
 Patent: JP 2002525127-A 29 13-AUG-2002;  
 MASSACHUSETTS INSTITUTE OF TECHNOLOGY  
 OS Homo sapiens (human)  
 PN JP 2002525127-A/29  
 PD 13-AUG-2002  
 PF 24-SEP-1999 JP 2000572407  
 PR 25-SEP-1998 US 60/101757  
 PI JOHN E LANDERS, BARBARA JORDAN, DAVID E HOUSMAN, ALAIN CHAREST PC  
 C12N15/09, C12Q1/68, G01N33/53, G01N33/566, G01N37/00, PC  
 G01N37/00,  
 PC C12N15/00  
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 /db\_xref='taxon:9606'  
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 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1379 TGGCTTGAAGAATGTTA 1395  
 DB 17 TGGCTTGAAGAATGTTA 1  
 RESULT 195  
 BD241091/c 17 bp DNA linear PAT 17-JUL-2003  
 LOCUS Methods and products related to genotyping and DNA analysis.  
 DEFINITION  
 ACCESSION BD241091.1 GI:33050861  
 VERSION JP 2002525127-A/38.  
 KEYWORDS Homo sapiens (human)  
 SOURCE  
 ORGANISM  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 Lenders,J.E., Jordan,B., Housman,D.E. and Charest,A.  
 Methods and products related to genotyping and DNA analysis  
 Patent: JP 2002525127-A 38 13-AUG-2002;  
 MASSACHUSETTS INSTITUTE OF TECHNOLOGY  
 OS Homo sapiens (human)  
 PN JP 2002525127-A/38  
 PD 13-AUG-2002  
 PF 24-SEP-1999 JP 2000572407  
 PR 25-SEP-1998 US 60/101757  
 PI JOHN E LANDERS, BARBARA JORDAN, DAVID E HOUSMAN, ALAIN CHAREST PC  
 C12N15/09, C12Q1/68, G01N33/53, G01N33/566, G01N37/00, PC  
 G01N37/00,  
 PC C12N15/00  
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 /db\_xref='taxon:9606'  
 Query Match 1.3%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 1.4e+02;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1379 TGGCTTGAAGAATGTTA 1395  
 DB 17 TGGCTTGAAGAATGTTA 1  
 RESULT 195  
 BD241091/c 17 bp DNA linear PAT 17-JUL-2003  
 LOCUS Methods and products related to genotyping and DNA analysis.  
 DEFINITION  
 ACCESSION BD241091.1 GI:33050861  
 VERSION JP 2002525127-A/38.  
 KEYWORDS Homo sapiens (human)  
 SOURCE  
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 Lenders,J.E., Jordan,B., Housman,D.E. and Charest,A.  
 Methods and products related to genotyping and DNA analysis  
 Patent: JP 2002525127-A 38 13-AUG-2002;  
 MASSACHUSETTS INSTITUTE OF TECHNOLOGY  
 OS Homo sapiens (human)  
 PN JP 2002525127-A/38  
 PD 13-AUG-2002  
 PF 24-SEP-1999 JP 2000572407  
 PR 25-SEP-1998 US 60/101757  
 PI JOHN E LANDERS, BARBARA JORDAN, DAVID E HOUSMAN, ALAIN CHAREST PC  
 C12N15/09, C12Q1/68, G01N33/53, G01N33/566, G01N37/00, PC  
 G01N37/00,  
 PC C12N15/00  
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 /mol\_type='genomic DNA'  
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Best Local Similarity 88.2%; Pred. No. 1.4e+02;  
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 DB 17 TGGCTTGAAGAATGTTA 1  
 RESULT 196  
 BD241132/c 17 bp DNA linear PAT 17-JUL-2003  
 LOCUS Methods and products related to genotyping and DNA analysis.  
 DEFINITION  
 ACCESSION BD241132.1 GI:33050902  
 VERSION JP 2002525127-A/79.  
 KEYWORDS Homo sapiens (human)  
 SOURCE  
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 Lenders,J.E., Jordan,B., Housman,D.E. and Charest,A.  
 Methods and products related to genotyping and DNA analysis  
 Patent: JP 2002525127-A 79 13-AUG-2002;  
 MASSACHUSETTS INSTITUTE OF TECHNOLOGY  
 OS Homo sapiens (human)  
 PN JP 2002525127-A/79  
 PD 13-AUG-2002  
 PF 24-SEP-1999 JP 2000572407  
 PR 25-SEP-1998 US 60/101757  
 PI JOHN E LANDERS, BARBARA JORDAN, DAVID E HOUSMAN, ALAIN CHAREST PC  
 C12N15/09, C12Q1/68, G01N33/53, G01N33/566, G01N37/00, PC  
 G01N37/00,  
 PC C12N15/00  
 CC Methods and products related to genotyping and DNA analysis FH  
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 /mol\_type='genomic DNA'  
 /db\_xref='taxon:9606'  
 Query Match 1.3%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 1.4e+02;  
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 QY 1379 TGGCTTGAAGAATGTTA 1395  
 DB 17 TGGCTTGAAGAATGTTA 1  
 RESULT 197  
 BD241617 17 bp DNA linear PAT 17-JUL-2003  
 LOCUS Methods and products related to genotyping and DNA analysis.  
 DEFINITION  
 ACCESSION BD241617.1 GI:33051387  
 VERSION JP 2002525127-A/564.  
 KEYWORDS Homo sapiens (human)  
 SOURCE  
 ORGANISM  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 Lenders,J.E., Jordan,B., Housman,D.E. and Charest,A.  
 Methods and products related to genotyping and DNA analysis  
 Patent: JP 2002525127-A 564 13-AUG-2002;  
 MASSACHUSETTS INSTITUTE OF TECHNOLOGY  
 OS Homo sapiens (human)  
 PN JP 2002525127-A/564  
 PD 13-AUG-2002  
 PF 24-SEP-1999 JP 2000572407  
 PR 25-SEP-1998 US 60/101757

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PI JOHN E LANDERS, BARBARA JORDAN, DAVID E HOUSMAN, ALAIN CHAREST PC
C12N15/09, C12Q1/68, G01N33/53, G01N33/566, G01N33/58, G01N37/00, PC
GOIN37/00,
PC C12N15/00
CC Methods and products related to genotyping and DNA analysis FH
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FT /organism='Homo sapiens (human)'.

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Location/Qualifiers
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Query Match 1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGT 1809
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Db 1 TGTGTGTGTGTGTGTCT 17

RESULT 198
BD254547
LOCUS 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Regulation of repressor genes using nucleic acid molecules.
ACCESSION BD254547
VERSION BD254547.1 GI:33064317
KEYWORDS JP 2002541795-A/2340.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Blatt, L., Zwick, M., Pavco, P. and McSwiggen, J.
TITLE Regulation of repressor genes using nucleic acid molecules
JOURNAL Patent: JP 2002541795-A 2340 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
COMMENT OS Eukaryote
PN JP 2002541795-A/2340
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN PC
C12N15/09, A61K38/00, A61K48/00, A61P43/00, A61P43/00, C12N5/10, PC
C12P21/02,
PC
C12P21/02, C12P21/02//A61K31/711, (C12N5/10, C12R1:91), (C12P21/02, PC
C12R1:91),
PC (C12P21/02, C12R1:91), (C12P21/02, C12R1:91), C12N15/00, C12N5/00,
PC A61K37/02,
PC (C12N5/00, C12R1:91)
CC Regulation of repressor genes using nucleic acid molecules FH
Key source Location/Qualifiers
FT source 1..17
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FEATURES
source
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Query Match 1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1760 AGCAGATTTTATAAA 1776
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Db 1 AGAGAGATTTTATAAA 17

RESULT 200
I53133
LOCUS 17 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 874 from patent US 5646042.
ACCESSION I53133
VERSION I53133.1 GI:2474336
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Strichcomb, D.T., Draper, K., McSwiggen, J. and Jarvis, T.
TITLE C-myc targeted ribozymes
JOURNAL Patent: US 5646042-A 874 08-JUL-1997;
FEATURES Location/Qualifiers
source 1..17
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/mol_type='unassigned DNA'

Query Match 1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1765 GATTTTAAATTTAT 1781
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Db 1 GATTTTAAATATATAT 1

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LOCUS 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Regulation of repressor genes using nucleic acid molecules.
ACCESSION BD255193
VERSION BD255193.1 GI:33064963
KEYWORDS JP 2002541795-A/2986.
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Blatt, L., Zwick, M., Pavco, P. and McSwiggen, J.
TITLE Regulation of repressor genes using nucleic acid molecules
JOURNAL Patent: JP 2002541795-A 2986 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
COMMENT OS Eukaryote
PN JP 2002541795-A/2986
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN PC
C12N15/09, A61K38/00, A61K48/00, A61P43/00, A61P43/00, C12N5/10, PC
C12P21/02,
PC
C12P21/02, C12P21/02//A61K31/711, (C12N5/10, C12R1:91), (C12P21/02, PC
C12R1:91),
PC (C12P21/02, C12R1:91), (C12P21/02, C12R1:91), C12N15/00, C12N5/00,
PC A61K37/02,
PC (C12N5/00, C12R1:91)
CC Regulation of repressor genes using nucleic acid molecules FH
Key source Location/Qualifiers
FT source 1..17
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FEATURES
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/mol_type='genomic DNA'
/db_xref='taxon:32644'

Query Match 1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1760 AGCAGATTTTATAAA 1776
|||||
Db 1 AGAGAGATTTTATAAA 17

RESULT 200
I53133
LOCUS 17 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 874 from patent US 5646042.
ACCESSION I53133
VERSION I53133.1 GI:2474336
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Strichcomb, D.T., Draper, K., McSwiggen, J. and Jarvis, T.
TITLE C-myc targeted ribozymes
JOURNAL Patent: US 5646042-A 874 08-JUL-1997;
FEATURES Location/Qualifiers
source 1..17
/organism='unknown'
/mol_type='unassigned DNA'

Query Match 1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1765 GATTTTAAATTTAT 1781
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Db 1 GATTTTAAATATATAT 1

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RESULT 201  
LOCUS AR187062 17 bp DNA linear PAT 20-APR-2002  
DEFINITION Sequence 2550 from patent US 6346398.  
ACCESSION AR187062  
VERSION AR187062.1 GI:20233027  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.  
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor  
JOURNAL Patent: US 6346398-A 2550 12-FEB-2002;  
FEATURES Location/Qualifiers  
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/mol\_type="unassigned DNA"  
Query Match 1.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.4e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1864 CTTTATTATTTGTTTT 1880  
DB 1 CTTTTTTTTTTTTTTT 17  
RESULT 202  
LOCUS AR190559 17 bp DNA linear PAT 20-APR-2002  
DEFINITION Sequence 6047 from patent US 6346398.  
ACCESSION AR190559  
VERSION AR190559.1 GI:20236524  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.  
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor  
JOURNAL Patent: US 6346398-A 6047 12-FEB-2002;  
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QY 1639 TGTTCCTTAAGTCAGAA 1655  
DB 1 TGTGCCTTAATTCAGAA 17  
RESULT 203  
LOCUS AR190561 17 bp DNA linear PAT 20-APR-2002  
DEFINITION Sequence 6049 from patent US 6346398.  
ACCESSION AR190561  
VERSION AR190561.1 GI:20236526  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.  
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor

JOURNAL Patent: US 6346398-A 6049 12-FEB-2002;  
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/mol\_type="unassigned DNA"  
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Best Local Similarity 88.2%; Pred. No. 1.4e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1643 CCTTAAGTCAGAACGC 1659  
DB 1 CCTTAATTCAGAACCC 17  
RESULT 204  
LOCUS AR222463 17 bp DNA linear PAT 26-SEP-2002  
DEFINITION Sequence 23 from patent US 6429300.  
ACCESSION AR222463  
VERSION AR222463.1 GI:23329994  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Kurz,M., Lohse,P. and Wagner,R.  
TITLE Peptide acceptor ligation methods  
JOURNAL Patent: US 6429300-A 23 06-AUG-2002;  
FEATURES Location/Qualifiers  
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Query Match 1.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.4e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1865 TTTTATTTTGTGTTTT 1881  
DB 1 TTTTATTTTGTGTTTT 1  
RESULT 205  
LOCUS AR236087 17 bp DNA linear PAT 20-DEC-2002  
DEFINITION Sequence 5 from patent US 6462184.  
ACCESSION AR236087  
VERSION AR236087.1 GI:27279786  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Manoharan,M. and Maier,M.A.  
TITLE Compounds, processes and intermediates for synthesis of mixed backbone oligomeric compounds  
JOURNAL Patent: US 6462184-A 5 08-OCT-2002;  
FEATURES Location/Qualifiers  
source 1..17  
/organism="unknown"  
/mol\_type="genomic DNA"  
Query Match 1.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.4e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1865 TTTTATTTTGTGTTTT 1881  
DB 1 TTTTATTTTGTGTTTT 17  
RESULT 206

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AR323672          AR323672          17 bp  RNA          linear  PAT 17-AUG-2003
LOCUS              Sequence 1074 from patent US 6566127.
DEFINITION
ACCESSION          AR323672
VERSION            AR323672.1  GI:33709480
KEYWORDS
SOURCE             Unknown.
ORGANISM            Unclassified.
REFERENCE           1 (bases 1 to 17)
AUTHORS            Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE              Method and reagent for the treatment of diseases or conditions
                  related to levels of vascular endothelial growth factor receptor
JOURNAL            Patent: US 6566127-A 1074 20-MAY-2003;
FEATURES            Location/Qualifiers
source             1..17
                  /organism="unknown"
                  /mol_type="unassigned RNA"

Query Match
Best Local Similarity 1.3%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1864 CTTTATTATTTGTTT 1880
Db 1 CTTTATTTTATTTT 17

RESULT 207
LOCUS              AR325482          17 bp  RNA          linear  PAT 17-AUG-2003
DEFINITION          Sequence 2884 from patent US 6566127.
ACCESSION          AR325482
VERSION            AR325482.1  GI:33711290
KEYWORDS
SOURCE             Unknown.
ORGANISM            Unclassified.
REFERENCE           1 (bases 1 to 17)
AUTHORS            Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE              Method and reagent for the treatment of diseases or conditions
                  related to levels of vascular endothelial growth factor receptor
JOURNAL            Patent: US 6566127-A 2884 20-MAY-2003;
FEATURES            Location/Qualifiers
source             1..17
                  /organism="unknown"
                  /mol_type="unassigned RNA"

Query Match
Best Local Similarity 1.3%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1639 TGTTCCTTAAGTCAGAA 1655
Db 1 TGTGCCTTAATTCAGAA 17

RESULT 208
LOCUS              AR325484          17 bp  RNA          linear  PAT 17-AUG-2003
DEFINITION          Sequence 2886 from patent US 6566127.
ACCESSION          AR325484
VERSION            AR325484.1  GI:33711292
KEYWORDS
SOURCE             Unknown.
ORGANISM            Unclassified.
REFERENCE           1 (bases 1 to 17)
AUTHORS            Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE              Method and reagent for the treatment of diseases or conditions
                  related to levels of vascular endothelial growth factor receptor
JOURNAL            Patent: US 6566127-A 2886 20-MAY-2003;
FEATURES            Location/Qualifiers
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source             1..17
                  /organism="unknown"
                  /mol_type="unassigned RNA"

Query Match
Best Local Similarity 1.3%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1643 CCTTAAGTCAGACACG 1659
Db 1 CCTTAATTCAGAACCC 17

RESULT 209
LOCUS              AR433961          17 bp  DNA          linear  PAT 18-DEC-2003
DEFINITION          Sequence 384 from patent US 6656700.
ACCESSION          AR433961
VERSION            AR433961.1  GI:40196804
KEYWORDS
SOURCE             Unknown.
ORGANISM            Unclassified.
REFERENCE           1 (bases 1 to 17)
AUTHORS            Gu,Y. and Shannon,M.E.
TITLE              Isoforms of human pregnancy-associated protein-E
JOURNAL            Patent: US 6656700-A 384 02-DEC-2003;
FEATURES            Location/Qualifiers
source             1..17
                  /organism="unknown"
                  /mol_type="genomic DNA"

Query Match
Best Local Similarity 1.3%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTG 1810
Db 1 GTGTGTGTGTGTGTGTG 17

RESULT 210
LOCUS              AR433962          17 bp  DNA          linear  PAT 18-DEC-2003
DEFINITION          Sequence 385 from patent US 6656700.
ACCESSION          AR433962
VERSION            AR433962.1  GI:40196805
KEYWORDS
SOURCE             Unknown.
ORGANISM            Unclassified.
REFERENCE           1 (bases 1 to 17)
AUTHORS            Gu,Y. and Shannon,M.E.
TITLE              Isoforms of human pregnancy-associated protein-E
JOURNAL            Patent: US 6656700-A 385 02-DEC-2003;
FEATURES            Location/Qualifiers
source             1..17
                  /organism="unknown"
                  /mol_type="genomic DNA"

Query Match
Best Local Similarity 1.3%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTG 1809
Db 1 TGTGTGTGTGTGTGTGTG 17

RESULT 211
LOCUS              AR433963          17 bp  DNA          linear  PAT 18-DEC-2003
DEFINITION          Sequence 386 from patent US 6656700.
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ACCESSION AR433963  
VERSION AR433963.1 GI:40196806  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Gu, Y. and Shannon, M.E.  
TITLE Isoforms of human pregnancy-associated protein-E  
JOURNAL Patent: US 6556700-A 386 02-DEC-2003;  
FEATURES Location/Qualifiers  
1..17  
/organism="unknown"  
/mol\_type="genomic DNA"  
Query Match 1.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.4e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1794 GTGTGTGTGTGTGTGTG 1810  
Db 1 GTGTGTGTGTGTGTGTG 17  
RESULT 212  
LOCUS AR433964  
DEFINITION Sequence 387 from patent US 6656700.  
ACCESSION AR433964  
VERSION AR433964.1 GI:40196807  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Gu, Y. and Shannon, M.E.  
TITLE Isoforms of human pregnancy-associated protein-E  
JOURNAL Patent: US 6556700-A 387 02-DEC-2003;  
FEATURES Location/Qualifiers  
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/organism="unknown"  
/mol\_type="genomic DNA"  
Query Match 1.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.4e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1793 TGTGTGTGTGTGTGTGT 1809  
Db 1 TGTGTGTGTGTGTGTGT 17  
RESULT 213  
LOCUS AR433965  
DEFINITION Sequence 388 from patent US 6656700.  
ACCESSION AR433965  
VERSION AR433965.1 GI:40196808  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Gu, Y. and Shannon, M.E.  
TITLE Isoforms of human pregnancy-associated protein-E  
JOURNAL Patent: US 6556700-A 388 02-DEC-2003;  
FEATURES Location/Qualifiers  
1..17  
/organism="unknown"  
/mol\_type="genomic DNA"  
Query Match 1.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.4e+02;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1798 GTGTGTGTGTGTGTGTA 1814  
Db 1 GTGTGTGTGTGTGTGTA 17  
RESULT 214  
LOCUS AR433966  
DEFINITION Sequence 389 from patent US 6656700.  
ACCESSION AR433966  
VERSION AR433966.1 GI:40196809  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Gu, Y. and Shannon, M.E.  
TITLE Isoforms of human pregnancy-associated protein-E  
JOURNAL Patent: US 6556700-A 389 02-DEC-2003;  
FEATURES Location/Qualifiers  
1..17  
/organism="unknown"  
/mol\_type="genomic DNA"  
Query Match 1.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.4e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1799 TGTGTGTGTGTGTGTAT 1815  
Db 1 TGTGTGTGTGTGTGTAT 17  
RESULT 215  
LOCUS AX502780  
DEFINITION Sequence 4087 from Patent EP1229046.  
ACCESSION AX502780  
VERSION AX502780.1 GI:23385073  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Zhan, J.  
TITLE Human testis expressed patched like protein  
JOURNAL Patent: EP 1229046-A 4087 07-AUG-2002;  
FEATURES Location/Qualifiers  
1..17  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 1.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.4e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2160 AACGATTGTTTCTACT 2176  
Db 1 ATGCAATTGTTTCTAGT 17  
RESULT 216  
LOCUS AX578222/c  
DEFINITION Sequence 60 from Patent WO2011674.  
ACCESSION AX578222  
VERSION AX578222.1 GI:27647424  
KEYWORDS

SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1  
 AUTHORS Thompson, J., Mcswiggen, J., Mckenzie, T., Ayers, D., Szymkowski, D.E.  
 and Grupe, A.  
 TITLE Method and reagent for the inhibition of calcium activated chloride  
 channel-1 (clca-1)  
 JOURNAL Patent: WO 0211674-A 60 14-FEB-2002;  
 RIBOZYME PHARMACEUTICALS, INC. (US); Syntex (U.S.A.) LLC (US);  
 Thompson, James (US)

FEATURES  
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 1. .17  
 /organism="Homo sapiens"  
 /mol\_type="unassigned RNA"  
 /db\_xref="taxon:9606"

Query Match 1.3%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 1.4e+02;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1821 TATATATGACAGTAT 1837  
 |||||  
 Db 17 TATATATACAGAT 1

RESULT 217  
 AX634823/c 17 bp RNA linear PAT 21-FEB-2003  
 LOCUS AX634823  
 DEFINITION Sequence 1962 from Patent EP1260586.  
 ACCESSION AX634823  
 VERSION AX634823.1 GI:28470437  
 KEYWORDS  
 SOURCE unidentified  
 ORGANISM unidentified  
 unclassified.

REFERENCE 1  
 AUTHORS Stinchcomb D.T., Dudycz L.W., Chowrika B., Grimm S., Drenzo, A.,  
 Karpeisky, A., Draper K.G., Kisich K., Matulic-Adamic J.,  
 Mcswiggen, J.A., Modak, A., Favco, P., Beigelman, L., Sullivan, S.M.,  
 Sweedler, D., Thompson, J.D., Tracz, D., Usman, N., Wincott, F.E. and  
 Woolf, T.  
 TITLE Method and reagent for inhibiting the expression of disease related  
 genes  
 JOURNAL Patent: EP 1260586-A 1962 27-NOV-2002;  
 RIBOZYME PHARMACEUTICALS, INC. (US)

FEATURES  
 source  
 1. .17  
 /organism="unidentified"  
 /mol\_type="unassigned RNA"  
 /db\_xref="taxon:32644"

Query Match 1.3%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 1.4e+02;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1537 GTGTAATTGAGAGGAA 1553  
 |||||  
 Db 17 GCGTAATAGAGAGGAA 1

RESULT 218  
 AX692525 17 bp DNA linear PAT 31-MAR-2003  
 LOCUS AX692525  
 DEFINITION Sequence 5257 from Patent EP1281758.  
 ACCESSION AX692525  
 VERSION AX692525.1 GI:29415483  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1  
 AUTHORS Shannon, M., Gu, Y. and Nguyen, C.T.  
 TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and  
 mdz12  
 JOURNAL Patent: EP 1281758-A 5257 05-FEB-2003;  
 Aeomica, Inc. (US)

FEATURES  
 source  
 1. .17  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

Query Match 1.3%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 1.4e+02;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1864 CTTTTATTATTTTGT 1880  
 |||||  
 Db 1 CTTTTTTTTTTTTT 17

RESULT 219  
 AX735506 17 bp DNA linear PAT 08-MAY-2003  
 LOCUS AX735506  
 DEFINITION Sequence 1096 from Patent WO03025177.  
 ACCESSION AX735506  
 VERSION AX735506.1 GI:30514783  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1  
 AUTHORS Teلمان, A., Anson, R. and Tuijinder, M.  
 TITLE Sequences involved in phenomena of tumour suppression, tumour  
 reversion, apoptosis and/or resistance to viruses and the use  
 thereof as medicaments  
 JOURNAL Patent: WO 03025177-A 1096 27-MAR-2003;  
 Molecular Engines Laboratories (FR)

FEATURES  
 source  
 1. .17  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

Query Match 1.3%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 1.4e+02;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1695 GTTCAGGAATCGGAATC 1711  
 |||||  
 Db 1 GATCAGAAATCGGAATC 17

RESULT 220  
 AR050983 15 bp DNA linear PAT 29-SEP-1999  
 LOCUS AR050983  
 DEFINITION Sequence 52 from patent US 5830644.  
 ACCESSION AR050983  
 VERSION AR050983.1 GI:5974347  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 unclassified.

REFERENCE 1 (bases 1 to 15)  
 AUTHORS West, M.D., Shay, J. and Wright, W.E.  
 TITLE Method for screening for agents which increase telomerase activity  
 in a cell  
 JOURNAL Patent: US 5830644-A 52 03-NOV-1998;  
 Location/Qualifiers  
 1. 15  
 /organism="unknown"  
 /mol\_type="unassigned DNA"

Query Match 1.3%; Score 13.4; DB 1; Length 15;  
Best Local Similarity 93.3%; Pred. No. 1.3e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1792 TTGTGTGTGTGTG 1806  
Db 1 TGGTGTGTGTGTG 15

RESULT 221  
LOCUS I51784 15 bp DNA linear PAT 07-OCT-1997  
DEFINITION Sequence 52 from patent US 5645986.  
ACCESSION I51784  
VERSION I51784.1 GI:2472985  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS West, M.D., Harley, C.B., Strahl, C.M., McEachern, M.J., Shay, J.,  
Wright, W.E., Blackburn, E.H. and Vaziri, H.  
TITLE Therapy and diagnosis of conditions related to telomere length  
and/or telomerase activity  
JOURNAL Patent: US 5645986-A 52 08-JUL-1997;  
FEATURES Location/Qualifiers  
1..15  
source /organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.3%; Score 13.4; DB 1; Length 15;  
Best Local Similarity 93.3%; Pred. No. 1.3e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1792 TTGTGTGTGTGTG 1806  
Db 1 TGGTGTGTGTGTG 15

RESULT 222  
LOCUS I84393 15 bp DNA linear PAT 04-APR-1998  
DEFINITION Sequence 51 from patent US 5695932.  
ACCESSION I84393  
VERSION I84393.1 GI:3021913  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS West, M.D., Shay, J., Wright, W., Blackburn, E.H. and McEachern, M.J.  
TITLE Telomerase activity assays for diagnosing pathogenic infections  
JOURNAL Patent: US 5695932-A 51 09-DEC-1997;  
FEATURES Location/Qualifiers  
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source /organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.3%; Score 13.4; DB 1; Length 15;  
Best Local Similarity 93.3%; Pred. No. 1.3e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1792 TTGTGTGTGTGTG 1806  
Db 1 TGGTGTGTGTGTG 15

RESULT 223  
LOCUS AR204601 15 bp DNA linear PAT 20-JUN-2002  
DEFINITION Sequence 51 from patent US 6368789.  
ACCESSION AR204601

VERSION AR204601.1 GI:21501969  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS West, M.D., Shay, J., Wright, W. and Blackburn, E.H.  
TITLE Screening methods to identify inhibitors of telomerase activity  
JOURNAL Patent: US 6368789-A 51 09-APR-2002;  
FEATURES Location/Qualifiers  
1..15  
source /organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.3%; Score 13.4; DB 1; Length 15;  
Best Local Similarity 93.3%; Pred. No. 1.3e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1792 TTGTGTGTGTGTG 1806  
Db 1 TGGTGTGTGTGTG 15

RESULT 224  
LOCUS AR241795/c 15 bp DNA linear PAT 20-DEC-2002  
DEFINITION Sequence 83 from patent US 6472154.  
ACCESSION AR241795  
VERSION AR241795.1 GI:27287607  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Garner, H.R., Wren, J.D., Minna, J.D. and Fondon, J.W. III.  
TITLE Polymorphic repeats in human genes  
JOURNAL Patent: US 6472154-A 83 29-OCT-2002;  
FEATURES Location/Qualifiers  
1..15  
source /organism="unknown"  
/mol\_type="genomic DNA"

Query Match 1.3%; Score 13.4; DB 1; Length 15;  
Best Local Similarity 93.3%; Pred. No. 1.3e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1811 TGTATATATATATAT 1825  
Db 15 TTTATATATATATAT 1

RESULT 225  
LOCUS AR307316 15 bp DNA linear PAT 12-JUN-2003  
DEFINITION Sequence 79 from patent US 6551774.  
ACCESSION AR307316  
VERSION AR307316.1 GI:31697843  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS West, M.D., Harley, C.B., Weinrich, S.L., Strahl, C.M., McEachern, M.J.,  
Shay, J., Wright, W.E., Blackburn, E.H., Kim, N.W. and Vaziri, H.  
TITLE Diagnostic methods for conditions associated with elevated cellular  
levels of telomerase activity  
JOURNAL Patent: US 6551774-A 79 22-APR-2003;  
FEATURES Location/Qualifiers  
1..15  
source /organism="unknown"  
/mol\_type="genomic DNA"

Query Match 1.3%; Score 13.4; DB 1; Length 15;

Best Local Similarity 93.3%; Pred. No. 1.3e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1792 TTGTGTGTGTGTGTG 1806  
Db 1 TGTGTGTGTGTGTG 15

RESULT 226  
AX663411 15 bp DNA PAT 22-MAR-2003  
LOCUS Sequence 37 from Patent WO2097126.  
DEFINITION AX663411  
ACCESSION AX663411  
VERSION AX663411.1 GI:29163751  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM artificial sequences.

REFERENCE 1  
AUTHORS Weizenegger, M.  
TITLE Method for detecting gram-positive bacteria  
JOURNAL Patent: WO 02097126-A 37 05-DEC-2002;  
Hain Lifescience GmbH (DE)  
FEATURES Location/Qualifiers  
source 1..15  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Sonde"

Query Match 1.3%; Score 13.4; DB 1; Length 15;  
Best Local Similarity 93.3%; Pred. No. 1.3e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGT 1807  
Db 1 TGTGTGGTGTGTGT 15

RESULT 227  
AR328665 16 bp RNA PAT 17-AUG-2003  
LOCUS Sequence 6067 from patent US 6566127.  
DEFINITION AR328665  
ACCESSION AR328665  
VERSION AR328665.1 GI:33714473  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 16)  
AUTHORS Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.  
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor  
JOURNAL Patent: US 6566127-A 6067 20-MAY-2003;  
FEATURES Location/Qualifiers  
source 1..16  
/organism="unknown"  
/mol\_type="unassigned RNA"

Query Match 1.3%; Score 13.4; DB 1; Length 16;  
Best Local Similarity 93.3%; Pred. No. 1.5e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1791 ATTGTGTGTGTGTGT 1805  
Db 2 ACTGTGTGTGTGTGT 16

RESULT 228  
AR435926/c 16 bp RNA PAT 18-DEC-2003  
LOCUS Sequence 185 from patent US 6656731.  
DEFINITION AR435926  
ACCESSION AR435926

VERSION AR435926.1 GI:40199010  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 16)  
AUTHORS Eckstein, F., Ludwig, J. and Beigelman, L.  
TITLE Nucleic acid catalysts with endonuclease activity  
JOURNAL Patent: US 6656731-A 185 02-DEC-2003;  
FEATURES Location/Qualifiers  
source 1..16  
/organism="unknown"  
/mol\_type="unassigned RNA"

Query Match 1.3%; Score 13.4; DB 1; Length 16;  
Best Local Similarity 93.3%; Pred. No. 1.5e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGT 1879  
Db 15 TTTTATTTTATTT 1

RESULT 229  
AR046267 17 bp DNA PAT 29-SEP-1999  
LOCUS Sequence 1060 from patent US 5817796.  
DEFINITION AR046267  
ACCESSION AR046267  
VERSION AR046267.1 GI:5967732  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 17)  
AUTHORS Stinchcomb, D.T., Draper, K., McSwiggen, J. and Jarvis, T.  
TITLE C-myb ribozymes having 2'-5'-linked adenylate residues  
JOURNAL Patent: US 5817796-A 1060 06-OCT-1998;  
FEATURES Location/Qualifiers  
source 1..17  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.3%; Score 13.4; DB 1; Length 17;  
Best Local Similarity 93.3%; Pred. No. 1.6e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1813 TATATATATATATAT 1827  
Db 2 TATATATATATATACAT 16

RESULT 230  
I53319 17 bp DNA PAT 07-OCT-1997  
LOCUS Sequence 1060 from patent US 5646042.  
DEFINITION I53319  
ACCESSION I53319  
VERSION I53319.1 GI:2474522  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 17)  
AUTHORS Stinchcomb, D.T., Draper, K., McSwiggen, J. and Jarvis, T.  
TITLE C-myb targeted ribozymes  
JOURNAL Patent: US 5646042-A 1060 08-JUL-1997;  
FEATURES Location/Qualifiers  
source 1..17  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.3%; Score 13.4; DB 1; Length 17;  
Best Local Similarity 93.3%; Pred. No. 1.6e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;



QY 1813 TATATATATATAT 1827  
Db 2 TATATATATACAT 16  
RESULT 231  
AR074716/c 13 bp DNA linear PAT 28-AUG-2000  
LOCUS Sequence 13 from patent US 5955276.  
DEFINITION AR074716  
ACCESSION AR074716.1 GI:10001469  
VERSION AR074716.1  
KEYWORDS Location/Qualifiers  
SOURCE 1. .13  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 13)  
AUTHORS Morgante,M. and Vogel,J.Marie.  
TITLE Compound microsatellite primers for the detection of genetic polymorphisms  
JOURNAL Patent: US 5955276-A 13 21-SEP-1999;  
FEATURES Location/Qualifiers  
source 1. .13  
/organism="unknown"  
/mol\_type="unassigned DNA"  
Query Match 1.2%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02; Mismatches 0; Indels 0; Gaps 0;  
Matches 13; Conservative 0;  
QY 1793 TGTGTGTGTGTGT 1805  
Db 13 TGTGTGTGTGTGT 1  
RESULT 232  
AR074718 13 bp DNA linear PAT 28-AUG-2000  
LOCUS Sequence 15 from patent US 5955276.  
DEFINITION AR074718  
ACCESSION AR074718  
VERSION AR074718.1 GI:10001471  
KEYWORDS Location/Qualifiers  
SOURCE 1. .13  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 13)  
AUTHORS Morgante,M. and Vogel,J.Marie.  
TITLE Compound microsatellite primers for the detection of genetic polymorphisms  
JOURNAL Patent: US 5955276-A 15 21-SEP-1999;  
FEATURES Location/Qualifiers  
source 1. .13  
/organism="unknown"  
/mol\_type="unassigned DNA"  
Query Match 1.2%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02; Mismatches 0; Indels 0; Gaps 0;  
Matches 13; Conservative 0;  
QY 1793 TGTGTGTGTGTGT 1805  
Db 1 TGTGTGTGTGTGT 13  
RESULT 233  
AR199332 13 bp DNA linear PAT 20-APR-2002  
LOCUS Sequence 41 from patent US 6355428.  
DEFINITION AR199332  
ACCESSION AR199332  
VERSION AR199332.1 GI:20249406  
KEYWORDS Location/Qualifiers  
SOURCE 1. .13  
ORGANISM Unknown.

Unclassified.  
REFERENCE 1 (bases 1 to 13)  
AUTHORS Schroth,G.P., Bruce,T.Wayne. and Suh,Y.J.  
TITLE Nucleic acid ligand interaction assays  
JOURNAL Patent: US 6355428-A 41 12-MAR-2002;  
FEATURES Location/Qualifiers  
source 1. .13  
/organism="unknown"  
/mol\_type="unassigned DNA"  
Query Match 1.2%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02; Mismatches 0; Indels 0; Gaps 0;  
Matches 13; Conservative 0;  
QY 1794 GTGTGTGTGTGTG 1806  
Db 1 GTGTGTGTGTGTG 13  
RESULT 234  
AR218382 13 bp DNA linear PAT 25-SEP-2002  
LOCUS Sequence 41 from patent US 6420109.  
DEFINITION AR218382  
ACCESSION AR218382  
VERSION AR218382.1 GI:23319079  
KEYWORDS Location/Qualifiers  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 13)  
AUTHORS Schroth,G.P., Bruce,T.W. and Suh,Y.J.  
TITLE Nucleic acid ligand interaction assays  
JOURNAL Patent: US 6420109-A 41 16-JUL-2002;  
FEATURES Location/Qualifiers  
source 1. .13  
/organism="unknown"  
/mol\_type="genomic DNA"  
Query Match 1.2%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02; Mismatches 0; Indels 0; Gaps 0;  
Matches 13; Conservative 0;  
QY 1794 GTGTGTGTGTGTG 1806  
Db 1 GTGTGTGTGTGTG 13  
RESULT 235  
AR241795 15 bp DNA linear PAT 20-DEC-2002  
LOCUS Sequence 83 from patent US 6472154.  
DEFINITION AR241795  
ACCESSION AR241795  
VERSION AR241795.1 GI:27287607  
KEYWORDS Location/Qualifiers  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Garner,H.R., Wren,J.D., Minna,J.D. and Fondon,J.W. III.  
TITLE Polymorphic repeats in human genes  
JOURNAL Patent: US 6472154-A 83 29-OCT-2002;  
FEATURES Location/Qualifiers  
source 1. .15  
/organism="unknown"  
/mol\_type="genomic DNA"  
Query Match 1.2%; Score 13; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.15e+02; Mismatches 0; Indels 0; Gaps 0;  
Matches 13; Conservative 0;  
QY 1814 ATATATATATATA 1826  
Db 1 ATATATATATATA 13

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RESULT 236
ARI170919
LOCUS          ARI170919          15 bp      DNA          linear          PAT 17-DEC-2001
DEFINITION     Sequence 1 from patent US 6297006.
ACCESSION      ARI170919
VERSION        ARI170919.1  GI:17909869
KEYWORDS       Unknown.
SOURCE         Unknown.
ORGANISM       Unknown.
REFERENCE      1 (bases 1 to 15)
AUTHORS       Drmanac,R.T., Drmanac,S., Hou,A. and Hauser,B.
TITLE         Methods for sequencing repetitive sequences and for determining the
              order of sequence subfragments
JOURNAL       Patent: US 6297006-A 1 02-OCT-2001;
FEATURES      Location/Qualifiers
              1..15
              /organism="unknown"
              /mol_type="unassigned DNA"
Query Match   1.2%; Score 13; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1863 CCTTTTATTTTG 1876
Db 1 CCTTTTNTTTTG 14

RESULT 237
ARI170920/C
LOCUS          ARI170920          15 bp      DNA          linear          PAT 17-DEC-2001
DEFINITION     Sequence 2 from patent US 6297006.
ACCESSION      ARI170920
VERSION        ARI170920.1  GI:17909870
KEYWORDS       Unknown.
SOURCE         Unknown.
ORGANISM       Unknown.
REFERENCE      1 (bases 1 to 15)
AUTHORS       Drmanac,R.T., Drmanac,S., Hou,A. and Hauser,B.
TITLE         Methods for sequencing repetitive sequences and for determining the
              order of sequence subfragments
JOURNAL       Patent: US 6297006-A 2 02-OCT-2001;
FEATURES      Location/Qualifiers
              1..15
              /organism="unknown"
              /mol_type="unassigned DNA"
Query Match   1.2%; Score 13; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1863 CCTTTTATTTTG 1876
Db 1 CCTTTTNTTTTG 14

RESULT 238
ARI175435
LOCUS          ARI175435          15 bp      DNA          linear          PAT 17-DEC-2001
DEFINITION     Sequence 2 from patent US 6309824.
ACCESSION      ARI175435
VERSION        ARI175435.1  GI:17916734
KEYWORDS       Unknown.
SOURCE         Unknown.
ORGANISM       Unknown.
REFERENCE      1 (bases 1 to 15)
AUTHORS       Drmanac,R.T.
TITLE         Methods for analyzing a target nucleic acid using immobilized
              heterogeneous mixtures of oligonucleotide probes
JOURNAL       Patent: US 6309824-A 2 30-OCT-2001;
FEATURES      Location/Qualifiers
              1..15
              /organism="unknown"
              /mol_type="unassigned DNA"
Query Match   1.2%; Score 13; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1863 CCTTTTATTTTG 1876
Db 1 CCTTTTNTTTTG 14

RESULT 239
ARI175436/C
LOCUS          ARI175436          15 bp      DNA          linear          PAT 17-DEC-2001
DEFINITION     Sequence 3 from patent US 6309824.
ACCESSION      ARI175436
VERSION        ARI175436.1  GI:17916735
KEYWORDS       Unknown.
SOURCE         Unknown.
ORGANISM       Unknown.
REFERENCE      1 (bases 1 to 15)
AUTHORS       Drmanac,R.T.
TITLE         Methods for analyzing a target nucleic acid using immobilized
              heterogeneous mixtures of oligonucleotide probes
JOURNAL       Patent: US 6309824-A 3 30-OCT-2001;
FEATURES      Location/Qualifiers
              1..15
              /organism="unknown"
              /mol_type="unassigned DNA"
Query Match   1.2%; Score 13; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1863 CCTTTTATTTTG 1876
Db 1 CCTTTTNTTTTG 14

RESULT 240
I61567/C
LOCUS          I61567            15 bp      DNA          linear          PAT 07-OCT-1997
DEFINITION     Sequence 121 from patent US 5658780.
ACCESSION      I61567
VERSION        I61567.1  GI:2479515
KEYWORDS       Unknown.
SOURCE         Unknown.
ORGANISM       Unknown.
REFERENCE      1 (bases 1 to 15)
AUTHORS       Stinchcomb,D.T., Draper,K.G. and McSwiggen,J.
TITLE         Rel a targeted ribozymes
JOURNAL       Patent: US 5658780-A 121 19-AUG-1997;
FEATURES      Location/Qualifiers
              1..15
              /organism="unknown"
              /mol_type="unassigned DNA"
Query Match   1.2%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2152 TCACCTGGAGCA 2164
Db 15 TCACCTGGAGCA 3
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RESULT 241
I61640/c
LOCUS      161640          15 bp      DNA      linear      PAT 07-OCT-1997
DEFINITION Sequence 194 from patent US 5658780.
ACCESSION  I61640
VERSION     I61640.1  GI:2479588
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 15)
AUTHORS     Stinchcomb,D.T., Draper,K.G. and McSwiggen,J.
TITLE       Rel a targeted ribozymes
JOURNAL     Patent: US 5658780-A 194 19-AUG-1997;
FEATURES    Location/Qualifiers
             1..15
             /organism="unknown"
             /mol_type="unassigned DNA"

Query Match      1.2%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2152 TCACCTGGAGCA 2164
Db      15 TCACCTGGAGCA 3

RESULT 242
I61756/c
LOCUS      161756          15 bp      DNA      linear      PAT 07-OCT-1997
DEFINITION Sequence 310 from patent US 5658780.
ACCESSION  I61756
VERSION     I61756.1  GI:2479704
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 15)
AUTHORS     Stinchcomb,D.T., Draper,K.G. and McSwiggen,J.
TITLE       Rel a targeted ribozymes
JOURNAL     Patent: US 5658780-A 310 19-AUG-1997;
FEATURES    Location/Qualifiers
             1..15
             /organism="unknown"
             /mol_type="unassigned DNA"

Query Match      1.2%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2152 TCACCTGGAGCA 2164
Db      15 TCACCTGGAGCA 3

RESULT 243
AR242245
LOCUS      AR242245          15 bp      DNA      linear      PAT 20-DEC-2002
DEFINITION Sequence 9 from patent US 6472173.
ACCESSION  AR242245
VERSION     AR242245.1  GI:27288069
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 15)
AUTHORS     Ford,J. and Yeung,G.
TITLE       Chemokine receptor obtained from a cdna library of fetal
             liver-spleen
JOURNAL     Patent: US 6472173-A 9 29-OCT-2002;
FEATURES    Location/Qualifiers
             1..15
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             /organism="unknown"
             /mol_type="genomic DNA"

Query Match      1.2%; Score 13; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1863 CCTTTTATTTTG 1876
Db      1 CCTTTTATTTTG 14

RESULT 244
AR242247/c
LOCUS      AR242247          15 bp      DNA      linear      PAT 20-DEC-2002
DEFINITION Sequence 10 from patent US 6472173.
ACCESSION  AR242247
VERSION     AR242247.1  GI:27288070
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 15)
AUTHORS     Ford,J. and Yeung,G.
TITLE       Chemokine receptor obtained from a cdna library of fetal
             liver-spleen
JOURNAL     Patent: US 6472173-A 10 29-OCT-2002;
FEATURES    Location/Qualifiers
             1..15
             /organism="unknown"
             /mol_type="genomic DNA"

Query Match      1.2%; Score 13; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1863 CCTTTTATTTTG 1876
Db      15 CCTTTTATTTTG 2

RESULT 245
AX635886/c
LOCUS      AX635886          15 bp      RNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 3025 from Patent EPI260586.
ACCESSION  AX635886
VERSION     AX635886.1  GI:28471500
KEYWORDS    unidentified
SOURCE      unidentified
ORGANISM    unclassified.
REFERENCE   1
AUTHORS     Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A.,
             Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
             McSwiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
             Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.B. and
             Woolf,T.
TITLE       Method and reagent for inhibiting the expression of disease related
             genes
JOURNAL     Patent: EP 1260586-A 3025 27-NOV-2002;
FEATURES    RIBOZYME PHARMACEUTICALS, INC. (US)
             Location/Qualifiers
             1..15
             /organism="unidentified"
             /mol_type="unassigned RNA"
             /db_xref="taxon:32644"

Query Match      1.2%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2152 TCACCTGGAGCA 2164
Db      15 TCACCTGGAGCA 3
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Db      15 TCACCTGGAAGCA 3

RESULT 246
LOCUS   AX636032/c
DEFINITION Sequence 3171 from Patent EP1260586.
ACCESSION AX636032
VERSION  AX636032.1 GI:28471646
KEYWORDS
SOURCE  unidentified
        unclassified.
REFERENCE
AUTHORS  Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A.,
        Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
        McSwiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
        Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
        Woolf,T.
TITLE    Method and reagent for inhibiting the expression of disease related
        genes
JOURNAL  Patent: EP 1260586-A 3171 27-NOV-2002;
FEATURES
SOURCE  Location/Qualifiers
        1..15
        /organism="unidentified"
        /mol_type="unassigned RNA"
        /db_xref="taxon:32644"

Query Match      1.2%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2152 TCACCTGGAAGCA 2164
      |||||
Db   15 TCACCTGGAAGCA 3

RESULT 247
LOCUS   AX636075/c
DEFINITION Sequence 3214 from Patent EP1260586.
ACCESSION AX636075
VERSION  AX636075.1 GI:28471699
KEYWORDS
SOURCE  unidentified
        unclassified.
REFERENCE
AUTHORS  Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A.,
        Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
        McSwiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
        Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
        Woolf,T.
TITLE    Method and reagent for inhibiting the expression of disease related
        genes
JOURNAL  Patent: EP 1260586-A 3214 27-NOV-2002;
FEATURES
SOURCE  Location/Qualifiers
        1..15
        /organism="unidentified"
        /mol_type="unassigned RNA"
        /db_xref="taxon:32644"

Query Match      1.2%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2152 TCACCTGGAAGCA 2164
      |||||
Db   15 TCACCTGGAAGCA 3

RESULT 248
LOCUS   AR435858
DEFINITION Sequence 117 from patent US 6856731.
ACCESSION AR435858
VERSION  AR435858.1 GI:40198942
KEYWORDS
SOURCE  Unknown.
        Unclassified.
REFERENCE
AUTHORS  Eckstein,F., Ludwig,J. and Beigelman,L.
TITLE    Nucleic acid catalysts with endonuclease activity
JOURNAL  Patent: US 6856731-A 117 02-DEC-2003;
FEATURES
SOURCE  Location/Qualifiers
        1..16
        /organism="unknown"
        /mol_type="unassigned RNA"

Query Match      1.2%; Score 13; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2268 TTTTTCCTATAAA 2280
      |||||
Db   1 TTTTTCCTATAAA 13

RESULT 249
LOCUS   AR027678
DEFINITION Sequence 15 from patent US 5856435.
ACCESSION AR027678
VERSION  AR027678.1 GI:5938498
KEYWORDS
SOURCE  Unknown.
        Unclassified.
REFERENCE
AUTHORS  Bazile,D., Emile,C., Helene,C. and Spenlehauer,G.
TITLE    Nucleic acid-containing composition, its preparation and use
JOURNAL  Patent: US 5856435-A 15 05-JAN-1999;
FEATURES
SOURCE  Location/Qualifiers
        1..16
        /organism="unknown"
        /mol_type="unassigned DNA"

Query Match      1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  1865 TTTTTCCTATAAA 1880
      |||||
Db   1 TTTTTCCTATAAA 16

RESULT 250
LOCUS   AR037355
DEFINITION Sequence 2 from patent US 5801155.
ACCESSION AR037355
VERSION  AR037355.1 GI:5955211
KEYWORDS
SOURCE  Unknown.
        Unclassified.
REFERENCE
AUTHORS  Kutvavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
TITLE    Covalently linked oligonucleotide minor groove binder conjugates
JOURNAL  Patent: US 5801155-A 2 01-SEP-1998;
FEATURES
SOURCE  Location/Qualifiers
        1..16
        /organism="unknown"

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RESULT 248
LOCUS   AR435858
DEFINITION Sequence 117 from patent US 6856731.
ACCESSION AR435858
VERSION  AR435858.1 GI:40198942
KEYWORDS
SOURCE  Unknown.
        Unclassified.
REFERENCE
AUTHORS  Eckstein,F., Ludwig,J. and Beigelman,L.
TITLE    Nucleic acid catalysts with endonuclease activity
JOURNAL  Patent: US 6856731-A 117 02-DEC-2003;
FEATURES
SOURCE  Location/Qualifiers
        1..16
        /organism="unknown"
        /mol_type="unassigned RNA"

Query Match      1.2%; Score 13; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2268 TTTTTCCTATAAA 2280
      |||||
Db   1 TTTTTCCTATAAA 13

RESULT 249
LOCUS   AR027678
DEFINITION Sequence 15 from patent US 5856435.
ACCESSION AR027678
VERSION  AR027678.1 GI:5938498
KEYWORDS
SOURCE  Unknown.
        Unclassified.
REFERENCE
AUTHORS  Bazile,D., Emile,C., Helene,C. and Spenlehauer,G.
TITLE    Nucleic acid-containing composition, its preparation and use
JOURNAL  Patent: US 5856435-A 15 05-JAN-1999;
FEATURES
SOURCE  Location/Qualifiers
        1..16
        /organism="unknown"
        /mol_type="unassigned DNA"

Query Match      1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  1865 TTTTTCCTATAAA 1880
      |||||
Db   1 TTTTTCCTATAAA 16

RESULT 250
LOCUS   AR037355
DEFINITION Sequence 2 from patent US 5801155.
ACCESSION AR037355
VERSION  AR037355.1 GI:5955211
KEYWORDS
SOURCE  Unknown.
        Unclassified.
REFERENCE
AUTHORS  Kutvavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
TITLE    Covalently linked oligonucleotide minor groove binder conjugates
JOURNAL  Patent: US 5801155-A 2 01-SEP-1998;
FEATURES
SOURCE  Location/Qualifiers
        1..16
        /organism="unknown"

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/mol_type="unassigned DNA"

Query Match      1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTT 1880
DB 1 TTTTATTTTGTGTTT 16

RESULT 251
AR104584/c      16 bp      DNA
LOCUS          AR104584
DEFINITION     Sequence 131 from patent US 6093809.
ACCESSION      AR104584
VERSION        AR104584.1 GI:12817292
KEYWORDS       Unknown.
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 16)
AUTHORS       Cech,T.R. and Lingner,J.
TITLE         Telomerase
JOURNAL       Patent: US 6093809-A 131 25-JUL-2000;
FEATURES       Location/Qualifiers
                source
                1..16
                /organism="unknown"
                /mol_type="unassigned DNA"

Query Match      1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTT 1880
DB 16 TTTTATTTTGTGTTT 1

RESULT 252
AR175845/c      16 bp      DNA
LOCUS          AR175845
DEFINITION     Sequence 131 from patent US 6309867.
ACCESSION      AR175845
VERSION        AR175845.1 GI:17917144
KEYWORDS       Unknown.
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 16)
AUTHORS       Cech,T.R. and Nakamura,T.
TITLE         Telomerase
JOURNAL       Patent: US 6309867-A 131 30-OCT-2001;
FEATURES       Location/Qualifiers
                source
                1..16
                /organism="unknown"
                /mol_type="unassigned DNA"

Query Match      1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTT 1880
DB 16 TTTTATTTTGTGTTT 1

RESULT 253
E32226/c        16 bp      DNA
LOCUS          E32226
DEFINITION     Method for isolating satellite sequence.
ACCESSION      E32226
VERSION        E32226.1 GI:13021862
KEYWORDS       
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```
KEYWORDS       JP 2000060559-A/28.
SOURCE         Haliotis discus discus
ORGANISM       Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
                Vetigastropoda; Haliotoidea; Haliotidae; Haliotis.
REFERENCE      Hideaki,T. and Masashi,S.
                Method for isolating satellite sequence
                Patent: JP 2000060559-A 28 29-FEB-2000;
                NATL INST OF AGROBIOLOGICAL RESOURCES
COMMENT        OS Haliotis discus discus
                PN JP 2000060559-A/28
                PD 29-FEB-2000
                PF 18-AUG-1998 JP 1998232153
                PR HIDEAKI TAKAHASHI,MASASHI SEKINO
                PC C12N15/09,C12Q1/68,C12N15/00
                CC CC
                FH Key
                FT source
                Location/Qualifiers
                1..16
                /organism="Haliotis discus discus"
                /mol_type="genomic DNA"
                /sub_species="discus"
                /db_xref="taxon:91233"

Query Match      1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTG 1808
DB 16 TCTCTGTGTGTGTG 1

RESULT 254
I38676          16 bp      DNA
LOCUS          I38676
DEFINITION     Sequence 36 from patent US 5614617.
ACCESSION      I38676
VERSION        I38676.1 GI:2084730
KEYWORDS       Unknown.
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 16)
AUTHORS       Cook,P.D. and Sanghvi,Y.S.
TITLE         Nuclease resistant, pyrimidine modified oligonucleotides that
                detect and modulate gene expression
                Patent: US 5614617-A 36 25-MAR-1997;
JOURNAL
FEATURES       Location/Qualifiers
                source
                1..16
                /organism="unknown"
                /mol_type="unassigned DNA"

Query Match      1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTT 1880
DB 1 TTTTATTTTGTGTTT 16

RESULT 255
I38682          16 bp      DNA
LOCUS          I38682
DEFINITION     Sequence 42 from patent US 5614617.
ACCESSION      I38682
VERSION        I38682.1 GI:2084736
KEYWORDS       
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SOURCE  
ORGANISM  
Unknown.  
Unclassified.  
REFERENCE  
1 (bases 1 to 16)  
AUTHORS  
Cook,P.D. and Sanghvi,Y.S.  
TITLE  
Nuclease resistant, pyrimidine modified oligonucleotides that  
detect and modulate gene expression  
JOURNAL  
Patent: US 5614617-A 42 25-MAR-1997;  
FEATURES  
Location/Qualifiers  
1..16  
/organism="unknown"  
/mol\_type="unassigned DNA"  
Query Match 1.2%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 1.7e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1865 TTTTATTTTGTGTTT 1880  
Db 1 TTTTATTTTGTGTTT 16  
RESULT 256  
LOCUS I38700 16 bp DNA linear PAT 13-MAY-1997  
DEFINITION  
Sequence 60 from patent US 5614617.  
ACCESSION I38700  
VERSION I38700.1 GI:2084754  
KEYWORDS  
Unknown.  
ORGANISM  
Unknown.  
Unclassified.  
REFERENCE  
1 (bases 1 to 16)  
AUTHORS  
Cook,P.D. and Sanghvi,Y.S.  
TITLE  
Nuclease resistant, pyrimidine modified oligonucleotides that  
detect and modulate gene expression  
JOURNAL  
Patent: US 5614617-A 60 25-MAR-1997;  
FEATURES  
Location/Qualifiers  
1..16  
/organism="unknown"  
/mol\_type="unassigned DNA"  
Query Match 1.2%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 1.7e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1865 TTTTATTTTGTGTTT 1880  
Db 1 TTTTATTTTGTGTTT 16  
RESULT 257  
LOCUS AR221692 16 bp DNA linear PAT 26-SEP-2002  
DEFINITION  
Sequence 2 from patent US 6426408.  
ACCESSION AR221692  
VERSION AR221692.1 GI:23328764  
KEYWORDS  
Unknown.  
ORGANISM  
Unknown.  
Unclassified.  
REFERENCE  
1 (bases 1 to 16)  
AUTHORS  
Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.  
TITLE  
Covalently linked oligonucleotide minor groove binder conjugates  
JOURNAL  
Patent: US 6426408-A 2 30-JUL-2002;  
FEATURES  
Location/Qualifiers  
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/mol\_type="genomic DNA"  
Query Match 1.2%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 1.7e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1865 TTTTATTTTGTGTTT 1880  
Db 1 TTTTATTTTGTGTTT 16  
RESULT 258  
LOCUS AR222462 16 bp DNA linear PAT 26-SEP-2002  
DEFINITION  
Sequence 22 from patent US 6429300.  
ACCESSION AR222462  
VERSION AR222462.1 GI:23329993  
KEYWORDS  
Unknown.  
ORGANISM  
Unknown.  
Unclassified.  
REFERENCE  
1 (bases 1 to 16)  
AUTHORS  
Kurz,M., Lohse,P. and Wagner,R.  
TITLE  
Peptide acceptor ligation methods  
JOURNAL  
Patent: US 6429300-A 22 06-AUG-2002;  
FEATURES  
Location/Qualifiers  
1..16  
/organism="unknown"  
/mol\_type="genomic DNA"  
Query Match 1.2%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 1.7e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1865 TTTTATTTTGTGTTT 1880  
Db 1 TTTTATTTTGTGTTT 16  
RESULT 259  
LOCUS AR257437 16 bp DNA linear PAT 20-DEC-2002  
DEFINITION  
Sequence 2 from patent US 6486308.  
ACCESSION AR257437  
VERSION AR257437.1 GI:27307448  
KEYWORDS  
Unknown.  
ORGANISM  
Unknown.  
Unclassified.  
REFERENCE  
1 (bases 1 to 16)  
AUTHORS  
Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.  
TITLE  
Covalently linked oligonucleotide minor groove binder conjugates  
JOURNAL  
Patent: US 6486308-A 2 26-NOV-2002;  
FEATURES  
Location/Qualifiers  
1..16  
/organism="unknown"  
/mol\_type="genomic DNA"  
Query Match 1.2%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 1.7e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1865 TTTTATTTTGTGTTT 1880  
Db 1 TTTTATTTTGTGTTT 16  
RESULT 260  
LOCUS AR328670 16 bp RNA linear PAT 17-AUG-2003  
DEFINITION  
Sequence 6072 from patent US 6566127.  
ACCESSION AR328670  
VERSION AR328670.1 GI:33714478  
KEYWORDS  
Unknown.  
ORGANISM  
Unknown.  
Unclassified.  
REFERENCE  
1 (bases 1 to 16)

SOURCE  
ORGANISM  
Unknown.  
Unclassified.  
REFERENCE  
1 (bases 1 to 16)  
AUTHORS  
Cook,P.D. and Sanghvi,Y.S.  
TITLE  
Nuclease resistant, pyrimidine modified oligonucleotides that  
detect and modulate gene expression  
JOURNAL  
Patent: US 5614617-A 42 25-MAR-1997;  
FEATURES  
Location/Qualifiers  
1..16  
/organism="unknown"  
/mol\_type="unassigned DNA"  
Query Match 1.2%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 1.7e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1865 TTTTATTTTGTGTTT 1880  
Db 1 TTTTATTTTGTGTTT 16  
RESULT 256  
LOCUS I38700 16 bp DNA linear PAT 13-MAY-1997  
DEFINITION  
Sequence 60 from patent US 5614617.  
ACCESSION I38700  
VERSION I38700.1 GI:2084754  
KEYWORDS  
Unknown.  
ORGANISM  
Unknown.  
Unclassified.  
REFERENCE  
1 (bases 1 to 16)  
AUTHORS  
Cook,P.D. and Sanghvi,Y.S.  
TITLE  
Nuclease resistant, pyrimidine modified oligonucleotides that  
detect and modulate gene expression  
JOURNAL  
Patent: US 5614617-A 60 25-MAR-1997;  
FEATURES  
Location/Qualifiers  
1..16  
/organism="unknown"  
/mol\_type="unassigned DNA"  
Query Match 1.2%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 1.7e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1865 TTTTATTTTGTGTTT 1880  
Db 1 TTTTATTTTGTGTTT 16  
RESULT 257  
LOCUS AR221692 16 bp DNA linear PAT 26-SEP-2002  
DEFINITION  
Sequence 2 from patent US 6426408.  
ACCESSION AR221692  
VERSION AR221692.1 GI:23328764  
KEYWORDS  
Unknown.  
ORGANISM  
Unknown.  
Unclassified.  
REFERENCE  
1 (bases 1 to 16)  
AUTHORS  
Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.  
TITLE  
Covalently linked oligonucleotide minor groove binder conjugates  
JOURNAL  
Patent: US 6426408-A 2 30-JUL-2002;  
FEATURES  
Location/Qualifiers  
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/mol\_type="genomic DNA"  
Query Match 1.2%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 1.7e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1865 TTTTATTTTGTGTTT 1880  
Db 1 TTTTATTTTGTGTTT 16  
RESULT 258  
LOCUS AR222462 16 bp DNA linear PAT 26-SEP-2002  
DEFINITION  
Sequence 22 from patent US 6429300.  
ACCESSION AR222462  
VERSION AR222462.1 GI:23329993  
KEYWORDS  
Unknown.  
ORGANISM  
Unknown.  
Unclassified.  
REFERENCE  
1 (bases 1 to 16)  
AUTHORS  
Kurz,M., Lohse,P. and Wagner,R.  
TITLE  
Peptide acceptor ligation methods  
JOURNAL  
Patent: US 6429300-A 22 06-AUG-2002;  
FEATURES  
Location/Qualifiers  
1..16  
/organism="unknown"  
/mol\_type="genomic DNA"  
Query Match 1.2%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 1.7e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1865 TTTTATTTTGTGTTT 1880  
Db 1 TTTTATTTTGTGTTT 16  
RESULT 259  
LOCUS AR257437 16 bp DNA linear PAT 20-DEC-2002  
DEFINITION  
Sequence 2 from patent US 6486308.  
ACCESSION AR257437  
VERSION AR257437.1 GI:27307448  
KEYWORDS  
Unknown.  
ORGANISM  
Unknown.  
Unclassified.  
REFERENCE  
1 (bases 1 to 16)  
AUTHORS  
Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.  
TITLE  
Covalently linked oligonucleotide minor groove binder conjugates  
JOURNAL  
Patent: US 6486308-A 2 26-NOV-2002;  
FEATURES  
Location/Qualifiers  
1..16  
/organism="unknown"  
/mol\_type="genomic DNA"  
Query Match 1.2%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 1.7e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1865 TTTTATTTTGTGTTT 1880  
Db 1 TTTTATTTTGTGTTT 16  
RESULT 260  
LOCUS AR328670 16 bp RNA linear PAT 17-AUG-2003  
DEFINITION  
Sequence 6072 from patent US 6566127.  
ACCESSION AR328670  
VERSION AR328670.1 GI:33714478  
KEYWORDS  
Unknown.  
ORGANISM  
Unknown.  
Unclassified.  
REFERENCE  
1 (bases 1 to 16)

AUTHORS Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.  
 TITLE Method and reagent for the treatment of diseases or conditions  
 related to levels of vascular endothelial growth factor receptor  
 JOURNAL Patent: US 6566127-A 6072 20-MAY-2003;  
 FEATURES Location/Qualifiers

source  
 1..16  
 /organism="unknown"  
 /mol\_type="unassigned RNA"

Query Match 1.2%; Score 12.8; DB 1; Length 16;  
 Best Local Similarity 87.5%; Pred. No. 1.7e+02;  
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1794 GGTGTGTGTGTGTGT 1809  
 Db 1 GTGTGTGGGTGTGGGT 16

RESULT 261  
 AR328672 16 bp RNA linear PAT 17-AUG-2003  
 LOCUS  
 DEFINITION Sequence 6074 from patent US 6566127.  
 ACCESSION AR328672  
 VERSION AR328672.1 GI:33714480  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 16)  
 AUTHORS Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.  
 TITLE Method and reagent for the treatment of diseases or conditions  
 related to levels of vascular endothelial growth factor receptor  
 JOURNAL Patent: US 6566127-A 6074 20-MAY-2003;  
 FEATURES Location/Qualifiers

source  
 1..16  
 /organism="unknown"  
 /mol\_type="unassigned RNA"

Query Match 1.2%; Score 12.8; DB 1; Length 16;  
 Best Local Similarity 87.5%; Pred. No. 1.7e+02;  
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1794 GGTGTGTGTGTGTGT 1809  
 Db 1 GTGGGTGTGTGTGTGT 16

RESULT 262  
 AR436263 16 bp RNA linear PAT 18-DEC-2003  
 LOCUS  
 DEFINITION Sequence 522 from patent US 6656731.  
 ACCESSION AR436263  
 VERSION AR436263.1 GI:40199347  
 KEYWORDS  
 SOURCE Unknown.

REFERENCE 1 (bases 1 to 16)  
 AUTHORS Eckstein, F., Ludwig, J. and Beigelman, L.  
 TITLE Nucleic acid catalysts with endonuclease activity  
 JOURNAL Patent: US 6656731-A 522 02-DEC-2003;  
 FEATURES Location/Qualifiers

source  
 1..16  
 /organism="unknown"  
 /mol\_type="unassigned RNA"

Query Match 1.2%; Score 12.8; DB 1; Length 16;  
 Best Local Similarity 87.5%; Pred. No. 1.7e+02;  
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1832 AGTTATCTAGTTAAT 1847  
 Db 1 AGTTATGTATGTTAAT 16

RESULT 263  
 AX039049/c 16 bp DNA linear PAT 16-NOV-2000  
 LOCUS  
 DEFINITION Sequence 2 from Patent WO0061594.  
 ACCESSION AX039049  
 VERSION AX039049.1 GI:11228345  
 KEYWORDS  
 SOURCE synthetic construct  
 ORGANISM synthetic construct  
 artificial sequences.

REFERENCE 1  
 AUTHORS Beier, M. and Hchelsel, J.  
 TITLE Nucleoside derivatives with photo-unstable protective groups  
 JOURNAL Patent: WO 0061594-A 2 19-OCT-2000;  
 DEUTSCHES KREBSFORSCH (DE); BEIER MARKUS (DE); HOHEISEL JOERG (DE)

FEATURES Location/Qualifiers  
 source  
 1..16  
 /organism="synthetic construct"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:32630"  
 /note="Oligonucleotide"

Query Match 1.2%; Score 12.8; DB 1; Length 16;  
 Best Local Similarity 87.5%; Pred. No. 1.7e+02;  
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTT 1880  
 Db 16 TTTTATTTTGTGTTT 1

RESULT 264  
 AX135448/c 16 bp DNA linear PAT 29-MAY-2001  
 LOCUS  
 DEFINITION Sequence 5 from Patent EP1113080.  
 ACCESSION AX135448  
 VERSION AX135448.1 GI:14271796  
 KEYWORDS  
 SOURCE synthetic construct  
 ORGANISM synthetic construct  
 artificial sequences.

REFERENCE 1  
 AUTHORS Wang, X.B.  
 TITLE Personal gene library  
 JOURNAL Patent: EP 1113080-A 5 04-JUL-2001;  
 Wang, Xiao Bing (US); Morisawa, Shinkatsu (JP)

FEATURES Location/Qualifiers  
 source  
 1..16  
 /organism="synthetic construct"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:32630"  
 /note="Oligonucleotide primer"

Query Match 1.2%; Score 12.8; DB 1; Length 16;  
 Best Local Similarity 87.5%; Pred. No. 1.7e+02;  
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2130 TCTATATAGCTGATCA 2145  
 Db 16 TCTACAGAGCTGATCA 1

RESULT 265  
 AX235176 16 bp DNA linear PAT 11-SEP-2001  
 LOCUS  
 DEFINITION Sequence 9 from Patent WO0163282.  
 ACCESSION AX235176  
 VERSION AX235176.1 GI:15593767  
 KEYWORDS  
 SOURCE synthetic construct

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ORGANISM    synthetic construct
KEYWORDS    artificial sequences.
REFERENCE   1
AUTHORS     Cuzin,M., Pettie,P., Fontecave,M., Decout,J.L. and Dueyimes,C.
TITLE       Analysis of biological targets using a biochip comprising a
            fluorescent marker
JOURNAL     Patent: WO 0163282-A 9 30-AUG-2001;
            COMMISSARIAT A L'ENERGIE ATOMIQUE (FR)
FEATURES    Location/Qualifiers
            1..16
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="sequence synthetic"

Query Match      1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1865 TTTTATTGTTT 1880
Db 1 TTTTATTGTTT 16

RESULT 266
BD16420/c
LOCUS      16 bp DNA linear PAT 27-AUG-2002
DEFINITION Personal gene library.
ACCESSION  BD016420
VERSION     BD016420.1 GI:22557558
KEYWORDS    JP 2001186882-A/5.
SOURCE      unidentified
            unclassified.
ORGANISM    Wang,X
REFERENCE   1 (bases 1 to 16)
AUTHORS     Personal gene library
TITLE       Patent: JP 2001186882-A 5 10-JUL-2001;
            XIAOBING WANG,SHINKATSU MORISAWA
JOURNAL     OS Unidentified
COMMENT     PN JP 2001186882-A/5
            PD 10-JUL-2001
            PF 17-NOV-2000 JP 2000350702
            PR 01-DEC-1999 US 60/168297,09-NOV-2000 US 09/708493 PI
            XIAOBING WANG
            PC C12N15/09,C12N15/09,C12M1/00,C12Q1/68,C12N15/00,C12N15/00 CC
            Strandedness: Single;
            CC Topology: Linear;
            CC Personal gene library
            FH Key Location/Qualifiers
            FT source 1..16
            /organism="Unidentified".

FEATURES    Location/Qualifiers
            1..16
            /organism="unidentified"
            /mol_type="genomic DNA"
            /db_xref="taxon:32644"

Query Match      1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2130 TCTATATAGCTGATCA 2145
Db 16 TCTACAGGCTGATCA 1

RESULT 267
BD167413/c
LOCUS      15 bp DNA linear PAT 17-JAN-2003
DEFINITION Surface-roughened slide glass and method of analyzing biological
            substance using the same.
ACCESSION  BD167413

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VERSION     BD167413.1 GI:27873225
KEYWORDS    JP 2002211954-A/1.
SOURCE      unidentified
            unclassified.
REFERENCE   1 (bases 1 to 16)
AUTHORS     Okamura,H., Tanga,M., Oba,M., Yamakawa,K. and Takagi,K.
TITLE       Surface-roughened slide glass and method of analyzing biological
            substance using the same
JOURNAL     Patent: JP 2002211954-A 1 31-JUL-2002;
            TOYO KOHAN CO LTD
            OS Artificial Sequence
            PN JP 2002211954-A/1
            PD 31-JUL-2002
            PF 30-OCT-2001 JP 2001332778
            PI HIROSHI OKAMURA,MICHIFUMI TANGA,MITSUYOSHI OBA,KAORU YAMAKAWA,
            KENICHI TAKAGI
            PC C03C15/00,C03C17/245,C12M1/00,C12N11/14,C12N15/09,C12N15/09,
            C12Q1/68,
            PC GO1N33/53,GO1N33/53,GO1N37/00,C12N15/00,C12N15/00 CC
            Surface-roughened slide glass and method of analyzing CC
            biological substance
            CC using the same
            FH Key Location/Qualifiers
            FT source 1..16
            /organism="Artificial Sequence".

FEATURES    Location/Qualifiers
            1..16
            /organism="unidentified"
            /mol_type="genomic DNA"
            /db_xref="taxon:32644"

Query Match      1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1865 TTTTATTGTTT 1880
Db 16 TTTTATTGTTT 1

RESULT 268
BD167414/c
LOCUS      16 bp DNA linear PAT 17-JAN-2003
DEFINITION Surface-roughened slide glass and method of analyzing biological
            substance using the same.
ACCESSION  BD167414
VERSION     BD167414.1 GI:27873226
KEYWORDS    JP 2002211954-A/2.
SOURCE      unidentified
            unclassified.
ORGANISM    1 (bases 1 to 16)
REFERENCE   1 (bases 1 to 16)
AUTHORS     Okamura,H., Tanga,M., Oba,M., Yamakawa,K. and Takagi,K.
TITLE       Surface-roughened slide glass and method of analyzing biological
            substance using the same
JOURNAL     Patent: JP 2002211954-A 2 31-JUL-2002;
            TOYO KOHAN CO LTD
            OS Artificial Sequence
            PN JP 2002211954-A/2
            PD 31-JUL-2002
            PF 30-OCT-2001 JP 2001332778
            PI HIROSHI OKAMURA,MICHIFUMI TANGA,MITSUYOSHI OBA,KAORU YAMAKAWA,
            KENICHI TAKAGI
            PC C03C15/00,C03C17/245,C12M1/00,C12N11/14,C12N15/09,C12N15/09,
            C12Q1/68,
            PC GO1N33/53,GO1N33/53,GO1N37/00,C12N15/00,C12N15/00 CC
            Surface-roughened slide glass and method of analyzing CC
            biological substance
            CC using the same
            FH Key Location/Qualifiers
            FT source 1..16
            /organism="Artificial Sequence".

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FEATURES
  source
    Location/Qualifiers
      1..16
        /organism="unidentified"
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        /db_xref="taxon:32644"
    Query Match
      1.2%; Score 12.8; DB 1; Length 16;
    Best Local Similarity
      87.5%; Pred. No. 1.7e+02;
    Matches
      14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1865 TTTTATTTTGTGTTT 1880
Db 16 TTTTATTTTGTGTTT 1

RESULT 269
AR046265 AR046265 17 bp DNA linear PAT 29-SEP-1999
LOCUS
DEFINITION Sequence 1058 from patent US 5817796.
ACCESSION AR046265
VERSION AR046265.1 GI:5967730
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE
  1 (bases 1 to 17)
  AUTHORS Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
  TITLE C-myb ribozymes having 2'-5'-linked adenylate residues
  JOURNAL Patent: US 5817796-A 1058 06-OCT-1998;
  FEATURES
    Location/Qualifiers
      1..17
        /organism="unknown"
        /mol_type="unassigned DNA"
    Query Match
      1.2%; Score 12.8; DB 1; Length 17;
    Best Local Similarity
      87.5%; Pred. No. 1.8e+02;
    Matches
      14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1811 TGTATATATATATA 1826
Db 2 TTTATATATATATA 17

RESULT 270
AR050988 AR050988 14 bp DNA linear PAT 29-SEP-1999
LOCUS
DEFINITION Sequence 57 from patent US 5830644.
ACCESSION AR050988
VERSION AR050988.1 GI:5974352
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE
  1 (bases 1 to 14)
  AUTHORS West,M.D., Shay,J. and Wright,W.E.
  TITLE Method for screening for agents which increase telomerase activity
  JOURNAL Patent: US 5830644-A 57 03-NOV-1998;
  FEATURES
    Location/Qualifiers
      1..14
        /organism="unknown"
        /mol_type="unassigned DNA"
    Query Match
      1.2%; Score 12.4; DB 1; Length 14;
    Best Local Similarity
      92.9%; Pred. No. 1.6e+02;
    Matches
      13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTGTG 1806
Db 1 TGGGTGTGTGTGTG 14

RESULT 273
AR050988 AR050988 14 bp DNA linear PAT 07-OCT-1997
LOCUS
DEFINITION Sequence 57 from patent US 5645986.
ACCESSION AR050988
VERSION AR050988.1 GI:2472990
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE
  1 (bases 1 to 14)
  AUTHORS West,M.D., Harley,C.B., Strahl,C.M., McEachern,M.J., Shay,J.,

```

```

LOCUS
DEFINITION Sequence 60 from Patent WO0211674.
ACCESSION AX578222
VERSION AX578222.1 GI:27647424
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
  1
  AUTHORS Thompson,J., McSwiggen,J., McKenzie,T., Ayers,D., Szymkowski,D.E.
  TITLE Method and reagent for the inhibition of calcium activated chloride
  JOURNAL Patent: WO 0211674-A 60 14-FEB-2002;
  FEATURES
    Location/Qualifiers
      1..17
        /organism="Homo sapiens"
        /mol_type="unassigned RNA"
        /db_xref="taxon:9606"
    Query Match
      1.2%; Score 12.8; DB 1; Length 17;
    Best Local Similarity
      87.5%; Pred. No. 1.8e+02;
    Matches
      14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1807 TGTGTGTATATATA 1822
Db 2 TATCTGTATATATA 17

RESULT 272
AR050988 AR050988 14 bp DNA linear PAT 29-SEP-1999
LOCUS
DEFINITION Sequence 57 from patent US 5830644.
ACCESSION AR050988
VERSION AR050988.1 GI:5974352
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE
  1 (bases 1 to 14)
  AUTHORS West,M.D., Shay,J. and Wright,W.E.
  TITLE Method for screening for agents which increase telomerase activity
  JOURNAL Patent: US 5830644-A 57 03-NOV-1998;
  FEATURES
    Location/Qualifiers
      1..14
        /organism="unknown"
        /mol_type="unassigned DNA"
    Query Match
      1.2%; Score 12.4; DB 1; Length 14;
    Best Local Similarity
      92.9%; Pred. No. 1.6e+02;
    Matches
      13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTGTG 1806
Db 1 TGGGTGTGTGTGTG 14

RESULT 273
AR050988 AR050988 14 bp DNA linear PAT 07-OCT-1997
LOCUS
DEFINITION Sequence 57 from patent US 5645986.
ACCESSION AR050988
VERSION AR050988.1 GI:2472990
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE
  1 (bases 1 to 14)
  AUTHORS West,M.D., Harley,C.B., Strahl,C.M., McEachern,M.J., Shay,J.,

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Wright, W.E., Blackburn, E.H. and Vaziri, H.
Therapy and diagnosis of conditions related to telomere length
and/or telomerase activity
JOURNAL Patent: US 5645986-A 57 08-JUL-1997;
FEATURES Location/Qualifiers
SOURCE 1..14
/mol_type="unassigned DNA"

Query Match 1.2%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 1.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTGTG 1806
Db 1 TGGGTGTGTGTGTG 14

RESULT 274
184398 I84398 14 bp DNA linear PAT 04-APR-1998
LOCUS
DEFINITION Sequence 56 from patent US 5695932.
ACCESSION I84398
VERSION I84398.1 GI:3021918
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 14)
AUTHORS West, M.D., Shay, J., Wright, W., Blackburn, E.H. and McEachern, M.J.
TITLE Telomerase activity assays for diagnosing pathogenic infections
JOURNAL Patent: US 5695932-A 56 09-DEC-1997;
FEATURES Location/Qualifiers
SOURCE 1..14
/mol_type="unassigned DNA"

Query Match 1.2%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 1.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTGTG 1806
Db 1 TGGGTGTGTGTGTG 14

RESULT 275
AR204606 I84398 14 bp DNA linear PAT 20-JUN-2002
LOCUS
DEFINITION Sequence 56 from patent US 6368789.
ACCESSION AR204606
VERSION AR204606.1 GI:21501975
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 14)
AUTHORS West, M.D., Shay, J., Wright, W. and Blackburn, E.H.
TITLE Screening methods to identify inhibitors of telomerase activity
JOURNAL Patent: US 6368789-A 56 09-APR-2002;
FEATURES Location/Qualifiers
SOURCE 1..14
/mol_type="unassigned DNA"

Query Match 1.2%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 1.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTGTG 1806
Db 1 TGGGTGTGTGTGTG 14

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RESULT 276
AR307315 I84398 14 bp DNA linear PAT 12-JUN-2003
LOCUS
DEFINITION Sequence 78 from patent US 6551774.
ACCESSION AR307315
VERSION AR307315.1 GI:31697842
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 14)
AUTHORS West, M.D., Harley, C.B., Weinrich, S.L., Strahl, C.M., McEachern, M.J.,
Shay, J., Wright, W.E., Blackburn, E.H., Kim, N.W. and Vaziri, H.
TITLE Diagnostic methods for conditions associated with elevated cellular
levels of telomerase activity
JOURNAL Patent: US 6551774-A 78 22-APR-2003;
FEATURES Location/Qualifiers
SOURCE 1..14
/mol_type="genomic DNA"

Query Match 1.2%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 1.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTGTG 1806
Db 1 TGGGTGTGTGTGTG 14

RESULT 277
BD185612 I84398 14 bp DNA linear PAT 17-JUN-2003
LOCUS
DEFINITION Analyses of double stranded nucleic acid using scanning probe
microscope.
ACCESSION BD185612
VERSION BD185612.1 GI:31877812
KEYWORDS Synthetic construct
SOURCE Synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 14)
AUTHORS Takeuchi, M.
TITLE Analyses of double stranded nucleic acid using scanning probe
JOURNAL Patent: JP 2002360300-A 1 17-DEC-2002;
COMMENT OLYMPUS OPTICAL CO LTD
OS Artificial Sequence
PN JP 2002360300-A/1
PD 17-DEC-2002
PF 06-JUN-2001 JP 2001171590
PI MINORU TAKEUCHI
PC C13Q1/68, C12N15/09, G01N33/483, G01N33/50, C12N15/00 CC
ANALYSES OF DOUBLE STRANDED NUCLEIC ACID USING SCANNING PROBE CC
FEATURES Location/Qualifiers
SOURCE FH Key Location/Qualifiers
FT source 1..14
/mol_type="Artificial Sequence"

Query Match 1.2%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 1.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTGTG 1806
Db 1 TGGGTGTGTGTGTG 14

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RESULT 278
BD185613/c
LOCUS      BD185613      14 bp      DNA      linear      PAT 17-JUN-2003
DEFINITION Analyzeys of double stranded nucleic acid using scanning probe
            microscope.
ACCESSION  BD185613
VERSION    BD185613.1 GI:31877813
KEYWORDS  JP 2002360300-A/2.
SOURCE    synthetic construct
ORGANISM  artificial sequences.
REFERENCE  1 (bases 1 to 14)
AUTHORS   Takeuchi, M.
TITLE     Analyzeys of double stranded nucleic acid using scanning probe
JOURNAL   Patent: JP 2002360300-A 2 17-DEC-2002;
COMMENT   OLYMPUS OPTICAL CO LTD
          OS Artificial Sequence
          PN JP 2002360300-A/2
          PD 17-DEC-2002
          PF 06-JUN-2001 JP 2001171590
          PI MINORU TAKEUCHI
          PC C1201/68, C12N15/09, G01N33/483, G01N33/50, C12N15/00 CC
          Analyzeys of double stranded nucleic acid using scanning probe CC
FH Key      Location/Qualifiers
FT source   1..14
            /organism='Artificial Sequence'
FEATURES
  source
    1..14
      Location/Qualifiers
      /organism='synthetic construct'
      /mol_type='genomic DNA'
      /db_xref='taxon:32630'
Query Match      1.2%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 1.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1793 TGTGTGTGTGTGTG 1806
Db 14 TGTGTGTGTGTGTG 1
RESULT 279
AR056127
LOCUS      AR056127      15 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION Sequence 331 from patent US 5837542.
ACCESSION  AR056127
VERSION    AR056127.1 GI:5981704
KEYWORDS  Unknown.
SOURCE    Unknown.
ORGANISM  Unknown.
REFERENCE  1 (bases 1 to 15)
AUTHORS   Grimm, S., Stinchcomb, D.T., McSwiggen, J., Sullivan, S. and
          Draper, K.G.
TITLE     Intercellular adhesion molecule-1 (ICAM-1) ribozymes
JOURNAL   Patent: US 5837542-A 331 17-NOV-1998;
FEATURES   Location/Qualifiers
            source
              1..15
                /organism='unknown'
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Query Match      1.2%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 1.7e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1801 TGTGTGTGTGTGTA 1814
Db 1 TGTGTGTGTGTGTA 14
RESULT 280
AR113885
LOCUS      AR113885      15 bp      DNA      linear      PAT 20-APR-2002
DEFINITION Sequence 331 from patent US 6132967.
ACCESSION  AR113885
VERSION    AR113885.1 GI:14094207
KEYWORDS  Unknown.
SOURCE    Unknown.
ORGANISM  Unknown.
REFERENCE  1 (bases 1 to 15)
AUTHORS   Grimm, S., Stinchcomb, D.T., McSwiggen, J., Sullivan, S. and
          Draper, K.G.
TITLE     Ribozyme treatment of diseases or conditions related to levels of
          intercellular adhesion molecule-1 (ICAM-1)
JOURNAL   Patent: US 6132967-A 331 17-OCT-2000;
FEATURES   Location/Qualifiers
            source
              1..15
                /organism='unknown'
                /mol_type='unassigned DNA'
Query Match      1.2%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 1.7e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1801 TGTGTGTGTGTGTA 1814
Db 1 TGTGTGTGTGTGTA 14

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LOCUS      AR113885      15 bp      DNA      linear      PAT 16-MAY-2001
DEFINITION Sequence 331 from patent US 6132967.
ACCESSION  AR113885
VERSION    AR113885.1 GI:14094207
KEYWORDS  Unknown.
SOURCE    Unknown.
ORGANISM  Unknown.
REFERENCE  1 (bases 1 to 15)
AUTHORS   Grimm, S., Stinchcomb, D.T., McSwiggen, J., Sullivan, S. and
          Draper, K.G.
TITLE     Ribozyme treatment of diseases or conditions related to levels of
          intercellular adhesion molecule-1 (ICAM-1)
JOURNAL   Patent: US 6132967-A 331 17-OCT-2000;
FEATURES   Location/Qualifiers
            source
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                /organism='unknown'
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Query Match      1.2%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 1.7e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1801 TGTGTGTGTGTGTA 1814
Db 1 TGTGTGTGTGTGTA 14
RESULT 281
AR118773
LOCUS      AR118773      15 bp      DNA      linear      PAT 16-MAY-2001
DEFINITION Sequence 203 from patent US 6150087.
ACCESSION  AR118773
VERSION    AR118773.1 GI:14100683
KEYWORDS  Unknown.
SOURCE    Unknown.
ORGANISM  Unknown.
REFERENCE  1 (bases 1 to 15)
AUTHORS   Chien, D.Y.
TITLE     NANEV diagnostics and vaccines
JOURNAL   Patent: US 6150087-A 203 21-NOV-2000;
FEATURES   Location/Qualifiers
            source
              1..15
                /organism='unknown'
                /mol_type='unassigned DNA'
Query Match      1.2%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 1.7e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1378 CTGGCTTGAAGAAT 1391
Db 1 CTGGCTTGAAGAAT 14
RESULT 282
AR179058
LOCUS      AR179058      15 bp      DNA      linear      PAT 20-APR-2002
DEFINITION Sequence 1 from patent US 6326139.
ACCESSION  AR179058
VERSION    AR179058.1 GI:20220613
KEYWORDS  Unknown.
SOURCE    Unknown.
ORGANISM  Unknown.
REFERENCE  1 (bases 1 to 15)
AUTHORS   Soreq, H. and Zakut, H.
TITLE     Method of screening for genetic predisposition to
          anticholinesterase therapy
JOURNAL   Patent: US 6326139-A 1 04-DEC-2001;
FEATURES   Location/Qualifiers
            source
              1..15

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/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 1.2%; Score 12.4; DB 1; Length 15;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2174 ACTTGATATGACT 2187
Db 2 ACTTGTCTAGACT 15

RESULT 283
LOCUS I06405
DEFINITION Sequence 25 from Patent EP 0318216.
ACCESSION I06405
VERSION I06405.1 GI:590295
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Houghton,M., Choo,Q.-L. and Kuo,G.
TITLE Nanbv diagnostics and vaccines
JOURNAL Patent: EP 0318216-A1 25 31-MAY-1989;
FEATURES
    Location/Qualifiers
        source
            1..15
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Query Match
Best Local Similarity 1.2%; Score 12.4; DB 1; Length 15;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1378 CTGGTTTGAAGAAAT 1391
Db 1 CTGGCTTGAAGAAAT 14

RESULT 284
LOCUS I06416
DEFINITION Sequence 36 from Patent EP 0318216.
ACCESSION I06416
VERSION I06416.1 GI:590306
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Houghton,M., Choo,Q.-L. and Kuo,G.
TITLE Nanbv diagnostics and vaccines
JOURNAL Patent: EP 0318216-A1 36 31-MAY-1989;
FEATURES
    Location/Qualifiers
        source
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Query Match
Best Local Similarity 1.2%; Score 12.4; DB 1; Length 15;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1378 CTGGTTTGAAGAAAT 1391
Db 1 CTGGCTTGAAGAAAT 14

RESULT 285
LOCUS I39436
DEFINITION Sequence 474 from patent US 5616488.
ACCESSION I39436
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VERSION I39436.1 GI:2083916
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Sullivan,S., Draper,K.G., McSwiggen,J. and Stinchcomb,D.T.
TITLE IL-5 targeted ribozymes
JOURNAL Patent: US 5616488-A 474 01-APR-1997;
FEATURES
    Location/Qualifiers
        source
            1..15
                /organism="unknown"
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Query Match
Best Local Similarity 1.2%; Score 12.4; DB 1; Length 15;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1956 AAAGCATGAATGG 1969
Db 1 AAAGCATAAATGG 14

RESULT 286
LOCUS I39453
DEFINITION Sequence 491 from patent US 5616488.
ACCESSION I39453
VERSION I39453.1 GI:2083933
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Sullivan,S., Draper,K.G., McSwiggen,J. and Stinchcomb,D.T.
TITLE IL-5 targeted ribozymes
JOURNAL Patent: US 5616488-A 491 01-APR-1997;
FEATURES
    Location/Qualifiers
        source
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Query Match
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Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1284 TTATTTAAATCTGT 1297
Db 2 TTATTTAATTCGT 15

RESULT 287
LOCUS I77628/c
DEFINITION Sequence 335 from patent US 5693532.
ACCESSION I77628
VERSION I77628.1 GI:3013782
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS McSwiggen,J., Draper,K., Pavco,P. and Woolf,T.
TITLE Respiratory syncytial virus ribozymes
JOURNAL Patent: US 5693532-A 335 02-DEC-1997;
FEATURES
    Location/Qualifiers
        source
            1..15
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                /mol_type="unassigned DNA"

Query Match
Best Local Similarity 1.2%; Score 12.4; DB 1; Length 15;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1378 CTGGTTTGAAGAAAT 1391
Db 1 CTGGCTTGAAGAAAT 14

RESULT 288
LOCUS I39436
DEFINITION Sequence 474 from patent US 5616488.
ACCESSION I39436
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ORGANISM unclassified  
REFERENCE 1  
AUTHORS Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A., Karpeisky,A., Draper,K.G., Kisch,X., Matulic-Adamic,J., McSwiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M., Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and Woolf,T.  
TITLE Method and reagent for inhibiting the expression of disease related genes  
JOURNAL Patent: EP 1260586-A 373 27-NOV-2002;  
RIBOZYME PHARMACEUTICALS, INC. (US)  
FEATURES Location/Qualifiers  
source 1..15  
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/mol\_type="unassigned RNA"  
/db\_xref="taxon:32644"  
Query Match 1.2%; Score 12.4; DB 1; Length 15;  
Best Local Similarity 92.9%; Pred. No. 1.7e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1801 TGTGTGTGTGTGTA 1814  
Db 1 TGTGTGTGTGTGTA 14  
RESULT 291  
LOCUS AX635692 15 bp RNA linear PAT 21-FEB-2003  
DEFINITION Sequence 2831 from Patent EP1260586.  
ACCESSION AX635692  
VERSION AX635692.1 GI:28471306  
KEYWORDS  
SOURCE unclassified  
ORGANISM unclassified  
REFERENCE 1  
AUTHORS Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A., Karpeisky,A., Draper,K.G., Kisch,X., Matulic-Adamic,J., McSwiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M., Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and Woolf,T.  
TITLE Method and reagent for inhibiting the expression of disease related genes  
JOURNAL Patent: EP 1260586-A 2831 27-NOV-2002;  
RIBOZYME PHARMACEUTICALS, INC. (US)  
FEATURES Location/Qualifiers  
source 1..15  
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/mol\_type="unassigned RNA"  
/db\_xref="taxon:32644"  
Query Match 1.2%; Score 12.4; DB 1; Length 15;  
Best Local Similarity 92.9%; Pred. No. 1.7e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1284 TTATTTAAATCTGT 1297  
Db 2 TTATTTAAATCTGT 15  
RESULT 292  
LOCUS AX635755 15 bp RNA linear PAT 21-FEB-2003  
DEFINITION Sequence 2894 from Patent EP1260586.  
ACCESSION AX635755  
VERSION AX635755.1 GI:28471369  
KEYWORDS  
SOURCE unclassified  
ORGANISM unclassified  
REFERENCE 1

QY 1784 TGTAAATATTGTGT 1797  
Db 14 TGTGAATATTGTGT 1  
RESULT 288  
LOCUS AR241870 15 bp DNA linear PAT 20-DEC-2002  
DEFINITION Sequence 158 from patent US 6472154.  
ACCESSION AR241870  
VERSION AR241870.1 GI:27287682  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Garner,H.R., Wren,J.D., Minna,J.D. and Fondon,J.W. III.  
TITLE Polymorphic repeats in human genes  
JOURNAL Patent: US 6472154-A 158 29-OCT-2002;  
FEATURES Location/Qualifiers  
source 1..15  
/organism="unknown"  
/mol\_type="genomic DNA"  
Query Match 1.2%; Score 12.4; DB 1; Length 15;  
Best Local Similarity 86.7%; Pred. No. 1.7e+02;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1865 TTTTATTTTGTGT 1879  
Db 1 TTTTATTTTGTGT 15  
RESULT 289  
LOCUS AX587098 15 bp DNA linear PAT 10-JAN-2003  
DEFINITION Sequence 120 from Patent WO02072883.  
ACCESSION AX587098  
VERSION AX587098.1 GI:27655973  
KEYWORDS  
SOURCE unclassified  
ORGANISM unclassified  
REFERENCE 1  
AUTHORS Roetger,A.  
TITLE Nucleotide carrier for diagnosing and treating oral diseases  
JOURNAL Patent: WO 02072883-A 120 19-SEP-2002;  
FEATURES Location/Qualifiers  
source 1..15  
/organism="unclassified"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32644"  
/note="Bacteria"  
Query Match 1.2%; Score 12.4; DB 1; Length 15;  
Best Local Similarity 92.9%; Pred. No. 1.7e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1275 TAGCACAGTATT 1288  
Db 15 TAGCACAGTATT 2  
RESULT 290  
LOCUS AX633234 15 bp RNA linear PAT 21-FEB-2003  
DEFINITION Sequence 373 from Patent EP1260586.  
ACCESSION AX633234  
VERSION AX633234.1 GI:28468848  
KEYWORDS  
SOURCE unclassified

**AUTHORS** Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A., Karpeisky,A., Draper,K.G., Kisch,K., Matulic-Adamic,J., McSwiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M., Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and Woolf,T.

**TITLE** Method and reagent for inhibiting the expression of disease related genes

**JOURNAL** Patent: EP 1260586-A 2894 27-NOV-2002;  
RIBOZYME PHARMACEUTICALS, INC. (US)

**FEATURES** source  
Location/Qualifiers  
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/organism="unidentified"  
/mol\_type="unassigned RNA"  
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**Query Match** 1.2%; Score 12.4; DB 1; Length 15;  
Best Local Similarity 92.9%; Pred. No. 1.7e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

**QY** 1956 AAAGCATGAATGG 1969  
|||||  
1 AAAGCATGAATGG 14

**Db**

**RESULT 293**  
AX637904/c  
LOCUS AX637904  
DEFINITION Sequence 5043 from Patent EP1260586.  
ACCESSION AX637904  
VERSION AX637904.1 GI:28473518  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1  
AUTHORS Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A., Karpeisky,A., Draper,K.G., Kisch,K., Matulic-Adamic,J., McSwiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M., Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and Woolf,T.

**TITLE** Method and reagent for inhibiting the expression of disease related genes

**JOURNAL** Patent: EP 1260586-A 5043 27-NOV-2002;  
RIBOZYME PHARMACEUTICALS, INC. (US)

**FEATURES** source  
Location/Qualifiers  
1..15  
/organism="unidentified"  
/mol\_type="unassigned RNA"  
/db\_xref="taxon:32644"

**Query Match** 1.2%; Score 12.4; DB 1; Length 15;  
Best Local Similarity 92.9%; Pred. No. 1.7e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

**QY** 1784 TGTAATATTGTGT 1797  
|||||  
14 TGTAATATTGTGT 1

**Db**

**RESULT 294**  
I31521/c  
LOCUS I31521  
DEFINITION Sequence 433 from patent US 5582979.  
ACCESSION I31521  
VERSION I31521.1 GI:1822312  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 12)  
AUTHORS Weber,J.L.  
TITLE Length polymorphisms in (dC-dA).sub.n.(dG-dT).sub.n sequences and method of using the same

**JOURNAL** Patent: US 5582979-A 433 10-DEC-1996;  
Location/Qualifiers  
1..12  
/organism="unknown"  
/mol\_type="unassigned DNA"

**FEATURES** source  
Location/Qualifiers  
1..12  
/organism="unknown"  
/mol\_type="unassigned DNA"

**Query Match** 1.1%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**QY** 1794 GTGTGTGTGTGT 1805  
|||||  
12 GTGTGTGTGTGT 1

**Db**

**RESULT 295**  
AR208365  
LOCUS AR208365  
DEFINITION Sequence 21 from patent US 6383747.  
ACCESSION AR208365  
VERSION AR208365.1 GI:21509500  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 12)  
AUTHORS Dawkins,R.Letts. and Abraham,L.Joseph.  
TITLE Method for determining ancestral haplotypes using haplo-specific geometric elements within the major histocompatibility complex multigene cluster  
JOURNAL Patent: US 6383747-A 21 07-MAY-2002;  
Location/Qualifiers  
1..12  
/organism="unknown"  
/mol\_type="unassigned DNA"

**Query Match** 1.1%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**QY** 1793 TGTGTGTGTGTG 1804  
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1 TGTGTGTGTGTG 12

**Db**

**RESULT 296**  
AR261535/c  
LOCUS AR261535  
DEFINITION Sequence 2 from patent US 6322971.  
ACCESSION AR261535  
VERSION AR261535.1 GI:28072603  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 12)  
AUTHORS Chetverin,A.B. and Kramer,F.R.  
TITLE Oligonucleotide arrays and their use for sorting, isolating, sequencing, and manipulating nucleic acids  
JOURNAL Patent: US 6322971-A 2 27-NOV-2001;  
Location/Qualifiers  
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/organism="unknown"  
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**Query Match** 1.1%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**QY** 1794 GTGTGTGTGTGT 1805  
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12 GTGTGTGTGTGT 1

**Db**

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RESULT 297
AX175249
LOCUS AX175249 12 bp DNA linear PAT 03-JUL-2001
DEFINITION Sequence 13 from Patent WO0144465.
ACCESSION AX175249
VERSION AX175249.1 GI:14598617
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Phillips,N.C. and Filion,M.C.
TITLE Therapeutically useful synthetic oligonucleotides
JOURNAL Patent: WO 0144465-A 13 21-JUN-2001;
Bioniche Life Sciences Inc. (CA)
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1793 TGTGTGTGTGTG 1804
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Db 1 TGTGTGTGTGTG 12

RESULT 298
AX175250
LOCUS AX175250 12 bp DNA linear PAT 03-JUL-2001
DEFINITION Sequence 14 from Patent WO0144465.
ACCESSION AX175250
VERSION AX175250.1 GI:14598618
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Phillips,N.C. and Filion,M.C.
TITLE Therapeutically useful synthetic oligonucleotides
JOURNAL Patent: WO 0144465-A 14 21-JUN-2001;
Bioniche Life Sciences Inc. (CA)
FEATURES
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
Query Match 1.1%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1793 TGTGTGTGTGTG 1804
| | | | |
Db 1 TGTGTGTGTGTG 12

RESULT 299
AX239661/c
LOCUS AX239661 12 bp DNA linear PAT 26-SEP-2001
DEFINITION Sequence 1 from Patent WO0164948.
ACCESSION AX239661
VERSION AX239661.1 GI:15797326
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS van Haeringen,W.A. and van Haeringen,H.

TITLE Universal variable fragments
JOURNAL Patent: WO 0164948-A 1 07-SEP-2001;
Dr. van Haeringen Laboratorium B.V. (NL)
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/organism="synthetic construct"
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/notes="primer"
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Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1793 TGTGTGTGTGTG 1804
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Db 12 TGTGTGTGTGTG 1

RESULT 300
AX644020/c
LOCUS AX644020 12 bp DNA linear PAT 27-FEB-2003
DEFINITION Sequence 1 from Patent WO02101088.
ACCESSION AX644020
VERSION AX644020.1 GI:28610172
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Dace,G.T., Kmerly,W.J., Goff,S.A. and Oeller,P.
TITLE In vitro capture of nucleic acids via modified oligonucleotides and
magnetic beads
JOURNAL Patent: WO 02101088-A 1 19-DEC-2002;
Syngenta Participations AG (CH)
FEATURES
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/organism="synthetic construct"
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/db_xref="taxon:32630"
/notes="Hypothetical SSR"
Query Match 1.1%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1793 TGTGTGTGTGTG 1804
| | | | |
Db 12 TGTGTGTGTGTG 1

RESULT 301
AX644021
LOCUS AX644021 12 bp DNA linear PAT 27-FEB-2003
DEFINITION Sequence 2 from Patent WO02101088.
ACCESSION AX644021
VERSION AX644021.1 GI:28610173
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Dace,G.T., Kmerly,W.J., Goff,S.A. and Oeller,P.
TITLE In vitro capture of nucleic acids via modified oligonucleotides and
magnetic beads
JOURNAL Patent: WO 02101088-A 2 19-DEC-2002;
Syngenta Participations AG (CH)
FEATURES
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/db_xref="taxon:32630"
/notes="Hypothetical probe"
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Query Match 1.1%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGT 1805  
|||||  
Db 1 GTGTGTGTGT 12

RESULT 302  
BD062286  
LOCUS BD062286 12 bp DNA linear PAT 27-AUG-2002  
DEFINITION Method for identifying organism by genotype.  
ACCESSION BD062286  
VERSION BD062286.1 GI:22607891  
KEYWORDS JP 2001299398-A/11.  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1 (bases 1 to 12)  
AUTHORS Nishigaki, K., Takasawa, T. and Hamano, K.  
TITLE Method for identifying organism by genotype  
JOURNAL Patent: JP 2001299398-A 11 30-OCT-2001;  
TIE TECH KK  
COMMENT OS Unknown  
PN JP 2001299398-A/11  
PD 30-OCT-2001  
PF 23-APR-2000 JP 2000123755  
PI KOICHI NISHIGAKI, TSUTOMU TAKASAWA, KEIICHI HAMANO PC  
C12Q1/68, C12N15/09, G01N27/447, G01N27/447, G01N33/50 CC  
FH Key Location/Qualifiers.

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Query Match 1.1%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1814 ATATATATAT 1825  
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Db 1 ATATATATAT 12

RESULT 303  
BD062286/c  
LOCUS BD062286 12 bp DNA linear PAT 27-AUG-2002  
DEFINITION Method for identifying organism by genotype.  
ACCESSION BD062286  
VERSION BD062286.1 GI:22607891  
KEYWORDS JP 2001299398-A/11.  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1 (bases 1 to 12)  
AUTHORS Nishigaki, K., Takasawa, T. and Hamano, K.  
TITLE Method for identifying organism by genotype  
JOURNAL Patent: JP 2001299398-A 11 30-OCT-2001;  
TIE TECH KK  
COMMENT OS Unknown  
PN JP 2001299398-A/11  
PD 30-OCT-2001  
PF 25-APR-2000 JP 2000123755  
PI KOICHI NISHIGAKI, TSUTOMU TAKASAWA, KEIICHI HAMANO PC  
C12Q1/68, C12N15/09, G01N27/447, G01N27/447, G01N33/50 CC  
FH Key Location/Qualifiers.

FEATURES  
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/organism="unidentified"  
/mol\_type="genomic DNA"

/db\_xref="taxon:32644"

Query Match 1.1%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1814 ATATATATAT 1825  
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Db 12 ATATATATAT 1

RESULT 304  
BD106556/c  
LOCUS BD106556 12 bp DNA linear PAT 18-SEP-2002  
DEFINITION Production of attenuated parainfluenza virus vaccines from cloned nucleotide sequence.  
ACCESSION BD106556  
VERSION BD106556.1 GI:23201374  
KEYWORDS JP 2002502241-A/50.  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.

REFERENCE 1 (bases 1 to 12)  
AUTHORS Murphy, B.R., Collins, P.L., Durbin, A.P., Skiadopoulos, M.H. and Ta, T.  
TITLE Production of attenuated parainfluenza virus vaccines from cloned nucleotide sequence  
JOURNAL Patent: JP 2002502241-A 50 22-JAN-2002;  
THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE MERCK & CO INC DEPARTMENT OF HEALTH AND HUMANSERVICES  
COMMENT PN JP 2002502241-A/50  
PD 22-JAN-2002  
PF 22-MAY-1998 JP 1998550704  
PI BRIAN R MURPHY, PETER L COLLINS, ANNA P DURBIN, MARIO H PI  
SKIADPOULOS, TAO TAO  
PC C12N15/45, C07K14/115, C12N5/10, C12N7/01, A61K39/155 CC  
Strandedness: Single;  
CC Topology: Linear;

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/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"

Query Match 1.1%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1844 TAATTTAAAGTT 1855  
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Db 12 TAATTTAAAGTT 1

RESULT 305  
A09237/c  
LOCUS A09237 15 bp RNA linear PAT 14-OCT-1993  
DEFINITION Sabin:codon 286-290 mRNA.  
ACCESSION A09237  
VERSION A09237.1 GI:492887  
KEYWORDS Human poliovirus 3  
SOURCE Human poliovirus 3  
ORGANISM Human poliovirus 3  
Viruses; ssRNA positive-strand viruses, no DNA stage;  
Picornaviridae; Enterovirus.

REFERENCE 1 (bases 1 to 15)  
AUTHORS Minor, P.D., Evans, D.M.A., Schild, G.C., Almond, J.W. and Ferguson, M.  
TITLE Peptides useful in vaccination against enteroviruses  
JOURNAL Patent: EP 0197772-A 1 15-OCT-1986;  
NATIONAL RESEARCH DEVELOPMENT CORPORATION  
Location/Qualifiers

FEATURES  
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/mol_type="unassigned RNA"
/db_xref="taxon:12086"

Query Match
  1.1%; Score 12; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1634 CAAGTTGTTCT 1645
Db 12 CAAGTTGTTCT 1

RESULT 306
161566/c
LOCUS 161566 15 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 120 from patent US 5658780.
ACCESSION I61566
VERSION I61566.1 GI:2479514
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 15)
AUTHORS Stinchcomb,D.T., Draper,K.G. and McSwiggen,J.
TITLE Rel a targeted ribozymes
JOURNAL Patent: US 5658780-A 120 19-AUG-1997;
FEATURES
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        /mol_type="unassigned DNA"

Query Match
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Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2153 CACCTGGAAGCA 2164
Db 15 CACCTGGAAGCA 4

RESULT 307
161639/c
LOCUS 161639 15 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 193 from patent US 5658780.
ACCESSION I61639
VERSION I61639.1 GI:2479587
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 15)
AUTHORS Stinchcomb,D.T., Draper,K.G. and McSwiggen,J.
TITLE Rel a targeted ribozymes
JOURNAL Patent: US 5658780-A 193 19-AUG-1997;
FEATURES
  Location/Qualifiers
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Query Match
  1.1%; Score 12; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2153 CACCTGGAAGCA 2164
Db 15 CACCTGGAAGCA 4

RESULT 308
161755/c
LOCUS 161755 15 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 309 from patent US 5658780.
ACCESSION I61755
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161755.1 GI:2479703
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 15)
AUTHORS Stinchcomb,D.T., Draper,K.G. and McSwiggen,J.
TITLE Rel a targeted ribozymes
JOURNAL Patent: US 5658780-A 309 19-AUG-1997;
FEATURES
  Location/Qualifiers
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Query Match
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Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2153 CACCTGGAAGCA 2164
Db 15 CACCTGGAAGCA 4

RESULT 309
166357
LOCUS 166357 15 bp DNA linear PAT 28-DEC-1997
DEFINITION Sequence 16 from patent US 5670330.
ACCESSION I66357
VERSION I66357.1 GI:2724334
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 15)
AUTHORS Sonenberg,N., Katze,M.G., Roy,S., Koromilas,A.E. and Barber,G.H.
TITLE Anti-tumor agent assay using PKR
JOURNAL Patent: US 5670330-A 16 23-SEP-1997;
FEATURES
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    source
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Query Match
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Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1784 TGTAAATATTGT 1795
Db 3 TGTAAATATTGT 14

RESULT 310
177325/c
LOCUS 177325 15 bp DNA linear PAT 03-APR-1998
DEFINITION Sequence 32 from patent US 5693532.
ACCESSION I77325
VERSION I77325.1 GI:3013479
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 15)
AUTHORS McSwiggen,J., Draper,K., Pavco,P. and Woolf,T.
TITLE Respiratory syncytial virus ribozymes
JOURNAL Patent: US 5693532-A 32 02-DEC-1997;
FEATURES
  Location/Qualifiers
    source
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        /organism="unknown"
        /mol_type="unassigned DNA"

Query Match
  1.1%; Score 12; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1347 TGTCAACAAT 1358  
 Db 13 TGTCAACAAT 2

RESULT 311  
 I77326/c  
 LOCUS 15 bp DNA linear PAT 03-APR-1998  
 DEFINITION Sequence 33 from patent US 5693532.  
 ACCESSION I77326  
 VERSION I77326.1 GI:3013480  
 KEYWORDS Unknown.  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 15)  
 AUTHORS McSwiggen, J., Draper, K., Pavco, P. and Woolf, T.  
 TITLE Respiratory syncytial virus ribozymes  
 JOURNAL Patent: US 5693532-A 33 02-DEC-1997;  
 FEATURES Location/Qualifiers  
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 /organism="unknown"  
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Query Match 1.1%; Score 12; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02; Indels 0; Gaps 0;  
 Matches 12; Conservative 0; Mismatches 0;

QY 1347 TGTCAACAAT 1358  
 Db 12 TGTCAACAAT 1

RESULT 312  
 AX635884/c  
 LOCUS 15 bp RNA linear PAT 21-FEB-2003  
 DEFINITION Sequence 3023 from Patent EP1260586.  
 ACCESSION AX635884  
 VERSION AX635884.1 GI:28471498  
 KEYWORDS unidentified  
 SOURCE unidentified  
 ORGANISM unclassified.  
 REFERENCE 1  
 AUTHORS Stinchcomb, D.T., Dudycz, L.W., Chowrira, B., Grimm, S., Drenzo, A., Karpeisky, A., Draper, K.G., Kisch, K., Matulic-Adamic, J., McSwiggen, J.A., Modak, A., Pavco, P., Beigelman, L., Sullivan, S.M., Sweedler, D., Thompson, J.D., Tracz, D., Usman, N., Wincott, F.E. and Woolf, T.  
 TITLE Method and reagent for inhibiting the expression of disease related genes  
 JOURNAL Patent: EP 1260586-A 3023 27-NOV-2002;  
 FEATURES Location/Qualifiers  
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 /organism="unidentified"  
 /mol\_type="unassigned RNA"  
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Query Match 1.1%; Score 12; DB 1; Length 15;  
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 Matches 12; Conservative 0; Mismatches 0;

QY 2153 CACCTGGAAGCA 2164  
 Db 15 CACCTGGAAGCA 4

RESULT 313  
 AX636030/c  
 LOCUS 15 bp RNA linear PAT 21-FEB-2003  
 DEFINITION Sequence 3169 from Patent EP1260586.

ACCESSION AX636030  
 VERSION AX636030.1 GI:28471644  
 KEYWORDS unidentified  
 SOURCE unidentified  
 ORGANISM unclassified.  
 REFERENCE 1  
 AUTHORS Stinchcomb, D.T., Dudycz, L.W., Chowrira, B., Grimm, S., Drenzo, A., Karpeisky, A., Draper, K.G., Kisch, K., Matulic-Adamic, J., McSwiggen, J.A., Modak, A., Pavco, P., Beigelman, L., Sullivan, S.M., Sweedler, D., Thompson, J.D., Tracz, D., Usman, N., Wincott, F.E. and Woolf, T.  
 TITLE Method and reagent for inhibiting the expression of disease related genes  
 JOURNAL Patent: EP 1260586-A 3169 27-NOV-2002;  
 FEATURES Location/Qualifiers  
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 /mol\_type="unassigned RNA"  
 /db\_xref="taxon:32644"

Query Match 1.1%; Score 12; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02; Indels 0; Gaps 0;  
 Matches 12; Conservative 0; Mismatches 0;

QY 2153 CACCTGGAAGCA 2164  
 Db 15 CACCTGGAAGCA 4

RESULT 314  
 AX636073/c  
 LOCUS 15 bp RNA linear PAT 21-FEB-2003  
 DEFINITION Sequence 3212 from Patent EP1260586.  
 ACCESSION AX636073  
 VERSION AX636073.1 GI:28471697  
 KEYWORDS unidentified  
 SOURCE unidentified  
 ORGANISM unclassified.  
 REFERENCE 1  
 AUTHORS Stinchcomb, D.T., Dudycz, L.W., Chowrira, B., Grimm, S., Drenzo, A., Karpeisky, A., Draper, K.G., Kisch, K., Matulic-Adamic, J., McSwiggen, J.A., Modak, A., Pavco, P., Beigelman, L., Sullivan, S.M., Sweedler, D., Thompson, J.D., Tracz, D., Usman, N., Wincott, F.E. and Woolf, T.  
 TITLE Method and reagent for inhibiting the expression of disease related genes  
 JOURNAL Patent: EP 1260586-A 3212 27-NOV-2002;  
 FEATURES Location/Qualifiers  
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 /organism="unidentified"  
 /mol\_type="unassigned RNA"  
 /db\_xref="taxon:32644"

Query Match 1.1%; Score 12; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02; Indels 0; Gaps 0;  
 Matches 12; Conservative 0; Mismatches 0;

QY 2153 CACCTGGAAGCA 2164  
 Db 15 CACCTGGAAGCA 4

RESULT 315  
 AX638069/c  
 LOCUS 15 bp RNA linear PAT 21-FEB-2003  
 DEFINITION Sequence 5208 from Patent EP1260586.  
 ACCESSION AX638069  
 VERSION AX638069.1 GI:28473683  
 KEYWORDS

SOURCE unidentified  
 ORGANISM unidentified  
 REFERENCE unclassified.  
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 AUTHORS  
 Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A.,  
 Karpelsky,A., Draper,K.G., Kisch,K., Matulic-Adamic,J.,  
 Meswigen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,  
 Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and  
 Woolf,T.  
 TITLE  
 Method and reagent for inhibiting the expression of disease related  
 genes  
 JOURNAL  
 Patent: EP 1260586-A 5208 27-NOV-2002;  
 RIBOZYME PHARMACEUTICALS, INC. (US)  
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 /organism="unidentified"  
 /mol\_type="unassigned RNA"  
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Qy 1347 TGTCAAAACAAAT 1358  
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 Db 13 TGTCAAAACAAAT 2

RESULT 316  
 AX638071/c  
 LOCUS AX638071 15 bp RNA linear PAT 21-FEB-2003  
 DEFINITION Sequence 5210 from Patent EP1260586.  
 ACCESSION AX638071  
 VERSION AX638071.1 GI:28473685  
 KEYWORDS  
 SOURCE unidentified  
 ORGANISM unidentified  
 unclassified.  
 REFERENCE  
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 AUTHORS  
 Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A.,  
 Karpelsky,A., Draper,K.G., Kisch,K., Matulic-Adamic,J.,  
 Meswigen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,  
 Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and  
 Woolf,T.  
 TITLE  
 Method and reagent for inhibiting the expression of disease related  
 genes  
 JOURNAL  
 Patent: EP 1260586-A 5210 27-NOV-2002;  
 RIBOZYME PHARMACEUTICALS, INC. (US)  
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Query Match 1.1%; Score 12; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1347 TGTCAAAACAAAT 1358  
 |||||  
 Db 12 TGTCAAAACAAAT 1

Search completed: April 2, 2004, 14:35:26  
 Job time : 6 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model  
Run on: April 2, 2004, 14:41:23 ; Search time 3 Seconds  
(without alignment)  
2.494 Million cell updates/sec

Title: us-10-006-191-19  
Perfect score: 1049  
Sequence: 1 ttgaacgattcacatctca.....gtgtatatttttttataaa 1049

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 0.5

Searched: 169 seqs, 3566 residues

Total number of hits satisfying chosen parameters: 338

Minimum DB seq length: 8  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 178 summaries

Database : rst.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	37	3.5	37	1	R06912
C 2	31	3.0	35	1	ACCSSION:R06912
C 3	23.4	2.2	26	1	ACCSSION:N41929
C 4	23.2	2.2	28	1	ACCSSION:AZ781130
C 5	23.2	2.2	28	1	ACCSSION:AZ405219
C 6	23.2	2.2	28	1	ACCSSION:AZ443611
C 7	22.8	2.2	27	1	ACCSSION:AZ648796
C 8	22.4	2.1	24	1	ACCSSION:AZ646963
C 9	22.4	2.1	25	1	ACCSSION:AZ446429
C 10	22.4	2.1	25	1	ACCSSION:AZ762101
C 11	22.4	2.1	28	1	ACCSSION:AZ780500
C 12	22.2	2.1	27	1	ACCSSION:AZ345426
C 13	22.2	2.1	27	1	ACCSSION:AZ638238
C 14	22.2	2.1	27	1	ACCSSION:AZ981811
C 15	22.2	2.1	26	1	ACCSSION:AZ774981
C 16	21.8	2.1	25	1	ACCSSION:BX563211
C 17	21.8	2.1	25	1	ACCSSION:BX39866
C 18	21.8	2.1	26	1	ACCSSION:BX569116
C 19	21.8	2.1	26	1	ACCSSION:AZ307889
C 20	21.8	2.1	26	1	ACCSSION:AZ345505
C 21	21.8	2.1	26	1	ACCSSION:AZ494537
C 22	21.8	2.1	26	1	ACCSSION:AZ503652
C 23	21.8	2.1	26	1	ACCSSION:AZ795803
C 24	21.8	2.1	26	1	ACCSSION:AZ806004
C 25	21.8	2.1	26	1	ACCSSION:AZ975568
C 26	21.8	2.1	27	1	ACCSSION:AZ329433
C 27	21.8	2.1	27	1	ACCSSION:AZ342492
C 28	21.8	2.1	27	1	ACCSSION:AZ404479
C 29	21.8	2.1	27	1	ACCSSION:AZ583081
C 30	21.8	2.1	27	1	ACCSSION:AZ758321
C 31	21.8	2.1	27	1	ACCSSION:AZ788874
C 32	21.8	2.1	27	1	ACCSSION:AZ801217
C 33	21.4	2.0	23	1	ACCSSION:BX557786

34	21.4	2.0	23	1	AZ483624
C 35	21.4	2.0	23	1	ACCSSION:AZ637290
C 36	21.4	2.0	23	1	ACCSSION:AZ789907
C 37	21.4	2.0	23	1	ACCSSION:AZ829195
C 38	21.4	2.0	24	1	ACCSSION:BX559963
C 39	21.4	2.0	24	1	ACCSSION:AZ419602
C 40	21.4	2.0	24	1	ACCSSION:AZ621455
C 41	21.4	2.0	24	1	ACCSSION:AZ807762
C 42	21.4	2.0	24	1	ACCSSION:AZ813106
C 43	21.4	2.0	24	1	ACCSSION:AZ846178
C 44	21.4	2.0	24	1	ACCSSION:AL472248
C 45	21.4	2.0	24	1	ACCSSION:AZ345553
C 46	21.4	2.0	25	1	ACCSSION:AZ404057
C 47	21.4	2.0	25	1	ACCSSION:AZ467470
C 48	21.4	2.0	25	1	ACCSSION:AZ769673
C 49	21.4	2.0	25	1	ACCSSION:AZ771881
C 50	21.4	2.0	26	1	ACCSSION:AZ419877
C 51	21.4	2.0	26	1	ACCSSION:AZ467063
C 52	21.4	2.0	26	1	ACCSSION:AZ646850
C 53	21.4	2.0	26	1	ACCSSION:AZ830551
C 54	21.4	2.0	26	1	ACCSSION:AZ310642
C 55	21.4	2.0	26	1	ACCSSION:AZ333309
C 56	21.4	2.0	26	1	ACCSSION:AZ762904
C 57	21.4	2.0	26	1	ACCSSION:AZ854856
C 58	21.4	2.0	26	1	ACCSSION:AZ484090
C 59	21.4	2.0	26	1	ACCSSION:AZ985497
C 60	21.4	2.0	26	1	ACCSSION:AZ328763
C 61	21.4	2.0	26	1	ACCSSION:AZ371475
C 62	21.4	2.0	26	1	ACCSSION:AZ824638
C 63	21.4	2.0	26	1	ACCSSION:AZ828699
C 64	21.4	2.0	26	1	ACCSSION:AZ647335
C 65	21.4	2.0	26	1	ACCSSION:AZ459694
C 66	21.4	2.0	26	1	ACCSSION:AZ506209
C 67	21.4	2.0	26	1	ACCSSION:AZ494629
C 68	20.4	1.9	26	1	ACCSSION:AZ602037
C 69	20.2	1.9	25	1	ACCSSION:AZ452273
C 70	20.2	1.9	25	1	ACCSSION:AZ368875
C 71	20.2	1.9	25	1	ACCSSION:AZ465453
C 72	20.2	1.9	25	1	ACCSSION:AZ470768
C 73	20.2	1.9	25	1	ACCSSION:AZ580200
C 74	20.2	1.9	25	1	ACCSSION:AZ634201
C 75	20.2	1.9	25	1	ACCSSION:AZ946508
C 76	20.2	1.9	25	1	ACCSSION:AZ959039
C 77	20.2	1.9	25	1	ACCSSION:AZ635627
C 78	20.2	1.9	25	1	ACCSSION:AZ641805
C 79	20.2	1.9	25	1	ACCSSION:AZ991225
C 80	20.2	1.9	25	1	ACCSSION:AZ514387
C 81	20.2	1.9	25	1	ACCSSION:AZ780002
C 82	20.2	1.9	25	1	ACCSSION:AZ780118
C 83	20.2	1.9	25	1	ACCSSION:AZ309945
C 84	20.2	1.9	25	1	ACCSSION:AZ452951
C 85	20.2	1.9	25	1	ACCSSION:AZ645446
C 86	20.2	1.9	25	1	ACCSSION:AZ451588
C 87	19.4	1.8	25	1	ACCSSION:AZ513902
C 88	19.4	1.8	25	1	ACCSSION:AZ784203
C 89	19.4	1.8	25	1	ACCSSION:AZ793094
C 90	19.4	1.8	25	1	ACCSSION:AZ801266
C 91	19.4	1.8	25	1	ACCSSION:AZ561191
C 92	19.4	1.8	25	1	ACCSSION:AZ822069
C 93	19.4	1.8	25	1	ACCSSION:AZ648796
C 94	19.4	1.8	25	1	ACCSSION:AZ431700
C 95	19.4	1.8	25	1	ACCSSION:AZ461642
C 96	19.4	1.8	25	1	ACCSSION:AZ649147
C 97	19.4	1.8	25	1	ACCSSION:AZ774954
C 98	19.4	1.8	25	1	ACCSSION:AZ795767
C 99	19.4	1.8	25	1	ACCSSION:AZ822936
C 100	19.4	1.8	25	1	ACCSSION:AZ827177
C 101	19.4	1.8	25	1	ACCSSION:AZ785549
C 102	19.4	1.8	25	1	ACCSSION:AZ818214
C 103	18.4	1.8	25	1	ACCSSION:AZ484241
C 104	18.4	1.8	25	1	ACCSSION:AZ632650
C 105	18.4	1.8	25	1	ACCSSION:AZ654458
C 106	18.4	1.8	25	1	ACCSSION:AZ793887



IMAGE:270507 5' similar to gb:M92934 CONNECTIVE TISSUE GROWTH  
FACTOR PRECURSOR (HUMAN) ; mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE

N41929 1 GI:1165960  
EST.  
Homo sapiens (human)

ORGANISM

Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 35)  
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,  
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,  
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,  
Trevasaki, E., Waterston, R., Williamson, A., Wohlmann, P. and  
Wilson, R.

AUTHORS

The WashU-Merck EST Project

TITLE

Unpublished (1995)

JOURNAL

Contact: Wilson RK

COMMENT

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

High quality sequence starts: 1

High quality sequence stops: 1

Source: IMAGE Consortium, LNL

This clone is available royalty-free through LNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Trace considered overall poor quality

Seq primer: 17

High quality sequence stop: 1.

FEATURES

source

1. .35

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="GDB:3880149"

/db\_xref="taxon:9606"

/clone="IMAGE:270507"

/sex="Male"

/tissue\_type="melanocyte"

/lab\_host="DH10B (ampicillin resistant)"

/clone\_lib="Soares melanocyte 2N5HM"

/note="Vector: p773D (Pharmacia) with a modified

polylinker; site 1: Not I; Site 2: Eco RI; 1st strand cDNA

was primed with a Not I - oligo(dT) primer [5].

TGTTACCAACTGAGTGGAGCGGCGAGTTTCTTTTCTTTT 3']

double-stranded cDNA was size selected, ligated to Eco RI

adapters (Pharmacia), digested with Not I and cloned into

the Not I and Eco RI sites of a modified p773 vector

(Pharmacia). Library constructed by Bento Soares and

M.Fatima Bonaldo. RNA from normal foreskin melanocytes

(FS374) was kindly provided by Dr. Anthony P. Albino."

Query Match

Best Local Similarity 3.0%; Score 31; DB 1; Length 35;

Matches 31; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY

1794 GTGTGTGTGTGTGTGTGTGTATATATATATATATATATAT 1827

Db

1 GNGTGTGTGTGTGTGTGTGTATATATATATATATATATAT 34

RESULT 3

AZ781130

LOCUS

AZ781130 26 bp DNA linear GSS 16-FEB-2001

DEFINITION 2M0019A07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC2M0019A07 F, genomic survey sequence.

ACCESSION

AZ781130

VERSION

AZ781130.1

KEYWORDS

GSS

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0019 row: A column: 07

Seq primer: CGTTGTAACACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 26.

FEATURES

source

1. .26

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC2M0019A07"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/notes="Vector: FWD42nv, Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnates/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pWD42 (GI:4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

Query Match

Best Local Similarity 2.2%; Score 23.4; DB 1; Length 26;

Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY

1793 TGTGTGTGTGTGTGTGTGTGTATAT 1817

|||||

Db

1 TGTGTGTGTGTGTGTGTGTGTAT 25

RESULT 4

AZ405219

LOCUS

DEFINITION

IM0173N21R Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC1M0173N21 R, genomic survey sequence.

ACCESSION

AZ405219

VERSION

AZ405219.1

KEYWORDS

GSS

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 26)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0019 row: A column: 07

Seq primer: CGTTGTAACACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 26.

FEATURES

source

1. .26

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC2M0019A07"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/notes="Vector: FWD42nv, Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnates/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pWD42 (GI:4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."







Niederhausern,A. and Wright,D.,Weiss,R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0242 row: A column: 24  
 Seq primer: CACACAGGAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 24.

# FEATURES

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 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0242A24"  
 /sex="Male"  
 /lab\_host="F. Coli strain XL10-Gold, Tl-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pPW42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 2.1%; Score 22.4; DB 1; Length 24;  
 Best Local Similarity 95.8%; Pred. No. 25;  
 Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1792 TTGTGTGTGTGTGTGTGTGTGTAT 1815  
 DB 1 TTGTGTGTGTGTGTGTGTGTGT 24

RESULT 9  
 AZ762101  
 LOCUS 25 bp DNA linear GSS 16-FEB-2001  
 DEFINITION 1M0556K17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0556K17 R, genomic survey sequence.  
 ACCESSION AZ762101  
 VERSION AZ762101.1 GI:12871750  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 25)  
 DUNN,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Stokes,R., Tingley,A., von Niederhausern,A. and Wright,D.,Weiss,R.

# TITLE

JOURNAL  
 COMMENT

Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0556 row: K column: 17  
 Seq primer: CACACAGGAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 25.

# FEATURES

1..25  
 Location/Qualifiers  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0556K17"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pPW42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 2.1%; Score 22.4; DB 1; Length 25;  
 Best Local Similarity 95.8%; Pred. No. 26;  
 Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTGTATA 1816  
 DB 2 TGTGTGTGTGTGTGTGTGTGTGTA 25

# RESULT 10

AZ780500/c  
 LOCUS 25 bp DNA linear GSS 16-FEB-2001  
 DEFINITION 2M0017J19R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0017J19 R, genomic survey sequence.  
 ACCESSION AZ780500  
 VERSION AZ780500.1 GI:12912224  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 25)  
 DUNN,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Stokes,R., Tingley,A., von Niederhausern,A. and Wright,D.,Weiss,R.

# TITLE

JOURNAL COMMENT	plasmid inserts		Unpublished (2000)		Contact: Robert B. Weiss		University of Utah Genome Center		Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT		84112, USA		Tel: 801 585 5606		Fax: 801 585 7177		Email: ddunn@genetics.utah.edu		Insert length: 10000 Std Error: 0.00		Plate: 0017 row: J column: 19		Seq primer: CACACAGGAACAGCTATGACC		Class: plasmid ends		High quality sequence stop: 25.		Location/Qualifiers		1. .25		/organism="Mus musculus"		/mol_type="genomic DNA"		/strain="C57BL/6J"		/db_xref="taxon:10090"		/clone="UUGC2M0017119"		/sex="Male"		/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"		/clone_lib="Mouse 10kb plasmid UUGC1M library"		/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [GII4732114 GB AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."		2.1%; Score 22.4; DB 1; Length 25;		Best Local Similarity 95.8%; Pred. No. 26;		Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		QY 1790 TATTGTGTGTGTGTGTGTGTGT 1813				Db 25 TTTTGTGTGTGTGTGTGTGTGT 2		RESULT 11		AZ345426/c		LOCUS		DEFINITION		ACCESSION		VERSION		KEYWORDS		SOURCE		ORGANISM		REFERENCE		AUTHORS		TITLE		JOURNAL		Unpublished (2000)		Contact: Robert B. Weiss		University of Utah Genome Center		Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT		84112, USA		Tel: 801 585 5606		Fax: 801 585 7177		Email: ddunn@genetics.utah.edu		Insert length: 10000 Std Error: 0.00		Plate: 0017 row: J column: 19		Seq primer: CACACAGGAACAGCTATGACC		Class: plasmid ends		High quality sequence stop: 28.		Location/Qualifiers		1. .28		/organism="Mus musculus"		/mol_type="genomic DNA"		/strain="C57BL/6J"		/db_xref="taxon:10090"		/clone="UUGC1M0080A09"		/sex="Male"		/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"		/clone_lib="Mouse 10kb plasmid UUGC1M library"		/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [GII4732114 GB AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. 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Location/Qualifiers		1. .28		/organism="Mus musculus"		/mol_type="genomic DNA"		/strain="C57BL/6J"		/db_xref="taxon:10090"		/clone="UUGC1M0080A09"		/sex="Male"		/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"		/clone_lib="Mouse 10kb plasmid UUGC1M library"		/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [GII4732114 GB AF129072.1], a copy-number inducible derivative of plasmid R1. 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Weiss		University of Utah Genome Center		Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT		84112, USA		Tel: 801 585 5606		Fax: 801 585 7177		Email: ddunn@genetics.utah.edu		Insert length: 10000 Std Error: 0.00		Plate: 0080 row: A column: 09		Seq primer: CGTGTAAACGACGCGCCAGT		Class: plasmid ends		High quality sequence stop: 28.		Location/Qualifiers		1. .28		/organism="Mus musculus"		/mol_type="genomic DNA"		/strain="C57BL/6J"		/db_xref="taxon:10090"		/clone="UUGC1M0080A09"		/sex="Male"		/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"		/clone_lib="Mouse 10kb plasmid UUGC1M library"		/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. 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Coli strain XL10-Gold, T1-resistant, F-"		/clone_lib="Mouse 10kb plasmid UUGC1M library"		/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [GII4732114 GB AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. 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No. 28;		Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		QY 1793 TGTGTGTGTGTGTGTGTGTGTATA 1816				Db 28 TGTGTGTGTGTGTGTGTGTGTGTA 5		RESULT 12		AZ435344		LOCUS		DEFINITION		ACCESSION		VERSION		KEYWORDS		SOURCE		ORGANISM		REFERENCE		AUTHORS		TITLE		JOURNAL		Unpublished (2000)		Contact: Robert B. Weiss		University of Utah Genome Center		Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT		84112, USA		Tel: 801 585 5606		Fax: 801 585 7177		Email: ddunn@genetics.utah.edu		Insert length: 10000 Std Error: 0.00		Plate: 0080 row: A column: 09		Seq primer: CGTGTAAACGACGCGCCAGT		Class: plasmid ends		High quality sequence stop: 28.		Location/Qualifiers		1. .28		/organism="Mus musculus"		/mol_type="genomic DNA"		/strain="C57
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## COMMENT

Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0222 row: K column: 17  
Seq primer: CGTTGTAACACGCGCCAGT  
Class: plasmid ends  
High quality sequence stop: 27.

## FEATURES

source

## FEATURES

source

1..27  
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/db\_xref="taxon:10090"  
/clone="UUGC1M0222K17"  
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Query Match 2.1%; Score 22.2; DB 1; Length 27;  
Best Local Similarity 88.9%; Pred. No. 29;  
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTATATAT 1819  
|||||  
Db 1 TGTGTGTGTGTGTGTGTGTGTGTGT 27

## RESULT 13

AZ638238 27 bp DNA linear GSS 13-DEC-2000  
LOCUS IM0498H05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
DEFINITION clone UUGC1M0498H05 F, genomic survey sequence.

## ACCESSION

AZ638238  
VERSION GI:11760428

## KEYWORDS

GSS.  
SOURCE Mus musculus (house mouse)

## ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 27)

## REFERENCE

## AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Rally, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.

## TITLE

Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

## JOURNAL

Unpublished (2000)

## COMMENT

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Query Match 2.1%; Score 22.2; DB 1; Length 27;  
Best Local Similarity 88.9%; Pred. No. 29;  
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTATATAT 1819  
|||||  
Db 1 TGTGTGTGTGTGTGTGTGTGTGTGT 27

## RESULT 14

AZ981811/c 27 bp DNA linear GSS 27-APR-2001  
LOCUS 2M0262D23f Mouse 10kb plasmid UUGC2M library Mus musculus genomic  
DEFINITION clone UUGC2M0262D23 F, genomic survey sequence.

## ACCESSION

AZ981811  
VERSION GI:13853038

## KEYWORDS

GSS.  
SOURCE Mus musculus (house mouse)

## ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
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Mouse whole genome scaffolding with paired end reads from 10kb  
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## JOURNAL

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## COMMENT

Contact: Robert B. Weiss

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University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0498 row: H column: 05

Seq primer: CGTTGTAACACGCGCCAGT

Class: plasmid ends

High quality sequence stop: 27.

Location/Qualifiers

1..27

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/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/notes="Vector: PWD42nv; Purified genomic DNA from M.

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 Insert Length: 10000 Std Error: 0.00  
 Plate: 0262 row: D column: 23  
 Seq primer: CGTTGTAACACGCGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 27.  
 Location/Qualifiers

# FEATURES

1. .27  
 /organism="Mus musculus"  
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 /clone\_lib="Mouse 10kb plasmid UUGC2M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 2.1%; Score 22.2; DB 1; Length 27;  
 Best Local Similarity 88.9%; Pred. No. 29;  
 Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTATAT 1819  
 |||||  
 Db 27 TGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1

RESULT 15  
 AZ774981/c  
 LOCUS 26 bp DNA linear GSS 16-FEB-2001  
 DEFINITION 2M0004D22R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC2M0004D22 R, genomic survey sequence.  
 AZ774981  
 VERSION AZ774981.1 GI:12900999  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 26)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D. Weiss, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
 Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: dunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0004 row: D column: 22  
 Seq primer: CACACAGAAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 26.  
 Location/Qualifiers

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 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC2M0004D22"  
 /sex="Male"  
 /lab\_host="E. coli strain XL10-Gold, Tl-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 2.1%; Score 22; DB 1; Length 26;  
 Best Local Similarity 100.0%; Pred. No. 29;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTGTGTGTGT 1814  
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 Db 25 TGTGTGTGTGTGTGTGTGTGTGTGTGT 4

RESULT 16  
 BX563211  
 LOCUS 25 bp mRNA linear EST 10-OCT-2003  
 DEFINITION BX563211 Glossina morsitans morsitans adult infected gut Glossina morsitans morsitans cDNA clone Tse65b06\_plc, mRNA sequence.  
 BX563211  
 ACCESSION BX563211.1 GI:33430473  
 VERSION BX563211.1  
 KEYWORDS EST.  
 SOURCE Glossina morsitans morsitans  
 ORGANISM Glossina morsitans morsitans  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscoidae; Glossinidae; Glossina.  
 1 (bases 1 to 25)  
 Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M., Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.  
 Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune response genes  
 Genome Biol. 4 (10), R63 (2003)  
 22881942  
 14519198  
 Contact: Hall N  
 Pathogen Sequencing Unit

The Sanger Institute The Wellcome Trust Genome Campus  
Hinxton, Cambridge, CB10 1SA, UK  
Request for clones, please contact: Mike Lehane  
Prof. W.J. Lehane  
School of Biological Sciences,  
University of Wales,  
Bangor LL57 2UW  
All clones with suffix q1c are reverse primer reads starting at 5'  
end of the cDNA all plc reads are from  
the 3' end.

#### FEATURES

source  
Location/Qualifiers  
1. .25  
/organism="Glossina morsitans morsitans"  
/mol\_type="mRNA"  
/sub\_species="morsitans"  
/db\_xref="taxon:37546"  
/clone="Tse65b06 plc"  
/tissue\_type="adult infected gut"  
/clone\_lib="Glossina morsitans morsitans adult infected  
gut"  
/note="country: Zimbabwe; EST from adult gut infected with  
T.brucei"

Query Match 2.1%; Score 21.8; DB 1; Length 25;  
Best Local Similarity 92.0%; Pred. No. 29;  
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTATAT 1817  
|||||  
Db 1 TGTGTGTGTGTGTGTGTGTGTGT 25

#### RESULT 17

AZ339866 25 bp DNA linear GSS 29-SEP-2000  
LOCUS 1M0071H01R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
DEFINITION clone UUGC1M0071H01 R, genomic survey sequence.  
ACCESSION AZ339866  
VERSION A2339866.1 GI:10414560  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 25)  
REFERENCE  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Rally,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D., Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0071 row: H column: 01  
Seq primer: CACACGGAACACTATGACC  
Class: plasmid ends  
High quality sequence stop: 25.  
Location/Qualifiers  
1. .25  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0071H01"  
/sex="Male"

#### FEATURES

source  
Location/Qualifiers  
1. .25  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0071H01"  
/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, P-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PWD42 (GI4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 2.1%; Score 21.8; DB 1; Length 25;  
Best Local Similarity 92.0%; Pred. No. 29;  
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTATAT 1817  
|||||  
Db 1 TGTGTGTGTGTGTGTGTGTGTGT 25

#### RESULT 18

BX569116 26 bp mRNA linear EST 14-OCT-2003  
LOCUS BX569116 Glossina morsitans morsitans adult infected gut Glossina  
DEFINITION morsitans morsitans cDNA clone Tse97f02\_plc, mRNA sequence.  
ACCESSION BX569116  
VERSION BX569116.1 GI:33437055  
KEYWORDS EST.  
SOURCE Glossina morsitans morsitans  
ORGANISM Glossina morsitans morsitans  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Hippoboscoidae; Glossinidae; Glossina.  
1 (bases 1 to 26)  
REFERENCE  
AUTHORS Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,  
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.  
TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina  
morsitans morsitans and expression analysis of putative immune  
response genes  
JOURNAL Genome Biol. 4 (10), R63 (2003)  
MEDLINE 22881942  
PUBMED 14519198  
COMMENT Contact: Hall N  
Pathogen Sequencing Unit  
The Sanger Institute The Wellcome Trust Genome Campus  
Hinxton, Cambridge, CB10 1SA, UK  
Request for clones, please contact: Mike Lehane  
Prof. W.J. Lehane  
School of Biological Sciences,  
University of Wales,  
Bangor LL57 2UW  
All clones with suffix q1c are reverse primer reads starting at 5'  
end of the cDNA all plc reads are from  
the 3' end.  
Location/Qualifiers  
1. .26  
/organism="Glossina morsitans morsitans"  
/mol\_type="mRNA"  
/sub\_species="morsitans"  
/db\_xref="taxon:37546"  
/clone="Tse97f02 plc"  
/tissue\_type="adult infected gut"

/clone\_lib="Glossina morsitans morsitans adult infected gut"  
 /note="country: Zimbabwe; EST from adult gut infected with T.brucei"

Query Match 2.1%; Score 21.8; DB 1; Length 26;  
 Best Local Similarity 92.0%; Pred. No. 30;  
 Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTATAT 1817  
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 Db 2 TGTGTGTGTGTGTGTGTGTGTGT 26

RESULT 19  
 AZ307889  
 LOCUS  
 DEFINITION  
 1M0010L18F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC1M0010L18 F, genomic survey sequence.

ACCESSION  
 AZ307889  
 VERSION  
 AZ307889.1 GI:10347331

KEYWORDS  
 GSS.

SOURCE  
 Mus musculus (house mouse)

ORGANISM  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;

REFERENCE

AUTHORS  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
 Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von  
 Niederhausern, A. and Wright, D., Weiss, R.

TITLE  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts

JOURNAL  
 Unpublished (2000)

COMMENT  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 1000 Std Error: 0.00

Plate: 0010 row: 1 column: 18

Seq primer: CGTTGTAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 26.

Location/Qualifiers

FEATURES

source

1..26

/organism="Mus musculus"

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/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC1M0010L18"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of PWD42 (G[14732114]gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into

adapted mouse DNA, and transformed into

adapted mouse DNA, and transformed into

adapted vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

Query Match 2.1%; Score 21.8; DB 1; Length 26;  
 Best Local Similarity 92.0%; Pred. No. 30;  
 Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTATAT 1817  
 |||||  
 Db 2 TGTGTGTGTGTGTGTGTGTGTGT 26

RESULT 20

AZ345505/c

LOCUS

DEFINITION

1M0080H01F Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC1M0080H01 F, genomic survey sequence.

ACCESSION

AZ345505

VERSION

AZ345505.1 GI:10424742

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 1000 Std Error: 0.00

Plate: 0080 row: H column: 01

Seq primer: CGTTGTAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 26.

Location/Qualifiers

FEATURES

source

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/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC1M0080H01"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of PWD42 (G[14732114]gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into

adapted mouse DNA, and transformed into

chemically-competent *E. coli* XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 2.1%; Score 21.8; DB 1; Length 26;  
Best Local Similarity 92.0%; Pred. No. 30;  
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTGTAT 1817  
|||||  
Db 26 TGTGTGTGTGTGTGTGTGTGTGT 2

RESULT 21  
AZ494537  
LOCUS 26 bp DNA linear GSS 05-OCT-2000  
DEFINITION IM0329D24R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0329D24 R, genomic survey sequence.  
ACCESSION AZ494537  
VERSION AZ494537.1 GI:10669212  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 26)  
REFERENCE Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0329 row: D column: 24  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 26.

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/organism="Mus musculus"  
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/db\_xref="taxon:10090"  
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/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/notes="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent *E. coli* XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

Query Match 2.1%; Score 21.8; DB 1; Length 26;  
Best Local Similarity 92.0%; Pred. No. 30;  
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTGTAT 1817  
|||||  
Db 2 TGTGTGTGTGTGTGTGTGTGTGT 26

RESULT 22  
AZ503652  
LOCUS 26 bp DNA linear GSS 05-OCT-2000  
DEFINITION IM0343FOIR Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0343FO1 R, genomic survey sequence.  
ACCESSION AZ503652  
VERSION AZ503652.1 GI:10684968  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 26)  
REFERENCE Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.  
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plasmid inserts  
Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
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University of Utah  
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84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
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Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 26.

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/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
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/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/notes="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
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was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent *E. coli* XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 2.1%; Score 21.8; DB 1; Length 26;  
 Best Local Similarity 92.0%; Pred. No. 30;  
 Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTAT 1817  
 |||||  
 DB 2 TGTGTGTGTGTGTGTGTGTGT 26

RESULT 23  
 AZ795803  
 LOCUS  
 DEFINITION 26 bp DNA linear GSS 16-FEB-2001  
 clone UUGC2M0051P11 F, genomic survey sequence.  
 AZ795803  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Mus musculus (house mouse)  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 1 (bases 1 to 26)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
 Reilly, M., Rose, R., Stokes, R., Tingey, A., von  
 Niederhausern, A. and Wright, D. Weiss, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0051 row: P column: 11  
 Seq primer: CGTTGTAACGACGCGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 26.  
 Location/Qualifiers  
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 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
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 /sex="Male"  
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 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /notes="Vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
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 with adaptors complementary to the insert adaptors and  
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 adaptor vector DNA, and transformed into  
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 and selected for ampicillin resistance."

FEATURES  
 source  
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 /strain="C57BL/6J"  
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Query Match 2.1%; Score 21.8; DB 1; Length 26;  
 Best Local Similarity 92.0%; Pred. No. 30;  
 Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTAT 1817  
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 DB 1 TGTGTGTGTGTGTGTGTGTGT 25

RESULT 24  
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 clone UUGC2M0067H16 R, genomic survey sequence.  
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 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Mus musculus (house mouse)  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
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 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0067 row: H column: 16  
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 High quality sequence stop: 26.  
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 /lab\_host="E. Coli strain XL10-Gold, TI-resistant, P-"  
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FEATURES  
 source  
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 Location/Qualifiers  
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 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
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 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, TI-resistant, P-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /notes="Vector: PWD42nv; Purified genomic DNA from M.  
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 inducible derivative of plasmid R1. The vector was ligated  
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 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

Query Match 2.1%; Score 21.8; DB 1; Length 26;



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Best Local Similarity 92.0%; Pred. No. 30;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTAT 1817
      |||||
Db 2 TGTGTGTGTGTGTGTGTGTGTGT 26

RESULT 25
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DEFINITION
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clone UUG2M0250L12 R, genomic survey sequence.
ACCESSION
AZ975568
VERSION
AZ975568.1 GI:13846795
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 26)
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
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plasmid inserts
JOURNAL
Unpublished (2000)
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84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0250 row: L column: 12
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 26.
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/clone_lib="Mouse 10kb plasmid UUG2M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
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Query Match 2.1%; Score 21.8; DB 1; Length 26;
Best Local Similarity 92.0%; Pred. No. 30;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTAT 1817
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Db 25 TGTGTGTGTGTGTGTGTGTGTGT 1

RESULT 26
AZ329433
LOCUS
DEFINITION
IM0053K11R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0053K11 R, genomic survey sequence.
ACCESSION
AZ329433
VERSION
AZ329433.1 GI:10390140
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 27)
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
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Niederhausern,A. and Wright,D., Weiss,R.
TITLE
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Unpublished (2000)
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84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0053 row: K column: 11
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Class: plasmid ends
High quality sequence stop: 27.
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/lab_host="E. coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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Query Match 2.1%; Score 21.8; DB 1; Length 27;
Best Local Similarity 92.0%; Pred. No. 31;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy 1793 TGTGTGTGTGTGTGTGTGTGTAT 1817
Db 1 TGTGTGTGTGTGTGTGTGTGTGTGT 26

RESULT 27
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LOCUS 1M0075004R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0075004 R, genomic survey sequence.
ACCESSION AZ342492
VERSION AZ342492.1 GI:10419783
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 27)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0075 row: 0 column: 04
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Class: plasmid ends
High quality sequence stop: 27.
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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Qy 1793 TGTGTGTGTGTGTGTGTGTGTAT 1817
Db 1 TGTGTGTGTGTGTGTGTGTGTGTGT 26

RESULT 28
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LOCUS 1M017218R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M017218 R, genomic survey sequence.
ACCESSION AZ404479
VERSION AZ404479.1 GI:10528408
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
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84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
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Best Local Similarity 92.0%; Pred. No. 31;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTGTGTGTGTGTAT 1817
Db 1 TGTGTGTGTGTGTGTGTGTGTGTGT 26

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LOCUS 1M017218R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M017218 R, genomic survey sequence.
ACCESSION AZ404479
VERSION AZ404479.1 GI:10528408
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0172 row: F column: 18
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Class: plasmid ends
High quality sequence stop: 27.
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/notes="Vector: PWD42nv; Purified genomic DNA from M.
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Query Match 2.1%; Score 21.8; DB 1; Length 27;
Best Local Similarity 92.0%; Pred. No. 31;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

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Db      3  TGTGTGTGTGTGTGTGTGTGTAT 27
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LOCUS   27 bp      DNA      linear      GSS 13-DEC-2000
DEFINITION
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clone UUGC1M0376L16 R, genomic survey sequence.
ACCESSION
AZ583081
VERSION
AZ583081.1 GI:11702607
KEYWORDS
GSS.
SOURCE  Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
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Tel: 801 585 5606
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Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0376 row: L column: 16
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 27.
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/organism="Mus musculus"
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/clone="UUGC1M0376L16"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (G|4732114|G|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
Query Match 2.1%; Score 21.8; DB 1; Length 27;
Best Local Similarity 92.0%; Pred. No. 31;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1793 TGTGTGTGTGTGTGTGTGTAT 1817
|||||
Db      2  TGTGTGTGTGTGTGTGTGTGTGT 26
|||||
RESULT 30
AZ758321
LOCUS   27 bp      DNA      linear      GSS 16-FEB-2001
DEFINITION
1M0550G18F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0550G18 F, genomic survey sequence.
ACCESSION
AZ758321
VERSION
AZ758321.1 GI:12863998
KEYWORDS
GSS.
SOURCE  Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 27)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0550 row: G column: 18
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 27.
FEATURES
Location/Qualifiers
1..27
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0550G18"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (G|4732114|G|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
Query Match 2.1%; Score 21.8; DB 1; Length 27;
Best Local Similarity 92.0%; Pred. No. 31;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1793 TGTGTGTGTGTGTGTGTGTAT 1817
|||||
Db      2  TGTGTGTGTGTGTGTGTGTGTGT 26
|||||

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RESULT 31
AZ788874
LOCUS
DEFINITION
  27 bp      DNA      linear      GSS 16-FEB-2001
  2M0036H16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
  clone UUGC2M0036H16 F, genomic survey sequence.
ACCESSION
  AZ788874
VERSION
  AZ788874.1
KEYWORDS
  GSS.
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Mus musculus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  1 (bases 1 to 27)
REFERENCE
  Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
  Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
  Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von
  Niederhausern, A. and Wright, D., Weiss, R.
  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts
JOURNAL
  Unpublished (2000)
COMMENT
  Contact: Robert B. Weiss
  University of Utah Genome Center
  University of Utah
  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
  84112, USA
  Tel: 801 585 5606
  Fax: 801 585 7177
  Email: ddunn@genetics.utah.edu
  Insert Length: 10000 Std Error: 0.00
  Plate: 0036 row: H column: 16
  Seq primer: CGTTGTAACGACGCGCAGT
  Class: plasmid ends
  High quality sequence stop: 27.
  Location/Qualifiers
  1..27
  /organism="Mus musculus"
  /mol_type="genomic DNA"
  /strain="C57BL/6J"
  /db_xref="taxon:10090"
  /clone="UUGC2M0036H16"
  /sex="Male"
  /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
  /clone_lib="Mouse 10kb plasmid UUGC1M library"
  /note="Vector: PWD42nv; Purified genomic DNA from M.
  musculus C57BL/6J (male) was obtained from the Jackson
  Laboratory Mouse DNA Resource
  (http://www.jax.org/resources/documents/dnares/). The DNA
  was hydrodynamically sheared by repeated passage through a
  0.005 inch orifice at constant velocity. The sheared DNA
  was blunt end-repaired with T4 DNA polymerase and T4
  polynucleotide kinase. Adaptor oligonucleotides were
  ligated to the blunt ends in high molar excess. The
  adaptor DNA was purified and size-selected for a 9.5 to
  10.5 kb range using preparative agarose gel
  electrophoresis. Vector DNA was prepared from a derivative
  of pWD42 (G|4732114|gb|AF129072.1), a copy-number
  inducible derivative of plasmid R1. The vector was ligated
  with adaptors complementary to the insert adaptors and
  purified. The sheared, adaptor mouse DNA was annealed to
  adaptor vector DNA, and transformed into
  chemically-competent E. coli XL10-Gold (Stratagene) cells
  and selected for ampicillin resistance."
  Query Match 2.1%; Score 21.8; DB 1; Length 27;
  Best Local Similarity 92.0%; Pred. No. 31;
  Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTATAT 1817
      |||||
      3 TGTGTGTGTGTGTGTGTGTGTGTGTGT 27

Db

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RESULT 32
AZ801217
LOCUS
DEFINITION
  27 bp      DNA      linear      GSS 16-FEB-2001
  2M0059P03R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
  clone UUGC2M0059P03 R, genomic survey sequence.
ACCESSION
  AZ801217
VERSION
  AZ801217.1
KEYWORDS
  GSS.
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Mus musculus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  1 (bases 1 to 27)
REFERENCE
  Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
  Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
  Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von
  Niederhausern, A. and Wright, D., Weiss, R.
  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts
JOURNAL
  Unpublished (2000)
COMMENT
  Contact: Robert B. Weiss
  University of Utah Genome Center
  University of Utah
  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
  84112, USA
  Tel: 801 585 5606
  Fax: 801 585 7177
  Email: ddunn@genetics.utah.edu
  Insert Length: 10000 Std Error: 0.00
  Plate: 0059 row: F column: 03
  Seq primer: CACACAGAAACAGCTATGACC
  Class: plasmid ends
  High quality sequence stop: 27.
  Location/Qualifiers
  1..27
  /organism="Mus musculus"
  /mol_type="genomic DNA"
  /strain="C57BL/6J"
  /db_xref="taxon:10090"
  /clone="UUGC2M0059P03"
  /sex="Male"
  /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
  /clone_lib="Mouse 10kb plasmid UUGC1M library"
  /note="Vector: PWD42nv; Purified genomic DNA from M.
  musculus C57BL/6J (male) was obtained from the Jackson
  Laboratory Mouse DNA Resource
  (http://www.jax.org/resources/documents/dnares/). The DNA
  was hydrodynamically sheared by repeated passage through a
  0.005 inch orifice at constant velocity. The sheared DNA
  was blunt end-repaired with T4 DNA polymerase and T4
  polynucleotide kinase. Adaptor oligonucleotides were
  ligated to the blunt ends in high molar excess. The
  adaptor DNA was purified and size-selected for a 9.5 to
  10.5 kb range using preparative agarose gel
  electrophoresis. Vector DNA was prepared from a derivative
  of pWD42 (G|4732114|gb|AF129072.1), a copy-number
  inducible derivative of plasmid R1. The vector was ligated
  with adaptors complementary to the insert adaptors and
  purified. The sheared, adaptor mouse DNA was annealed to
  adaptor vector DNA, and transformed into
  chemically-competent E. coli XL10-Gold (Stratagene) cells
  and selected for ampicillin resistance."
  Query Match 2.1%; Score 21.8; DB 1; Length 27;
  Best Local Similarity 92.0%; Pred. No. 31;
  Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTATAT 1817
      |||||
      3 TGTGTGTGTGTGTGTGTGTGTGTGTGT 27

Db

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RESULT 33
BX557786      23 bp  mRNA  linear  EST 10-OCT-2003
LOCUS
DEFINITION  BX557786 Glossina morsitans morsitans adult infected gut Glossina
              morsitans morsitans cDNA clone Tse34f11_p1c, mRNA sequence.
ACCESSION   BX557786
VERSION     BX557786.1 GI:33428961
KEYWORDS    EST.
SOURCE      Glossina morsitans morsitans
ORGANISM    Glossina morsitans morsitans
             Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
             Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
             Hippoboscidae; Glossinidae; Glossina.
REFERENCE   1 (bases 1 to 23)
AUTHORS     Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M.,
             Hamilton, J., Soares, M.B., Donald, M.F., Lehane, S. and Hall, N.
TITLE       Adult midgut expressed sequence tags from the tsetse fly Glossina
             morsitans morsitans and expression analysis of putative immune
             response genes
JOURNAL     Genome Biol. 4 (10), R63 (2003)
MEDLINE     22881942
PubMed     14519138
COMMENT     Contact: Hall N
             Pathogen Sequencing Unit
             The Sanger Institute The Wellcome Trust Genome Campus
             Hinxton, Cambridge, CB10 1SA, UK
             Request for clones, please contact: Mike Lehane
             Prof. M.J. Lehane
             School of Biological Sciences,
             University of Wales,
             Bangor LL57 2UW
             All clones with suffix q1c are reverse primer reads starting at 5'
             end of the cDNA all p1c reads are from
             the 3' end.
FEATURES             Location/Qualifiers
             1..23
             /organism="Glossina morsitans morsitans"
             /mol_type="mRNA"
             /sub_species="morsitans"
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             /tissue_type="adult infected gut"
             /clone_lib="Glossina morsitans morsitans adult infected
             gut"
             /notes="country: Zimbabwe; EST from adult gut infected with
             T.brucei"
             Query Match      2.0%; Score 21.4; DB 1; Length 23;
             Best Local Similarity 95.7%; Pred. No. 30;
             Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  1793  TGTGTGTGTGTGTGTGTGTGTAT 1815
          |||||
          1  TGTGTGTGTGTGTGTGTGTGTGTGTGT 23

Db

RESULT 34
A2483624      23 bp  DNA  linear  GSS 05-OCT-2000
LOCUS
DEFINITION  A2483624 Mouse 10kb plasmid UUGC1M library Mus musculus genomic
              clone UUGC1M0309C01 R, genomic survey sequence.
ACCESSION   A2483624
VERSION     A2483624.1 GI:10647786
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
             1 (bases 1 to 23)
REFERENCE   1 (bases 1 to 23)
AUTHORS     Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
             Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
             Reilly, M., Rose, R., Stokes, R., Tingey, A., von
             Niederhausern, A. and Wright, D., Weiss, R.
             Mouse whole genome scaffolding with paired end reads from 10kb

```

```

TITLE       Mouse whole genome scaffolding with paired end reads from 10kb
             plasmid inserts
JOURNAL     Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
             University of Utah Genome Center
             Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
             84112, USA
             Tel: 801 585 5606
             Fax: 801 585 7177
             Email: dduenne@genetics.utah.edu
             Insert Length: 10000 Std Error: 0.00
             Plate: 0309 row: C column: 01
             Seq primer: CACACAGGAACAGCTATGACC
             Class: plasmid ends
             High quality sequence stop: 23.
FEATURES             Location/Qualifiers
             1..23
             /organism="Mus musculus"
             /mol_type="genomic DNA"
             /strain="C57BL/6J"
             /db_xref="taxon:10090"
             /clone="UUGC1M0309C01"
             /sex="Male"
             /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
             /clone_lib="Mouse 10kb plasmid UUGC1M library"
             /note="Vector: pWD42nv; Purified genomic DNA from M.
             musculus C57BL/6J (male) was obtained from the Jackson
             Laboratory Mouse DNA Resource
             (http://www.jax.org/resources/documents/dnares/). The DNA
             was hydrodynamically sheared by repeated passage through a
             0.005 inch orifice at constant velocity. The sheared DNA
             was blunt end-repaired with T4 DNA polymerase and T4
             polynucleotide kinase. Adaptor oligonucleotides were
             ligated to the blunt ends in high molar excess. The
             adaptor DNA was purified and size-selected for a 9.5 to
             10.5 kb range using preparative agarose gel
             electrophoresis. Vector DNA was prepared from a derivative
             of pWD42 (GI4732114|GB|AF129072.1), a copy-number
             inducible derivative of plasmid R1. The vector was ligated
             with adaptors complementary to the insert adaptors and
             purified. The sheared, adaptor mouse DNA was annealed to
             adaptor vector DNA, and transformed into
             chemically-competent E. coli XL10-Gold (Stratagene) cells
             and selected for ampicillin resistance."
             Query Match      2.0%; Score 21.4; DB 1; Length 23;
             Best Local Similarity 95.7%; Pred. No. 30;
             Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  1793  TGTGTGTGTGTGTGTGTGTGTAT 1815
          |||||
          1  TGTGTGTGTGTGTGTGTGTGTGTGTGT 23

Db

RESULT 35
A2637290/c    23 bp  DNA  linear  GSS 13-DEC-2000
LOCUS
DEFINITION  A2637290 Mouse 10kb plasmid UUGC1M library Mus musculus genomic
              clone UUGC1M0496005 R, genomic survey sequence.
ACCESSION   A2637290
VERSION     A2637290.1 GI:11759480
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
             1 (bases 1 to 23)
REFERENCE   1 (bases 1 to 23)
AUTHORS     Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
             Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
             Reilly, M., Rose, R., Stokes, R., Tingey, A., von
             Niederhausern, A. and Wright, D., Weiss, R.
             Mouse whole genome scaffolding with paired end reads from 10kb

```

plasmid inserts  
 Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0496 row: 0 column: 05  
 Seq primer: CACACAGAAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 23.

# FEATURES

source

1. .23  
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 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0496C05"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G14732114|GB|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 2.0%; Score 21.4; DB 1; Length 23;  
 Best Local Similarity 95.7%; Pred. No. 30;  
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTAT 1815  
 |||||  
 DB 23 TGTGTGTGTGTGTGTGTGT 1

RESULT 36  
 AZ789907/c  
 LOCUS  
 DEFINITION  
 2M0038G13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC2M0038G13 F, genomic survey sequence.

ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM

Mus musculus  
 Mus musculus (house mouse)  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 23)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
 Niederhausern, A., and Wright, D., Weiss, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts

# JOURNAL COMMENT

Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0038 row: G column: 13  
 Seq primer: CGTTGTAACACGCGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 23.

# FEATURES

source

1. .23  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC2M0038G13"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G14732114|GB|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 2.0%; Score 21.4; DB 1; Length 23;  
 Best Local Similarity 95.7%; Pred. No. 30;  
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTAT 1815  
 |||||  
 DB 23 TGTGTGTGTGTGTGTGTGT 1

RESULT 37  
 AZ829195/c  
 LOCUS  
 DEFINITION  
 2M0106M12R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC2M0106M12 R, genomic survey sequence.

ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM

Mus musculus  
 Mus musculus (house mouse)  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 23)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
 Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von  
 Niederhausern, A., and Wright, D., Weiss, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 Unpublished (2000)

```

COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0106 row: M column: 12
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 23.

FEATURES
Location/Qualifiers
1..23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0106M12"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42hy; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 2.0%; Score 21.4; DB 1; Length 23;
Best Local Similarity 95.7%; Pred. No. 30;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTAT 1815
1 1 TGTGTGTGTGTGTGTGTGTGTGT 1
Db 23 TGTGTGTGTGTGTGTGTGTGTGT 1

RESULT 38
BX559963 24 bp mRNA linear EST 10-OCT-2003
LOCUS BX559963 Glossina morsitans morsitans adult infected gut Glossina morsitans morsitans cDNA clone Tse47a03_plc, mRNA sequence.
ACCESSION BX559963
VERSION BX559963.1 GI:33367923
KEYWORDS EST.
SOURCE Glossina morsitans morsitans
ORGANISM Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscidae; Glossinidae; Glossina.
1 (bases 1 to 24)
Lehane, M.J., Aksoy, S., Gibson, W., Kertihornou, A., Berriman, M., Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N. Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune response genes
Genome Biol. 4 (10), R63 (2003)
22881942

JOURNAL MEDLINE

REFERENCE
AUTHORS
Lehane, M.J., Aksoy, S., Gibson, W., Kertihornou, A., Berriman, M., Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N. Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune response genes
Genome Biol. 4 (10), R63 (2003)
22881942

TITLE
morsitans morsitans and expression analysis of putative immune response genes

JOURNAL MEDLINE

REFERENCE
AUTHORS
Lehane, M.J., Aksoy, S., Gibson, W., Kertihornou, A., Berriman, M., Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N. Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune response genes
Genome Biol. 4 (10), R63 (2003)
22881942

TITLE
morsitans morsitans and expression analysis of putative immune response genes

JOURNAL MEDLINE

REFERENCE
AUTHORS
Lehane, M.J., Aksoy, S., Gibson, W., Kertihornou, A., Berriman, M., Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N. Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune response genes
Genome Biol. 4 (10), R63 (2003)
22881942

PUBMED
COMMENT
14519198
Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J. Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix q1c are reverse primer reads starting at 5' end of the cDNA all plc reads are from the 3' end.

FEATURES
Location/Qualifiers
1..24
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse47a03_plc"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected gut"
/notes="country: Zimbabwe; EST from adult gut infected with T.brucei"

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Best Local Similarity 95.7%; Pred. No. 31;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTAT 1815
1 1 TGTGTGTGTGTGTGTGTGTGTGT 23
Db 23 TGTGTGTGTGTGTGTGTGTGTGT 1

RESULT 39
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LOCUS AZ419602 Clone UUGC1M0196L12 F, genomic survey sequence.
DEFINITION Clone UUGC1M0196L12 F, genomic survey sequence.
ACCESSION AZ419602
VERSION AZ419602.1 GI:10543615
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 24)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0196 row: L column: 12
Seq primer: CTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 24.

FEATURES
Location/Qualifiers
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/mol_type="genomic DNA"
/strain="C57BL/6J"

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/sex="Male"
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/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      2.0%; Score 21.4; DB 1; Length 24;
Best Local Similarity 95.7%; Pred. No. 31;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTAT 1815
DB 1 TGTGTGTGTGTGTGTGTGTGTGT 23

RESULT 40
AZ621455
LOCUS
DEFINITION
IM0454K11R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0454K11 R, genomic survey sequence.
ACCESSION
AZ621455
VERSION
AZ621455.1 GI:11743645
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 24)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D. Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0454 row: K column: 11
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 24.
Location/Qualifiers
1. .24
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"

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/clone="UUGC1M0454K11"
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      2.0%; Score 21.4; DB 1; Length 24;
Best Local Similarity 95.7%; Pred. No. 31;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTAT 1815
DB 1 TGTGTGTGTGTGTGTGTGTGTGT 23

RESULT 41
AZ807762
LOCUS
DEFINITION
AZ807762
24 bp DNA linear GSS 20-FEB-2001
clone UUGC2M0070014 R, genomic survey sequence.
ACCESSION
AZ807762
VERSION
AZ807762.1 GI:12972432
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 24)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D. Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0070 row: O column: 14
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High quality sequence stop: 24.
Location/Qualifiers
1. .24
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0070014"

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/sex="Male"  
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/note="Vector: pW42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pW42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 2.0%; Score 21.4; DB 1; Length 24;  
Best Local Similarity 95.7%; Pred. No. 31;  
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1793 TGTGTGTGTGTGTGTGTAT 1815  
|||||  
Db 1 TGTGTGTGTGTGTGTGTGT 23

RESULT 42  
AZ813106/c  
LOCUS  
DEFINITION  
AZ813106 Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC2M0080A16 F, genomic survey sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Mus musculus  
Mus musculus (house mouse)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 24)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: dunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0080 row: A column: 16  
Seq primer: CGTTGTAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 24.  
Location/Qualifiers  
1. 24  
/organism="Mus musculus"  
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/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0080A16"  
/sex="Male"

FEATURES  
source  
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/sex="Male"

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/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: pW42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pW42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 2.0%; Score 21.4; DB 1; Length 24;  
Best Local Similarity 95.7%; Pred. No. 31;  
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1793 TGTGTGTGTGTGTGTGTAT 1815  
|||||  
Db 24 TGTGTGTGTGTGTGTGTGTGT 2

RESULT 43  
AZ846178  
LOCUS  
DEFINITION  
AZ846178 Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC2M0146F14 F, genomic survey sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Mus musculus  
Mus musculus (house mouse)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 24)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: dunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0146 row: F column: 14  
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Class: plasmid ends  
High quality sequence stop: 24.  
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/mol\_type="genomic DNA"  
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/db\_xref="taxon:10090"  
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/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

FEATURES  
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1. 24  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
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/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone.lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

Query Match 2.0%; Score 21.4; DB 1; Length 24;

Best Local Similarity 95.7%; Pred. No. 31;

Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTAT 1815

Db 2 TGTGTGTGTGTGTGTGTGTGTGTGT 24

#### RESULT 44

TA163H11P/c 24 bp DNA linear GSS 13-DEC-2000  
 LOCUS T. brucei sheared genomic DNA clone 163h11, forward sequence,  
 genomic survey sequence.

ACCESSION AL472248

VERSION AL472248.1 GI:11837597

#### KEYWORDS

GSS.

#### SOURCE

Trypanosoma brucei

Trypanosoma brucei

Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;

Trypanosoma.

1 (bases 1 to 24)

Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,

Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,

McVillie, S.B., Rajandream, M.A. and Barrell, B.G.

Direct Submission

Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing

project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,

Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and

nh@sanger.ac.uk

Constructed at the Institute for Genomic Research (TIGR).

Rockville, MD. Genomic DNA isolated from a cloned population of

Trypanosoma brucei (REU927/4 Gnat 10.1) was mechanically sheared

to give a tight size distribution (

4 kb). The v + i method used for the library construction is

described in detail in Smith, H. and Venter, J.C. (Making small

insert libraries for whole genome shotgun sequencing projects. In

Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.

Barrell, Oxford University Press, 1999).

Email: nh@sanger.ac.uk

Details of T. brucei sequencing at the Sanger Centre are available

at http://www.sanger.ac.uk/Projects/T\_brucei/.

Location/Qualifiers

1..24

/organism="Trypanosoma brucei"

/mol\_type="genomic DNA"

/strain="REU927"

/db\_xref="taxon:5691"

/clone="163h11"

#### FEATURES

source

Query Match

Best Local Similarity

Matches

22; Conservative

0; Mismatches

1; Indels

0; Gaps

0;

Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTAT 1815

Db 23 TGTGTGTGTGTGTGTGTGTGTGTGT 1

#### RESULT 45

AZ345553

LOCUS

DEFINITION

AZ345553

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 25)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Jongacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

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Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: dunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0080 row: E column: 16

Seq primer: CGTTGTAACGACGCCACT

Class: plasmid ends

High quality sequence stop: 25.

Location/Qualifiers

1..25

/organism="Mus musculus"

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/db\_xref="taxon:10090"

/clone="UUGC1M0080E16"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, Ti-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

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polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adaptor DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pWD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adaptor mouse DNA was annealed to

adaptor vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

Query Match

Best Local Similarity

Matches

22; Conservative

0; Mismatches

1; Indels

0; Gaps

0;

QY 1793 TGTGTGTGTGTGTGTGTGTAT 1815  
 Db 2 TGTGTGTGTGTGTGTGTGTGT 24

RESULT 46  
 AZ404057/C  
 LOCUS  
 DEFINITION  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT  
 FEATURES  
 source

AZ404057 25 bp DNA linear GSS 03-OCT-2000  
 1M0172D10F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC1M0172D10 F, genomic survey sequence.  
 AZ404057  
 AZ404057.1 GI:10528070  
 GSS.  
 Mus musculus (house mouse)  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 25)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
 Niederhausern, A., and Wright, D., Weiss, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0172 row: D column: 10  
 Seq primer: CGTGTAAACGACGCGCAGT  
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 High quality sequence stop: 25.  
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 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /notes="Vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
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 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

Query Match 2.0%; Score 21.4; DB 1; Length 25;  
 Best Local Similarity 95.7%; Pred. No. 32;  
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTAT 1815  
 Db 24 TGTGTGTGTGTGTGTGTGTGT 2

RESULT 47  
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 LOCUS  
 DEFINITION  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT  
 FEATURES  
 source

AZ467470 25 bp DNA linear GSS 04-OCT-2000  
 1M0278E21R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC1M0278E21 R, genomic survey sequence.  
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 AZ467470.1 GI:10625595  
 GSS.  
 Mus musculus (house mouse)  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
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 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
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 and selected for ampicillin resistance."

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 Best Local Similarity 95.7%; Pred. No. 32;  
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTAT 1815

Db 3 TGTGTGTGTGTGTGTGTGT 25

RESULT 48  
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clone UUGC1M0570D12 R, genomic survey sequence.  
ACCESSION  
AZ769673  
VERSION  
AZ769673.1 GI:12890050  
KEYWORDS  
GSS.  
SOURCE  
Mus musculus (house mouse)  
ORGANISM  
Mus musculus  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
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Niederhausern,A. and Wright,D., Weiss,R.  
Niederhausern,A. and Wright,D., Weiss,R.  
TITLE  
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JOURNAL  
Unpublished (2000)  
COMMENT  
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84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
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/notes="Vector: PWD42nv; Purified genomic DNA from M.  
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Laboratory Mouse DNA Resource  
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10.5 kb range using preparative agarose gel  
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adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
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source  
1. .25  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
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/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
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/notes="Vector: PWD42nv; Purified genomic DNA from M.  
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Best Local Similarity 95.7%; Pred. NO. 32;  
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTAT 1815

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Db 2 TGTGTGTGTGTGTGTGTGT 24

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ACCESSION  
AZ771881  
VERSION  
AZ771881.1 GI:12894610  
KEYWORDS  
GSS.  
SOURCE  
Mus musculus (house mouse)  
ORGANISM  
Mus musculus  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
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Reilly,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D., Weiss,R.  
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TITLE  
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JOURNAL  
Unpublished (2000)  
COMMENT  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
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84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plats: 0574 row: F column: 23  
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High quality sequence stop: 25.  
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/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/notes="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
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source  
1. .25  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
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Query Match 2.0%; Score 21.4; DB 1; Length 25;  
Best Local Similarity 95.7%; Pred. NO. 32;  
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTAT 1815

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Db 2 TGTGTGTGTGTGTGTGTGT 24

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 LOCUS  
 DEFINITION  
 1M019N03R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC1M0196N03 R, genomic survey sequence.  
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 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 26)  
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
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 84112 USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: dunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0196 row: N column: 03  
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 Class: plasmid ends  
 High quality sequence stop: 26.

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 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
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Query Match 2.0%; Score 21.4; DB 1; Length 26;  
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 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
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 Email: dunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0278 row: 0 column: 07  
 Seq primer: CGTTGTAACACGACGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 26.

## FEATURES

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 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
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 /clone="UUGC1M0278O07"  
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 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
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 Best Local Similarity 95.7%; Pred. No. 33;  
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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 DB 4 TGTGTGTGTGTGTGTGTGT 26

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 clone UUGCLM0513L06 F, genomic survey sequence.  
 ACCESSION  
 AZ646850  
 VERSION  
 GSS.  
 SOURCE  
 Mus musculus (house mouse)  
 ORGANISM  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
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 TITLE  
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 Insert Length: 10000 Std Error: 0.00  
 Plate: 0513 row: L column: 06  
 Seq primer: CGTTGTAAACACGCGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 26.

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 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1793 TGTGTGTGTGTGTGTGTGTAT 1815  
 ||||||||||||||||||  
 DB 3 TGTGTGTGTGTGTGTGTGTGT 25

RESULT 53

AZ830551  
 LOCUS  
 DEFINITION  
 2M0109C19R Mouse 10kb plasmid UUGCLM library Mus musculus genomic  
 clone UUGC2M0109C19 R, genomic survey sequence.  
 ACCESSION  
 AZ830551  
 VERSION  
 GSS.  
 SOURCE  
 Mus musculus (house mouse)  
 ORGANISM  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 26)  
 Dunn, D., Aoyagi, A., Barber, M., Beacom, T., Duval, B., Hamil, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
 Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von  
 Niederhausern, A. and Wright, D., Weiss, R.  
 TITLE  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 JOURNAL  
 Unpublished (2000)  
 COMMENT  
 Contact: Robert B. Weiss  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0109 row: C column: 19  
 Seq primer: CACACAGAAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 26.

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 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGCLM library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of PWD42 [gi14732114|gb|AF129072.1], a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

Query Match 2.0%; Score 21.4; DB 1; Length 26;  
 Best Local Similarity 95.7%; Pred. No. 33;  
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1793 TGTGTGTGTGTGTGTGTGTAT 1815  
 ||||||||||||||||||  
 DB 3 TGTGTGTGTGTGTGTGTGTGT 25

RESULT 54  
 AZ310642

LOCUS	A2310642	21 bp	DNA	linear	GSS 29-SEP-2000
DEFINITION	IM0025N09R Mouse 10kb plasmid UGCM1M library Mus musculus genomic clone UGCM10025N09 R, genomic survey sequence.				
ACCESSION	A2310642				
VERSION	A2310642.1	GI:10352832			
KEYWORDS	GSS.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus; 1 (Bases 1 to 21)				
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D.,Weise,R.				
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts				
JOURNAL	Unpublished (2000)				
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLU, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0025 row: N column: 09 Seq primer: CACACAGGAACAGCTATGACC Class: plasmid ends High quality sequence stop: 21.				

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FEATURES
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="vector: pWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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Query Match      2.0%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTGTGTGTGT 1813
Db 1 TGTGTGTGTGTGTGTGTGT 21

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RESULT 55				
AZ333309				
AZ333309				
LOCUS	AZ333309	21 bp	DNA	linear
				GSS 29-SEP-2000

1M062P313F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC1M0062P313 F, genomic survey sequence.  
 AZ333309  
 AZ333309.1 GI:10397798  
 GSS.  
 Mus musculus (house mouse)  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 21)  
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T.,  
 Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von  
 Niederhausern,A. and Wright,D., Weiss,R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLCT, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunne@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0062 row: P column: 13  
 Seq primer: CGTGTAAACGACGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 21.  
 Location/Qualifiers  
 1 . 21  
 source

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1. 21
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/clone="UGGC:M0062P13"
/sex="Male"
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/clone_lib="Mouse 10kb plasmid UGCIM library"
/note="vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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Query Match	2.0%	Score 21;	DB 1;	Length 21;
Best Local Similarity	100.0%;	Pred. NO. 30;		
Matches	21;	Conservative	0;	Mismatches
			0;	Indels
			0;	Gaps
			0;	
Qy	1793	TGTGTGTGTGTGTGTGT	1813	
Db	1	TGTGTGTGTGTGTGTGT	21	

RESULT 56	LOCUS	21 bp	DNA	linear	GSS 16-FEB-2001
AZ762904	AZ762904	100558G12F	Mouse	10kb plasmid UUC1M	library Mus musculus genomic
AZ762904	AZ762904	DEFINITION			





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VERSION      AZ484090.1  GI:10648679
KEYWORDS     GSS.
SOURCE       Mus musculus (house mouse)
ORGANISM     Mus musculus
REFERENCE    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
              1 (bases 1 to 22)
              Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
              Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
              Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
              Niederhausern,A. and Wright,D. Weiss,R.
TITLE        Mouse whole genome scaffolding with paired end reads from 10kb
              plasmid inserts
JOURNAL      Unpublished (2000)
COMMENT      Contact: Robert B. Weiss
              University of Utah Genome Center
              Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
              84112, USA
              Tel: 801 585 5606
              Fax: 801 585 7177
              Email: ddunn@genetics.utah.edu
              Insert Length: 10000 Std Error: 0.00
              Plate: 0310 row: 1 column: 15
              Seq primer: CGTTGTAACGACGCGCAGT
              Class: plasmid ends
              High quality sequence stop: 22.
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                  /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                  /clone_lib="Mouse 10kb plasmid UUGC1M library"
                  /note="Vector: PWD42nv; Purified genomic DNA from M.
                  musculus C57BL/6J (male) was obtained from the Jackson
                  Laboratory Mouse DNA Resource
                  (http://www.jax.org/resources/documents/dnares/). The DNA
                  was hydrodynamically sheared by repeated passage through a
                  0.005 inch orifice at constant velocity. The sheared DNA
                  was blunt end-repaired with T4 DNA polymerase and T4
                  polynucleotide kinase. Adaptor oligonucleotides were
                  ligated to the blunt ends in high molar excess. The
                  adaptor DNA was purified and size-selected for a 9.5 to
                  10.5 kb range using preparative agarose gel
                  electrophoresis. Vector DNA was prepared from a derivative
                  of pWD42 [gi|4732114|gb|AF129072.1|, a copy-number
                  inducible derivative of plasmid R1. The vector was ligated
                  with adaptors complementary to the insert adaptors and
                  purified. The sheared, adaptor mouse DNA was annealed to
                  adaptor vector DNA, and transformed into
                  chemically-competent E. coli XL10-Gold (Stratagene) cells
                  and selected for ampicillin resistance."

Query Match      2.0%; Score 21; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTGT 1813
      |||||
Db 1 TGTGTGTGTGTGTGTGTGTGT 21

RESULT 59
AZ985497
LOCUS      22 bp DNA linear GSS 27-APR-2001
DEFINITION 2M0267D23F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0267D23 F, genomic survey sequence.
ACCESSION  AZ985497
VERSION     AZ985497.1  GI:13856724
KEYWORDS

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GSS.
Mus musculus (house mouse)
Mus musculus
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 22)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D. Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0267 row: D column: 23
Seq primer: CGTTGTAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 22.
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    musculus C57BL/6J (female) was obtained from the Jackson
    Laboratory Mouse DNA Resource
    (http://www.jax.org/resources/documents/dnares/). The DNA
    was hydrodynamically sheared by repeated passage through a
    0.005 inch orifice at constant velocity. The sheared DNA
    was blunt end-repaired with T4 DNA polymerase and T4
    polynucleotide kinase. Adaptor oligonucleotides were
    ligated to the blunt ends in high molar excess. The
    adaptor DNA was purified and size-selected for a 9.5 to
    10.5 kb range using preparative agarose gel
    electrophoresis. Vector DNA was prepared from a derivative
    of pWD42 [gi|4732114|gb|AF129072.1|, a copy-number
    inducible derivative of plasmid R1. The vector was ligated
    with adaptors complementary to the insert adaptors and
    purified. The sheared, adaptor mouse DNA was annealed to
    adaptor vector DNA, and transformed into
    chemically-competent E. coli XL10-Gold (Stratagene) cells
    and selected for ampicillin resistance."

Query Match      2.0%; Score 21; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTGT 1813
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Db 2 TGTGTGTGTGTGTGTGTGTGT 22

RESULT 60
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LOCUS      23 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0521L12R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0521L2 R, genomic survey sequence.
ACCESSION  AZ328763
VERSION     AZ328763.1  GI:10388815
KEYWORDS

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**SOURCE** Mus musculus (house mouse)  
**ORGANISM** Mus musculus  
**REFERENCE** Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 23)  
**AUTHORS** Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.  
**TITLE** Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
**JOURNAL** Unpublished (2000)  
**COMMENT** Contact: Robert B. Weiss  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0052 row: L column: 12  
 Seq primer: CACACAGGAAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 23.  
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 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

**Query Match** 2.0%; Score 21; DB 1; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 32;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**QY** 1793 TGTGTGTGTGTGTGTGTGTGTGTGTGT 1813  
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**DB** 2 TGTGTGTGTGTGTGTGTGTGTGTGTGT 22

**RESULT 61**  
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**LOCUS** AZ371475 23 bp DNA linear GSS 02-OCT-2000  
**DEFINITION** IM0122K19R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0122K19 R, genomic survey sequence.  
**ACCESSION** AZ371475  
**VERSION** AZ371475.1 GI:10485175  
**KEYWORDS** GSS.  
**SOURCE** Mus musculus (house mouse)

**ORGANISM** Mus musculus  
**REFERENCE** Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 23)  
**AUTHORS** Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.  
**TITLE** Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
**JOURNAL** Unpublished (2000)  
**COMMENT** Contact: Robert B. Weiss  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0122 row: K column: 19  
 Seq primer: CACACAGGAAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 23.  
**FEATURES** Location/Qualifiers  
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 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
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 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

**Query Match** 2.0%; Score 21; DB 1; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 32;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**QY** 1793 TGTGTGTGTGTGTGTGTGTGTGTGTGT 1813  
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**DB** 3 TGTGTGTGTGTGTGTGTGTGTGTGTGT 23

**RESULT 62**  
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**DEFINITION** 2M0099A22F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0099A22 F, genomic survey sequence.  
**ACCESSION** AZ824638  
**VERSION** AZ824638.1 GI:12994546  
**KEYWORDS** GSS.  
**SOURCE** Mus musculus (house mouse)  
**ORGANISM** Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 23)

REFERENCE  
AUTHORS  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb Plasmid inserts

JOURNAL  
COMMENT  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00  
Plate: 0099 row: A column: 22  
Seq primer: CGTTGTAACACGCGCCAGT  
Class: plasmid ends  
High quality sequence stop: 23.

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/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 2.0%; Score 21; DB 1; Length 23;  
Best Local Similarity 100.0%; Pred. No. 32;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTGT 1913  
DB 2 TGTGTGTGTGTGTGTGTGTGT 22

RESULT 63  
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LOCUS  
DEFINITION  
2M0106013F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC2M0106013 F, genomic survey sequence.

ACCESSION  
AZ828969  
VERSION  
KEYWORDS  
GSS.  
SOURCE  
Mus musculus (house mouse)  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 23)

REFERENCE  
AUTHORS  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb Plasmid inserts

JOURNAL  
COMMENT  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00  
Plate: 0106 row: O column: 13  
Seq primer: CGTTGTAACACGCGCCAGT  
Class: plasmid ends  
High quality sequence stop: 23.

FEATURES  
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/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0106013"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 2.0%; Score 21; DB 1; Length 23;  
Best Local Similarity 100.0%; Pred. No. 32;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTGT 1813  
DB 22 TGTGTGTGTGTGTGTGTGTGT 2

RESULT 64  
AZ647335  
LOCUS  
DEFINITION  
1M0513J15R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0513J15 R, genomic survey sequence.

ACCESSION  
AZ647335  
VERSION  
KEYWORDS  
GSS.  
SOURCE  
Mus musculus (house mouse)  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 24)  
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
 Niederhausern,A. and Wright,D., Weiss,R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, UGA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: dunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0513 row: J column: 15  
 Seq primer: CACACAGGAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 24.  
 Location/Qualifiers  
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 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0513J15"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, TI-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

Query Match 2.0%; Score 21; DB 1; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 34;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTGTGTGT 1813  
 |||||  
 Db 3 TGTGTGTGTGTGTGTGTGTGTGTGT 23

RESULT 65  
 AZ459694  
 LOCUS 25 bp DNA linear GSS 04-OCT-2000  
 DEFINITION 1M0264P10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC1M0264P10 R, genomic survey sequence.  
 ACCESSION AZ459694  
 VERSION AZ459694.1 GI:10617819  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 25)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
 Niederhausern,A. and Wright,D., Weiss,R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: dunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0264 row: P column: 10  
 Seq primer: CACACAGGAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 25.  
 Location/Qualifiers  
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 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0264P10"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, TI-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

Query Match 2.0%; Score 21; DB 1; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 35;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTGTGTGTGT 1814  
 |||||  
 Db 1 GTGTGTGTGTGTGTGTGTGTGTGT 21

RESULT 66  
 AZ506209  
 LOCUS 25 bp DNA linear GSS 05-OCT-2000  
 DEFINITION 1M0347F10F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC1M0347F10 F, genomic survey sequence.  
 ACCESSION AZ506209  
 VERSION AZ506209.1 GI:10687525  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 25)  
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
 Niederhausern, A. and Wright, D., Weiss, R.,  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0347 row: F column: 10  
 Seq primer: CGTTGTAACGACGCGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 25.  
 Location/Qualifiers

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1. .25  
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 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGCLM0347P10"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, Ti-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGCLM library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pWD42 (GII4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

Query Match 2.0%; Score 21; DB 1; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 35;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTGTGTGTGT 1813  
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 Db 4 TGTGTGTGTGTGTGTGTGTGTGTGTGT 24

RESULT 67  
 AZ494629 26 bp DNA linear GSS 05-OCT-2000  
 DEFINITION IM0330F01F Mouse 10kb plasmid UUGCLM library Mus musculus genomic  
 clone UUGCLM0330F01 F, Genomic survey sequence.  
 ACCESSION AZ494629  
 VERSION AZ494629.1 GI:10669392  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 26)  
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
 Niederhausern, A. and Wright, D., Weiss, R.,  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0330 row: F column: 01  
 Seq primer: CGTTGTAACGACGCGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 26.  
 Location/Qualifiers

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 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
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 /clone="UUGCLM0330F01"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, Ti-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGCLM library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pWD42 (GII4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

Query Match 2.0%; Score 21; DB 1; Length 26;  
 Best Local Similarity 100.0%; Pred. No. 36;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTGTGTGTGT 1813  
 |||||  
 Db 5 TGTGTGTGTGTGTGTGTGTGTGTGTGT 25

RESULT 68  
 AZ602037 23 bp DNA linear GSS 13-DEC-2000  
 DEFINITION IM0420A10R Mouse 10kb plasmid UUGCLM library Mus musculus genomic  
 clone UUGCLM0420A10 R, Genomic survey sequence.  
 ACCESSION AZ602037  
 VERSION AZ602037.1 GI:11724227  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 23)  
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.



plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0119 row: 1 column: 12  
Seq primer: CGTTGTAACGACGCGCCAGT  
Class: plasmid ends  
High quality sequence stop: 20.  
Location/Qualifiers  
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/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0119112"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.9%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 36;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1794 GTGTGTGTGTGTGTGTGTGT 1813  
Db 1 GTGTGTGTGTGTGTGTGTGT 20

RESULT 71  
AZ465453  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

AZ465453  
1M0275F24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0275F24 F, genomic survey sequence.  
GSS.  
AZ465453.1 GI:10623578  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
1 (bases 1 to 20)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
Unpublished (2000)

Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0275 row: F column: 24  
Seq primer: CGTTGTAACGACGCGCCAGT  
Class: plasmid ends  
High quality sequence stop: 20.  
Location/Qualifiers  
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/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0275F24"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.9%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 36;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1794 GTGTGTGTGTGTGTGTGTGT 1813  
Db 1 GTGTGTGTGTGTGTGTGTGT 20

RESULT 72  
AZ470768  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

AZ470768  
1M0285H09F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0285H09 F, genomic survey sequence.  
GSS.  
AZ470768.1 GI:10628893  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
1 (bases 1 to 20)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
Unpublished (2000)

## COMMENT

Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: dduun@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0285 row: H column: 09  
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Class: plasmid ends  
High quality sequence stop: 20.  
Location/Qualifiers

## FEATURES

source

1..20  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0285H09"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G[14732114|GB|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

1.9%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred.No. 36;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTG 1812

Db 1 TGTGTGTGTGTGTGTGTGTG 20

## RESULT 73

AZ580200

LOCUS

DEFINITION 1M0368A20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0368A20 F, genomic survey sequence.

ACCESSION

AZ580200

VERSION

GSS.

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

REFERENCE

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Ielam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL

Unpublished (2000)

COMMENT

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: dduun@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0368 row: A column: 20

Seq primer: CGTTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 20.

Location/Qualifiers

source

1..20  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0368A20"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G[14732114|GB|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

1.9%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred.No. 36;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTG 1812

Db 1 TGTGTGTGTGTGTGTGTGTG 20

## RESULT 74

AZ634201

LOCUS

DEFINITION

1M0489C19R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0489C19 R, genomic survey sequence.

ACCESSION

AZ634201

VERSION

GSS.

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

REFERENCE

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Ielam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL

Unpublished (2000)

COMMENT

Contact: Robert B. Weiss

University of Utah Genome Center



University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: [dgunn@genetics.utah.edu](mailto:dgunn@genetics.utah.edu)  
Insert Length: 10000 Std Error: 0.00  
Plate: 0489 row: C column: 19  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 20.

## FEATURES

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1. 20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0489C19"
/sex="Male"
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/seq\_base="E. Coli strain X110-Gold, T1-resistant, F-"  
/lab\_host="Mouse 10kb plasmid UUGC1M library"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/notes="Vector: PW42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(<http://www.jax.org/resources/documents/dnares/>). The DNA  
was hydronamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PW42 (G14732114[gb|AF129072.1], a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli X110-Gold (Stratagene) cells  
and selected for ampicillin resistance."

```
Query Match      1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 20; Conservative 0; Mismatches 0; Indels
```

QY	1794	GTGTGTGTGTGTGTGTGT	1813
DB	1	GTGTGTGTGTGTGTGTGT	20

RESULT 75  
AZ946508/C

Accession	LOCUS	DEFINITION	Accession	LOCUS	DEFINITION
AZ946508	20 bp	DNA linear	AZ946508	20 bp	DNA linear
2M0208P13F	Mouse 10kb	plasmid UUGC2M library Mus musculus genomic	2M0208P13F	Mouse 10kb	plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0308P13 F,	genomic survey	sequence.	clone UUGC2M0308P13 F,	genomic survey	sequence.

ACCESSION AZ946508  
VERSION AZ946508.1 GI:13815584  
KEYWORDS GSS.

SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus

REFERENCE 1 (bases 1 to 20)

**AUTHORS**

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausen, A. and Wright, D., Weiss, R.

TITLE	JOURNAL
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts	Unpublished (2000)

CONTACT: Robert B. Weiss  
University of Utah Genome Center  
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLUC, UT  
84112, USA  
Tel: 801 585 5606  
Tel: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0208 row: P column: 13  
Seq primer: CGTTGTAACAGCGCCAGT  
Class: plasmid ends  
High quality sequence stop: 20.

**FEATURES**

source

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/organism="Mus musculus"  
/mol_type="genomic DNA"  
/strain="C57BL/6J"  
/db_xref="taxon:10090"  
/clone="JUGC2M0208P13"  
/sex="Female"  
/lab_host="E. coli strain"
```

/lab host="E. coli strain XL10-Gold, T1-resistant, F-"  
 /clone lib="Mouse 10kb plasmid UUG2M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (female) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnaes/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of PWD42 [G14722114|gb|F12072.1], a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

Query Match 1.9%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 36;  
Matches 20; Conservative 0; Mismatches 0; Indels

QY 1793 TGTGTGTGTGTGTG 1812  
|||  
nB 20 TGTGTGTGTGTGTG 1

RESULT 76  
AZ959039/C

AZ959039 20 bp DNA linear GSS 27-APR-2001  
2M0226L05R Mouse 10kb plasmid UUGC2M library Mus musculus genomic  
clone UUGC2M0226L05 R. genomic survey sequence.

AZ959039  
AZ959039.1 GI:13830266  
GSS

GSS.  
Mus musculus (house mouse)  
Mus musculus

Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus  
1. (bases 1 to 20)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, H., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D. Weiss, R.

Niedermaier, A. and Wright, S., 2005.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 Unpublished (2000)

Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center

University of Utah Genome Center  
University of Utah  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

Tel:	801 585 5606
Fax:	801 585 7177
Email:	dcmn@genetics.utah.edu
Insert Length:	10000 Std Error: 0.00
Plate:	0493 row: D column: 06
Seq primer:	CCTGTATAAACGACGAGCCCACT
Class:	plasmid ends
High quality sequence stop:	21.
FEATURES	
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/organism=	"Mus musculus"
/mol_type=	"genomic DNA"
/strain=	"C57BL/6J"
/db_xref=	"taxon:10090"
/clone=	"UUGCIM0493D06"
/sex=	"Male"
/lab_host=	"E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib=	"Mouse 10kb plasmid UUC1M library"
/notes=	"vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource ( <a href="http://www.jax.org/resources/documents/dnares/">http://www.jax.org/resources/documents/dnares/</a> ). The DNA was hydrodynamically sheared by repeated passages through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (GI:4732114[gb]/AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent S. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
Query Match	1.9%; Score 20; DB 1; Length 21;
Best Local Similarity	100.0%; Pred. No. 37;
Matches	20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1794 GTGTGTGTGTGTGTGTGTGT 1813       1 GTGTGTGTGTGTGTGTGTGT 20
DB	
RESULT 78	
AZ641805	
LOCUS	21 bp DNA linear GSS 14-DEC-2000
DEFINITION	1M0504J0AR Mouse 10kb plasmid UUC1M library Mus musculus genomic clone UUC1M0504J04 R, genomic survey sequence.
ACCESSION	AZ641805
VERSION	AZ641805.1 GI:11766140
KEYWORDS	GSS.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS	1 (bases 1 to 21) Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D., Weiss,R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
TITLE	Unpublished (2000)
JOURNAL	Contact: Robert B. Weiss
COMMENT	University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLCT, UT 84112, USA Tel: 801 585 5606

Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0504 row: J column: 04  
 Seq primer: CACACAGGAAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 21.  
 Location/Qualifiers

## FEATURES

source

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1. .21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0504J04"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```

Query Match 1.9%; Score 20; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 37;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTGTGT 1813  
 |||||  
 Db 1 GTGTGTGTGTGTGTGTGTGT 20

RESULT 79  
 AZ991225/c  
 LOCUS  
 DEFINITION  
 2M0275K17F Mouse 10kb plasmid UUGC2M library Mus musculus genomic  
 clone UUGC2M0275K17 F, genomic survey sequence.

ACCESSION  
 AZ991225  
 VERSION  
 AZ991225.1 GI:13862452

KEYWORDS  
 GSS.  
 SOURCE  
 Mus musculus (house mouse)

ORGANISM  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
 1 (bases 1 to 21)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
 Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von  
 Niederhausern, A. and Wright, D., Weiss, R.

TITLE  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts

JOURNAL  
 Unpublished (2000)

COMMENT  
 Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0275 row: K column: 17  
 Seq primer: CGTGTAAACAGCGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 21.  
 Location/Qualifiers

## FEATURES

source

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1. .21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0275K17"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```

Query Match 1.9%; Score 20; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 37;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTGTGT 1813  
 |||||  
 Db 21 GTGTGTGTGTGTGTGTGTGT 2

RESULT 80  
 AZ514387/c

LOCUS  
 DEFINITION  
 1M03161H03F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC1M03161H03 F, genomic survey sequence.

ACCESSION  
 AZ514387  
 VERSION  
 AZ514387.1 GI:10695703

KEYWORDS  
 GSS.

SOURCE  
 Mus musculus (house mouse)

ORGANISM  
 Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
 1 (bases 1 to 22)

AUTHORS  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
 Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von  
 Niederhausern, A. and Wright, D., Weiss, R.

TITLE  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts

JOURNAL  
 Unpublished (2000)

COMMENT  
 Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0361 row: H column: 03

Seq primer: CGTGTAAACGACGCGCCAGT

Class: plasmid ends

High quality sequence stop: 22.

Location/Qualifiers

## FEATURES

source

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1. .22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC2M0016J20"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
```

Query Match 1.9%; Score 20; DB 1; Length 22;

Best Local Similarity 100.0%; Pred. No. 38;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1795 TGTGTGTGTGTGTGTGTGT 1814

Db 22 TGTGTGTGTGTGTGTGTGT 3

## RESULT 81

AZ780002/C

LOCUS

DEFINITION 2M0016J20R Mouse 10kb plasmid UUC1M library Mus musculus genomic

clone UUC2M0016J20 R, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

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22 bp DNA linear GSS 16-FEB-2001
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 22)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
```

Plate: 0016 row: J column: 20

Seq primer: CACACAGGAACACGCTATGACC

Class: plasmid ends

High quality sequence stop: 22.

Location/Qualifiers

## FEATURES

source

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1. .22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC2M0016J20"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
```

Query Match 1.9%; Score 20; DB 1; Length 22;

Best Local Similarity 100.0%; Pred. No. 38;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTGT 1813

Db 22 GTGTGTGTGTGTGTGTGT 3

## RESULT 82

AZ780118

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

```
22 bp DNA linear GSS 16-FEB-2001
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 22)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0017 row: G column: 07
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Seq primer: CGTTGTAACACGACGCCAGT

Class: plasmid ends  
High quality sequence stop: 22.  
Location/Qualifiers

1. 22

/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0017G07"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.9%; Score 20; DB 1; Length 22;  
Best Local Similarity 100.0%; Pred. No. 38;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTG 1812

DB 3 TGTGTGTGTGTGTGTGTGTG 22

RESULT 83  
AZ309945/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AZ309945 23 bp DNA linear GSS 29-SEP-2000  
M0017K22F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0017K22 F, genomic survey sequence.

ACCESSION  
AZ309945  
KEYWORDS  
GSS.  
SOURCE  
Mus musculus (house mouse)

ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
1 (bases 1 to 23)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D. Weiss, R.

TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL  
Unpublished (2000)

COMMENT  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0017 row: K column: 22  
Seq primer: CGTTGTAACACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 23.

Location/Qualifiers

1. 23

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/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.9%; Score 20; DB 1; Length 23;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTGTGTG 1813

DB 21 GTGTGTGTGTGTGTGTGTGTG 2

RESULT 84

AZ452951

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AZ452951 23 bp DNA linear GSS 04-OCT-2000  
M0254M05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0254M05 F, genomic survey sequence.

ACCESSION  
AZ452951  
KEYWORDS  
GSS.  
SOURCE  
Mus musculus (house mouse)

ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
1 (bases 1 to 23)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D. Weiss, R.

TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL  
Unpublished (2000)

COMMENT  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0254 row: M column: 05  
Seq primer: CGTTGTAACACGACGCCAGT  
Class: plasmid ends



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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (GI:4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.9%; Score 20; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTGT 1913
DB 25 GTGTGTGTGTGTGTGTGT 6

RESULT 87
A2513902/c
LOCUS
DEFINITION
A2513902 Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0360A13 F, genomic survey sequence.
ACCESSION
A2513902
VERSION
A2513902.1 GI:10695218
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 21)
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,R., Stokes,R., Tingley,A., von
Niederhausern,A. and Wright,D., Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0360 row: A column: 13
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Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers
1. .21
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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (GI:4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.8%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 42;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGT 1813
DB 21 TGTGTGTGTGTGTGTGTGT 1

RESULT 88
A2784203
LOCUS
DEFINITION
A2784203 Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0026G16 R, genomic survey sequence.
ACCESSION
A2784203
VERSION
A2784203.1 GI:12919695
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 22)
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,R., Stokes,R., Tingley,A., von
Niederhausern,A. and Wright,D., Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0026 row: G column: 16
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers
1. .22
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/organism="Mus musculus"

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 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.8%; Score 19.4; DB 1; Length 22;  
 Best Local Similarity 95.2%; Pred. No. 43;  
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTGT 1813  
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 DB 1 TGTGTGTGTGTGTGTGTGTGT 21

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 clone UUGC2M0045H20 R, genomic survey sequence.  
 ACCESSION AZ793094  
 VERSION  
 KEYWORDS  
 SOURCE GSS.  
 ORGANISM Mus musculus (house mouse)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 22)  
 DUNN, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
 Niederhausern, A. and Wright, D., Weiss, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0045 row: H column: 20  
 Seq primer: CACACAGGAACAGCATGACC  
 Class: plasmid ends  
 High quality sequence stop: 22.  
 Location/Qualifiers  
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 /organism="Mus musculus"  
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RESULT 90  
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 ACCESSION AZ801266  
 VERSION  
 KEYWORDS  
 SOURCE GSS.  
 ORGANISM Mus musculus (house mouse)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 22)  
 DUNN, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
 Niederhausern, A. and Wright, D., Weiss, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0059 row: I column: 07  
 Seq primer: CACACAGGAACAGCATGACC  
 Class: plasmid ends  
 High quality sequence stop: 22.  
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/strain="C57BL/6J"  
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 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
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 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.8%; Score 19.4; DB 1; Length 22;  
 Best Local Similarity 95.2%; Pred. No. 43;  
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTGT 1813  
 |||||  
 DB 2 TGTGTGTGTGTGTGTGTGTGT 22

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 LOCUS 22 bp DNA linear GSS 16-FEB-2001  
 DEFINITION 2M0059107R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC2M0059107 R, genomic survey sequence.  
 ACCESSION AZ801266  
 VERSION  
 KEYWORDS  
 SOURCE GSS.  
 ORGANISM Mus musculus (house mouse)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 22)  
 DUNN, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
 Niederhausern, A. and Wright, D., Weiss, R.  
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 plasmid inserts  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
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 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0059 row: I column: 07  
 Seq primer: CACACAGGAACAGCATGACC  
 Class: plasmid ends  
 High quality sequence stop: 22.  
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 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"

RESULT 90  
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 LOCUS 22 bp DNA linear GSS 16-FEB-2001  
 DEFINITION 2M0059107R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC2M0059107 R, genomic survey sequence.  
 ACCESSION AZ801266  
 VERSION  
 KEYWORDS  
 SOURCE GSS.  
 ORGANISM Mus musculus (house mouse)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 22)  
 DUNN, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
 Niederhausern, A. and Wright, D., Weiss, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
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 JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
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 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
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 Location/Qualifiers  
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/sex="Male"

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Query Match 1.8%; Score 19.4; DB 1; Length 22;  
Best Local Similarity 95.2%; Pred. No. 43;  
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTGTGTGTGT 1813  
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Db 2 TGTGTGTGTGTGTGTGTGTGTGTGTGT 22

RESULT 91  
AZ356191/c  
LOCUS  
DEFINITION  
clone UGC1M0097L07 F, genomic survey sequence.

ACCESSION  
AZ356191  
VERSION  
KEYWORDS  
GSS.

SOURCE  
Mus musculus (house mouse)

ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 23)

REFERENCE  
AUTHORS  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Langacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A., and Wright, D., Weiss, R.

TITLE  
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plasmid inserts

JOURNAL  
Unpublished (2000)

COMMENT  
Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0097 row: L column: 07

Seq primer: CGTTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 23.

Location/Qualifiers

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FEATURES

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/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

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/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/notes="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adaptor DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pWD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adaptor mouse DNA was annealed to

adaptor vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

Query Match 1.8%; Score 19.4; DB 1; Length 23;

Best Local Similarity 95.2%; Pred. No. 45;

Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 22 TGGGTGTGTGTGTGTGTGTGTGTGTGT 2

RESULT 92

AZ822069

LOCUS

DEFINITION

clone UGC2M0095D03 F, genomic survey sequence.

ACCESSION

AZ822069

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 24)

REFERENCE

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Langacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A., and Wright, D., Weiss, R.

TITLE

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plasmid inserts

JOURNAL

Unpublished (2000)

COMMENT

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University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0095 row: D column: 03

Seq primer: CGTTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 24.

Location/Qualifiers

1. .24

FEATURES

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/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC2M0095D03"



/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pWD42 (GI|4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

Query Match 1.8%; Score 19; DB 1; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 42;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTG 1812  
 |||||  
 Db 1 GTGTGTGTGTGTGTGTG 19

RESULT 95  
 AZ461642/c 19 bp DNA linear GSS 04-OCT-2000  
 LOCUS 1M0267P06R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 DEFINITION clone UUGC1M0267P06 R, genomic survey sequence.

ACCESSION AZ461642  
 VERSION AZ461642.1 GI:10619767  
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 19)  
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
 Niederhausern, A. and Wright, D. Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts

JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA

Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: dunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0267 row: P column: 06  
 Seq primer: CACACGGAACAGCTATGACC  
 Class: plasmid ends

High quality sequence stop: 19.  
 Location/Qualifiers  
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 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
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 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pWD42 (GI|4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

Query Match 1.8%; Score 19; DB 1; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 42;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTG 1812  
 |||||  
 Db 19 GTGTGTGTGTGTGTGTG 1

RESULT 96  
 AZ649147

LOCUS AZ649147 19 bp DNA linear GSS 14-DEC-2000  
 DEFINITION 1M0518B17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC1M0518B17 R, genomic survey sequence.

ACCESSION AZ649147  
 VERSION AZ649147.1 GI:11782334  
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 19)

REFERENCE 1 (bases 1 to 19)  
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
 Niederhausern, A. and Wright, D. Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts

JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA

Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: dunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0518 row: B column: 17  
 Seq primer: CACACGGAACAGCTATGACC  
 Class: plasmid ends

High quality sequence stop: 19.  
 Location/Qualifiers  
 1. .19

/organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0518B17"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M."

musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.8%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 42;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGT 1811  
|||||  
DB 1 TGTGTGTGTGTGTGTGT 19

RESULT 97  
LOCUS AZ774954/c  
DEFINITION 2M0004N15R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0004N15 R, genomic survey sequence.

ACCESSION AZ774954  
VERSION AZ774954.1 GI:12900943

KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 19)  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 19)  
AUTHORS Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177

Email: [ddunn@genetics.utah.edu](mailto:ddunn@genetics.utah.edu)  
Insert Length: 10000 Std Error: 0.00

Plate: 0004 row: N column: 15  
Seq primer: CACACGAAACAGCTATGACC

Class: plasmid ends  
High quality sequence stop: 19.

FEATURES  
Location/Qualifiers  
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/organism="Mus musculus"  
/mol\_type="genomic DNA"

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/db\_xref="taxon:10090"

/clone="UUGC2M0004N15"  
/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: pWD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.8%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 42;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTG 1812  
|||||  
DB 19 GTGTGTGTGTGTGTGTG 1

RESULT 98  
LOCUS AZ795767

DEFINITION 2M0051112P Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0051112 F, genomic survey sequence.

ACCESSION AZ795767  
VERSION AZ795767.1 GI:12943132

KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 19)  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 19)  
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177

Email: [ddunn@genetics.utah.edu](mailto:ddunn@genetics.utah.edu)  
Insert Length: 10000 Std Error: 0.00

Plate: 0051 row: I column: 12  
Seq primer: CGTGTAAACACGCGCAGT

Class: plasmid ends  
High quality sequence stop: 19.

FEATURES  
Location/Qualifiers  
1..19

/organism="Mus musculus"  
/mol\_type="genomic DNA"

/strain="C57BL/6J"  
/db\_xref="taxon:10090"

/clone="UUGC2M0051112"  
/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: pWD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.8%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 42;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1794 GTGTGTGTGTGTGTGTGTG 1812  
|||||  
Db 1 GTGTGTGTGTGTGTGTGTG 19

RESULT 99  
AZ822936  
LOCUS  
DEFINITION  
2M0096E08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC2M0096E08 R, genomic survey sequence.

ACCESSION  
AZ822936  
VERSION  
GSS.  
KEYWORDS  
Mus musculus (house mouse)

SOURCE  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 19)

REFERENCE  
AUTHORS  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, R., Stokes, R., Tingley, A., von  
Niederhausern, A. and Wright, D., Weiss, R.

TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL  
COMMENT  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0096 row: E column: 08  
Seq primer: CACACAGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 19.  
Location/Qualifiers  
1. .19

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/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0096E08"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: pMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(<http://www.jax.org/resources/documents/dnares/>). The DNA

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.8%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 42;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1794 GTGTGTGTGTGTGTGTGTG 1812  
|||||  
Db 1 GTGTGTGTGTGTGTGTGTG 19

RESULT 100  
AZ827177  
LOCUS  
DEFINITION  
2M0103A05R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC2M0103A05 R, genomic survey sequence.

ACCESSION  
AZ827177  
VERSION  
GSS.  
KEYWORDS  
Mus musculus (house mouse)

SOURCE  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 19)

REFERENCE  
AUTHORS  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, R., Stokes, R., Tingley, A., von  
Niederhausern, A. and Wright, D., Weiss, R.

TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL  
COMMENT  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0103 row: A column: 05  
Seq primer: CACACAGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 19.  
Location/Qualifiers  
1. .19

FEATURES  
source  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0103A05"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: pMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(<http://www.jax.org/resources/documents/dnares/>). The DNA

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Query Match 1.8%; Score 19; DB 1; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 42;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGT 1811  
 |||||  
 DB 1 TGTGTGTGTGTGTGTGT 19

RESULT 101  
 A2785549 20 bp DNA linear GSS 16-FEB-2001  
 LOCUS 2M0029F01R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 DEFINITION clone UUGC2M0029F01 R, Genomic survey sequence.

ACCESSION A2785549  
 VERSION A2785549  
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 20)  
 Authors Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
 Niederhausern, A. and Wright, D. Weiss, R.

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 University of Utah  
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 84112, USA

Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: dcunne@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0029 row: F column: 01  
 Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends  
 High quality sequence stop: 20.

FEATURES  
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 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC2M0029F01"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /notes="Vector: FWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA

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Query Match 1.8%; Score 19; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 44;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1792 TTGTGTGTGTGTGTGTGTG 1810  
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 DB 2 TTGTGTGTGTGTGTGTGTG 20

RESULT 102  
 A2818214 21 bp DNA linear GSS 20-FEB-2001  
 LOCUS 2M0088B08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 DEFINITION clone UUGC2M0088B08 F, Genomic survey sequence.

ACCESSION A2818214  
 VERSION A2818214  
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 21)  
 Authors Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
 Niederhausern, A. and Wright, D. Weiss, R.

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 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA

Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: dcunne@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0088 row: B column: 08  
 Seq primer: CGTTGTAAACGACGCCAGT

Class: plasmid ends  
 High quality sequence stop: 21.

FEATURES  
 source Location/Qualifiers  
 1..21  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC2M0088B08"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /notes="Vector: FWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF123072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.8%; Score 19; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 45;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGT 1811  
|||||  
Db 3 TGTGTGTGTGTGTGTGT 21

RESULT 103  
AZ482421  
LOCUS 20 bp DNA linear GSS 04-OCT-2000  
DEFINITION 1M0307P01R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0307P01 R, genomic survey sequence.

ACCESSION AZ482421  
VERSION 1  
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 20)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

CONTACT: Robert B. Weiss

UNIVERSITY OF UTAH GENOME CENTER

UNIVERSITY OF UTAH

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

TEL: 801 585 5606

FAX: 801 585 7177

EMAIL: ddunn@genetics.utah.edu

INSERT LENGTH: 10000 Std Error: 0.00

PLATE: 0307 row: P column: 01

SEQ PRIMER: CACACAGGAACAGCTATGACC

CLASS: plasmid ends

HIGH QUALITY SEQUENCE STOP: 20.

LOCATION/QUALIFIERS

1..20

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC1M0307P01"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF123072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.8%; Score 18.4; DB 1; Length 20;  
Best Local Similarity 95.0%; Pred. No. 49;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTG 1812  
|||||  
Db 1 TGTGTGTGTGTGTGTGTG 20

RESULT 104

AZ632650

LOCUS 20 bp DNA linear GSS 13-DEC-2000

DEFINITION 1M0487H23F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0487H23 F, genomic survey sequence.

ACCESSION AZ632650

VERSION 1

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 20)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

CONTACT: Robert B. Weiss

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Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

TEL: 801 585 5606

FAX: 801 585 7177

EMAIL: ddunn@genetics.utah.edu

INSERT LENGTH: 10000 Std Error: 0.00

PLATE: 0487 row: H column: 23

SEQ PRIMER: CGTGTAAACGACGCGCAGT

CLASS: plasmid ends

HIGH QUALITY SEQUENCE STOP: 20.

LOCATION/QUALIFIERS

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/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC1M0487H23"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

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0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.8%; Score 18.4; DB 1; Length 20;  
 Best Local Similarity 95.0%; Pred. No. 49;  
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1792 TTGTGTGTGTGTGTGTGTGT 1811  
 |||||  
 Db 1 TTGTGTGTGTGTGTGTGTGT 20

RESULT 105  
 AZ654458  
 LOCUS 20 bp DNA linear GSS 14-DEC-2000  
 DEFINITION IM0528G10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0528G10 R, genomic survey sequence.  
 ACCESSION AZ654458  
 VERSION  
 KEYWORDS GSS.  
 SOURCE AZ654458.1 GI:11791604  
 ORGANISM Mus musculus (house mouse)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 20)  
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D., Weiss,R.  
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
 Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0528 row: G column: 10  
 Seq primer: CACACAGGAAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 20.

FEATURES  
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 /organism="Mus musculus"  
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 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0528G10"  
 /sex="Male"  
 /lab\_hosts="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel

10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.8%; Score 18.4; DB 1; Length 20;  
 Best Local Similarity 95.0%; Pred. No. 49;  
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTGT 1812  
 |||||  
 Db 1 TGTGTGTGTGTGTGTGTGTGT 20

RESULT 106  
 AZ793887/c  
 LOCUS 20 bp DNA linear GSS 16-FEB-2001  
 DEFINITION 2M0047G21F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0047G21 F, genomic survey sequence.  
 ACCESSION AZ793887  
 VERSION  
 KEYWORDS GSS.  
 SOURCE AZ793887.1 GI:12939296  
 ORGANISM Mus musculus (house mouse)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 20)  
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D., Weiss,R.  
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 Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0047 row: G column: 21  
 Seq primer: CGTTGTAAACGACGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 20.

FEATURES  
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 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC2M0047G21"  
 /sex="Male"  
 /lab\_hosts="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel



electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.8%; Score 18.4; DB 1; Length 20;  
Best Local Similarity 95.0%; Pred. No. 49;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1792 TTGTGTGTGTGTGTGTGTGT 1811  
|||||  
Db 20 TTGTGTGTGTGTGTGTGT 1

RESULT 107  
AZ415089  
LOCUS 21 bp DNA linear GSS 03-OCT-2000  
DEFINITION 1M0189G17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0189G17 R, genomic survey sequence.

ACCESSION AZ415089  
VERSION AZ415089.1 GI:10539102  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 21)

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0189 row: G column: 17  
Seq primer: CACACAGAAACACTATGACC  
Class: plasmid ends  
High quality sequence stop: 21.  
Location/Qualifiers  
1. .21  
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/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
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/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative

FEATURES  
source

1. .21  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0367P06"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
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polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
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electrophoresis. Vector DNA was prepared from a derivative

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Query Match 1.8%; Score 18.4; DB 1; Length 21;  
Best Local Similarity 95.0%; Pred. No. 51;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTGTGT 1813  
|||||  
Db 1 GTGTGTGTGTGTGTGTGT 20

RESULT 108  
AZ579599

LOCUS 21 bp DNA linear GSS 13-DEC-2000  
DEFINITION 1M0367P06F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0367P06 F, genomic survey sequence.

ACCESSION AZ579599  
VERSION AZ579599.1 GI:11694028  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 21)

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0367 row: P column: 06  
Seq primer: CTTGTAAAACGACGGCCAGT  
Class: plasmid ends  
High quality sequence stop: 21.  
Location/Qualifiers  
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/db\_xref="taxon:10090"  
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/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
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was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number

FEATURES  
source

1. .21  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
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/clone="UUGC1M0367P06"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
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(http://www.jax.org/resources/documents/dnares/). The DNA  
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polynucleotide kinase. Adaptor oligonucleotides were  
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adapted DNA was purified and size-selected for a 9.5 to  
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electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.8%; Score 18.4; DB 1; Length 21;  
Best Local Similarity 95.0%; Pred. No. 51;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1808 GTGTGTATATATATATAT 1827  
Db 1 GTGTGTATATATATATCT 20

RESULT 109  
AZ621072/c 21 bp DNA linear GSS 13-DEC-2000  
LOCUS  
DEFINITION  
1M0454M05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0454M05 F, genomic survey sequence.

ACCESSION  
AZ621072  
VERSION  
AZ621072.1 GI:11743262  
KEYWORDS  
GSS.  
SOURCE  
Mus musculus (house mouse)

ORGANISM  
Mus musculus  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 21)

REFERENCE  
AUTHORS  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.

TITLE  
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JOURNAL  
Unpublished (2000)

COMMENT  
Contact: Robert B. Weiss  
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University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112 USA  
Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0454 row: M column: 05  
Seq primer: CGTGTAAACGACGCGCAGT  
Class: Plasmid ends  
High quality sequence stop: 21.  
Location/Qualifiers  
1. .21

FEATURES  
source  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0454M05"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
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inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.8%; Score 18.4; DB 1; Length 21;  
Best Local Similarity 95.0%; Pred. No. 51;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1796 GTGTGTGTGTGTGTGTAT 1815  
Db 21 GTGTGTGTGTGTGTGTAT 2

RESULT 110  
AZ665302/c 21 bp DNA linear GSS 14-DEC-2000  
LOCUS  
DEFINITION  
1M0546J09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0546J09 R, genomic survey sequence.

ACCESSION  
AZ665302  
VERSION  
AZ665302.1 GI:11802448  
KEYWORDS  
GSS.  
SOURCE  
Mus musculus (house mouse)

ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 21)

REFERENCE  
AUTHORS  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
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Niederhausern, A. and Wright, D., Weiss, R.

TITLE  
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plasmid inserts  
JOURNAL  
Unpublished (2000)

COMMENT  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112 USA  
Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0546 row: J column: 09  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 21.  
Location/Qualifiers  
1. .21

FEATURES  
source  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0546J09"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and XL10-Gold (Stratagene) cells chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.7%; Score 17.8; DB 1; Length 21;  
Best Local Similarity 90.5%; Pred. No. 58;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1790 TATTGTGTGTGTGTGTGTG 1810  
|||||  
Db 21 TTTTGTGTGTGTGTGTGTG 1

## RESULT 111

PCH303878/c 21 bp DNA linear GSS 03-APR-2001  
LOCUS Plasmodium chabaudi genome survey sequence, clone PC4c11.plt,  
DEFINITION genomic survey sequence.

ACCESSION AJ303878

VERSION AJ303878.1 GI:11140385

KEYWORDS GSS; genome survey sequence.

SOURCE Plasmodium chabaudi

ORGANISM Plasmodium chabaudi

REFERENCE 1 (bases 1 to 21)

AUTHORS Janssen,C.S., Barrett,M.P., Lawson,D., Quail,M.A., Harris,D.,

Bowman,S., Phillips,R.S. and Turner,C.M.

TITLE Gene discovery in Plasmodium chabaudi by genome survey sequencing

JOURNAL Mol. Biochem. Parasitol. 113 (2), 251-260 (2001)

MEDLINE 21192558

PUBMED 11295179

REFERENCE 2 (bases 1 to 21)

AUTHORS Janssen,C.S.

DIRECT SUBMISSION

TITLE Submitted (06-NOV-2000) Division of Infection &amp; Immunity,

JOURNAL University of Glasgow, Joseph Black Building, Glasgow G12 8QQ, UK

COMMENT bases 40 to 60 (SL to QR).

FEATURES Location/Qualifiers

source 1..21

/organism="Plasmodium chabaudi"

/mol\_type="genomic DNA"

/db\_xref="taxon:5825"

/clone="PC4c11.plt"

## Query Match

Best Local Similarity 1.7%; Score 17.8; DB 1; Length 21;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1767 TTTTAAAAATTATATGTA 1787  
|||||  
Db 21 TTTTAAAAATTATATTTTA 1

## RESULT 112

AZ464442 22 bp DNA linear GSS 04-OCT-2000  
LOCUS 1M0273N14R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
DEFINITION clone UUGC1M0273N14 R, genomic survey sequence.

ACCESSION AZ464442

VERSION AZ464442.1 GI:10622567

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 22)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T.,

Rally,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhauser,A. and Wright,D., Weises,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb

Plasmid inserts

## JOURNAL COMMENT

Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0273 row: N column: 14  
Seq primer: CACACAGGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 22.  
Location/Qualifiers  
1..22  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0273N14"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gil14732114[gb|AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## FEATURES

source

Query Match 1.7%; Score 17.8; DB 1; Length 22;

Best Local Similarity 90.5%; Pred. No. 60;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTGT 1813  
|||||  
Db 1 TGTGTGTGTGTGTGTGTGTGT 21

## RESULT 113

AA995094/c 19 bp mRNA linear EST 27-AUG-1998  
LOCUS ou9909.s1 NCI CGAP Kid3 Homo sapiens cDNA clone IMAGE1635040 3',  
DEFINITION similar to TR:Q69566 Q69566 ; contains TARI.t2 MER35 repetitive element ; mRNA sequence.

ACCESSION AA995094

VERSION AA995094.1 GI:3181583

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 19)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.  
 cDNA Library Preparation: M. Bento Soares, Ph.D.  
 cDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: [www.bio.llnl.gov/bbrp/image/image.html](http://www.bio.llnl.gov/bbrp/image/image.html)

Trace considered overall poor quality  
 Insert Length: 1087 Std Error: 0.00  
 Seq primer: -40m3 fwd. ET from Amersham  
 High quality sequence stop: 1.

#### FEATURES

Location/Qualifiers  
 1..19  
 /organism="Homo sapiens"  
 /mol\_type="rRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:1635040"  
 /lab\_host="DH10B"  
 /clone\_lib="NCI CGAP Kid3"  
 /notes="Organ: Kidney; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer, double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. mRNA source: 2 pooled kidneys. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo."

Query Match 1.7%; Score 17.4; DB 1; Length 19;  
 Best Local Similarity 94.7%; Pred. No. 58;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTG 1812  
 | | | | | | | | | | | | | | | | | | | | |  
 Db 19 GCGTGTGTGTGTGTGTG 1

RESULT 114  
 AZ786779 19 bp DNA linear GSS 16-FEB-2001  
 LOCUS 2M0032C01R Mouse 10kb plasmid UUGCLM library Mus musculus genomic  
 DEFINITION clone UUGC2M0032C01 R, genomic survey sequence.

ACCESSION AZ786779  
 VERSION AZ786779  
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 19)  
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D. Weiss,R.  
 Mouse whole genome scaffolding with paired end reads from 10kb

Plasmid inserts  
 Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: [ddunn@genetics.utah.edu](mailto:ddunn@genetics.utah.edu)  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0032 row: C column: 01  
 Seq primer: CACACAGGAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 19.

#### FEATURES

Location/Qualifiers  
 1..19  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC2M0032C01"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, TI-resistant, P-"  
 /clone\_lib="Mouse 10kb plasmid UUGCLM library"  
 /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI4732114|GB|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.6%; Score 17; DB 1; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 63;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1798 GTGTGTGTGTGTGTGTA 1814  
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 Db 3 GTGTGTGTGTGTGTGTA 19

#### RESULT 115

AZ597939 21 bp DNA linear GSS 13-DEC-2000  
 LOCUS 1M0412F22F Mouse 10kb plasmid UUGCLM library Mus musculus genomic  
 DEFINITION clone UUGC1M0412F22 F, genomic survey sequence.

ACCESSION AZ597939  
 VERSION AZ597939.1 GI:11720129  
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 21)  
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D. Weiss,R.  
 Mouse whole genome scaffolding with paired end reads from 10kb

Plasmid inserts  
 Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: [ddunn@genetics.utah.edu](mailto:ddunn@genetics.utah.edu)  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0412 row: F column: 22  
 Seq primer: CGTTGTAACAGCGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 21.  
 Location/Qualifiers

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source
1. 21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/cloned="UUCG1M0412F22"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUCG1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.6%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 70;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1811 TGTATATATATATATATGTA 1830
DB 1 TATATATATATATATATA 20

RESULT 116
AZ597939/c
LOCUS
DEFINITION
1M0412F22F Mouse 10kb plasmid UUCG1M library Mus musculus genomic
clone UUCG1M0412F22 F, genomic survey sequence.
ACCESSION
AZ597939
VERSION
AZ597939.1 GI:11720129
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 21)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0412 row: F column: 22
Seq primer: CGTTGTAACAGCGCCAGT
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers
1. 21
/organism="Mus musculus"

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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M0412F22"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUCG1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.6%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 70;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1811 TGTATATATATATATATGTA 1830
DB 20 TATATATATATATATATA 1

RESULT 117
AZ401252
LOCUS
DEFINITION
1M0167E20R Mouse 10kb plasmid UUCG1M library Mus musculus genomic
clone UUCG1M0167E20 R, genomic survey sequence.
ACCESSION
AZ401252
VERSION
AZ401252.1 GI:10516326
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0167 row: E column: 20
Seq primer: CACACAGGAACAGCATGACC
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
1. 19
/organism="Mus musculus"

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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0167E20"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.6%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 71;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1813 TATATATATATATATGTA 1830
DB 2 TATATATATATATATATA 19

RESULT 118
AZ401252/c 19 bp DNA linear GSS 03-OCT-2000
DEFINITION IM0167E20R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0167E20 R, genomic survey sequence.
ACCESSION AZ401252
VERSION AZ401252.1 GI:10516326
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0167 row: E column: 20
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"

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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0167E20"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.8%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 71;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1813 TATATATATATATATGTA 1830
DB 19 TATATATATATATATATA 2

RESULT 119
AZ630416 19 bp DNA linear GSS 13-DEC-2000
DEFINITION IM0484B03F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0484B03 F, genomic survey sequence.
ACCESSION AZ630416
VERSION AZ630416.1 GI:11752606
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0484 row: B column: 03
Seq primer: CGTTGTAACAGCGCCAGT
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"

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/db_xref="taxon:10090"
/clone="UUGC1M0484B03"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (GI4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Query Match 1.6%; Score 16.4; DB 1; Length 19;  
Best Local Similarity 94.4%; Pred. No. 71;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1813 TATATATATATATATGTA 1830  
|||||  
Db 2 TATATATATATATATA 19  
|||||

RESULT 120  
AZ630416/c  
LOCUS  
DEFINITION  
1M0484B03F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0484B03 F, genomic survey sequence.

ACCESSION  
AZ630416  
VERSION  
AZ630416.1 GI:11752606  
GSS.  
SOURCE  
Mus musculus (house mouse)  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 19)  
REFERENCE  
AUTHORS  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.  
TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL  
Unpublished (2000)  
COMMENT  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0484 row: B column: 03  
Seq primer: CGTTGTAACGACGCGCAGT  
Class: plasmid ends  
High quality sequence stop: 19.  
Location/Qualifiers  
1..19  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"

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/clone="UUGC1M0484B03"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (GI4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Query Match 1.6%; Score 16.4; DB 1; Length 19;  
Best Local Similarity 94.4%; Pred. No. 71;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1813 TATATATATATATATGTA 1830  
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Db 19 TATATATATATATATA 2  
|||||

RESULT 121  
AZ799396/c  
LOCUS  
DEFINITION  
2M005N18R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M005N18 R, genomic survey sequence.

ACCESSION  
AZ799396  
VERSION  
AZ799396.1 GI:12950471  
GSS.  
SOURCE  
Mus musculus (house mouse)  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 19)  
REFERENCE  
AUTHORS  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.  
TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL  
Unpublished (2000)  
COMMENT  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0056 row: N column: 18  
Seq primer: CACACAGGAACACGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 19.  
Location/Qualifiers  
1..19  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M005N18"

/sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G114732114|GB|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.6%; Score 16.4; DB 1; Length 19;  
 Best Local Similarity 94.4%; Pred. No. 71;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1808 GTGTGTATATATATATAT 1825  
 |||||  
 DB 19 GTATGTATATATATATAT 2

RESULT 122  
 AZ772074 20 bp DNA linear GSS 16-FEB-2001  
 LOCUS  
 DEFINITION  
 1M0574M10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC1M0574M10 R, genomic survey sequence.

ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM

REFERENCE  
 AUTHORS  
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE  
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL  
 COMMENT  
 Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0574 row: M column: 10  
 Seq primer: CACACAGGAACACGTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 20.

FEATURES  
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 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0574M10"  
 /sex="Male"

/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G114732114|GB|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.5%; Score 16; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 79;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTGT 1809  
 |||||  
 DB 5 GTGTGTGTGTGTGTGTGT 20

RESULT 123  
 AZ345795/c

LOCUS  
 DEFINITION  
 19 bp DNA linear GSS 29-SEP-2000  
 1M0808H09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC1M0808H09 R, genomic survey sequence.

ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM

REFERENCE  
 AUTHORS  
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE  
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL  
 COMMENT  
 Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0080 row: H column: 09  
 Seq primer: CACACAGGAACACGTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 19.

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 /mol\_type="genomic DNA"  
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 /db\_xref="taxon:10090"  
 /clone="UUGC1M0808H09"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"



/clone\_lib="Mouse 10kb plasmid UUGCLM library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.5%; Score 15.8; DB 1; Length 19;  
 Best Local Similarity 89.5%; Pred. No. 79;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTTAA 1883  
 |||||  
 DB 19 TTTTATTTTGTGTTTAA 1

RESULT 124  
 AZ491644  
 LOCUS  
 DEFINITION  
 1M0325A20F Mouse 10kb plasmid UUGCLM library Mus musculus genomic  
 clone UUGCLM0325A20 F, genomic survey sequence.

ACCESSION  
 AZ491644  
 VERSION  
 AZ491644.1 GI:10663543  
 GSS.  
 SOURCE  
 Mus musculus (house mouse)  
 ORGANISM  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 19)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
 Niederhausern, A. and Wright, D., Weiss, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts

JOURNAL  
 COMMENT  
 Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA

Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0325 row: A column: 20  
 Seq primer: CGTTGTAACGACGGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 19.  
 Location/Qualifiers

FEATURES  
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 /organism="Mus musculus"  
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 /db\_xref="taxon:10090"  
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 /sex="Male"  
 /lab\_hosts="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGCLM library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.5%; Score 15.8; DB 1; Length 19;  
 Best Local Similarity 89.5%; Pred. No. 79;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1792 TTGTGTGTGTGTGTGTG 1810  
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 DB 1 TCCTGTGTGTGTGTGTG 19

RESULT 125  
 AZ650575/c  
 LOCUS  
 DEFINITION  
 1M0520P13R Mouse 10kb plasmid UUGCLM library Mus musculus genomic  
 clone UUGCLM0520P13 R, genomic survey sequence.

ACCESSION  
 AZ650575  
 VERSION  
 AZ650575.1 GI:11785200  
 GSS.  
 SOURCE  
 Mus musculus (house mouse)  
 ORGANISM  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 19)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
 Niederhausern, A. and Wright, D., Weiss, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts

JOURNAL  
 COMMENT  
 Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA

Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0520 row: P column: 13  
 Seq primer: CACACAGAACACGATGACC  
 Class: plasmid ends  
 High quality sequence stop: 19.  
 Location/Qualifiers

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 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGCLM0520P13"  
 /sex="Male"  
 /lab\_hosts="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGCLM library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M."

musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance.

Query Match 1.5%; Score 15.4; DB 1; Length 19;  
 Best Local Similarity 89.5%; Pred. No. 79;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTTAA 1863  
 ||||| ||||| ||||| |||||  
 DB 19 TTTTATTTTGTGTTTAA 1

RESULT 126  
 CF276637/C

LOCUS 17 bp mRNA linear EST 14-AUG-2003

DEFINITION 14ETL--01-N18-g1 Rice etiolated leaf plasmid cDNA library (14ETL)

ACCESSION CF276637

VERSION CF276637.1 GI:33654023

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 17)  
 Kim J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)

TITLE Contact: Nahm B.H.

JOURNAL Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

COMMENT Yongin, Gyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES  
 source  
 1..17  
 /organism="Oryza sativa"  
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 /cultivar="Nackdong"  
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 /tissue\_type="leaf"  
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 /clone\_lib="Rice etiolated leaf plasmid cDNA library (14ETL)"  
 /notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 1.5%; Score 15.4; DB 1; Length 17;  
 Best Local Similarity 94.1%; Pred. No. 79;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTT 1881  
 ||||| ||||| ||||| |||||  
 DB 17 TTTTATTTTGTGTTT 1

RESULT 127  
 AZ654747

LOCUS 19 bp DNA linear GSS 14-DEC-2000

DEFINITION IM0529F08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0529F08 F, genomic survey sequence.

ACCESSION AZ654747

VERSION AZ654747.1 GI:11791893

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 19)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
 Unpublished (2000)

TITLE Contact: Robert B. Weiss

JOURNAL University of Utah

COMMENT Rm 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
 Tel: 801 585 5066  
 Fax: 801 585 7177  
 Email: dunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0529 row: F column: 08  
 Seq primer: CGTGTAAACGACGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 19.

FEATURES  
 Location/Qualifiers  
 1..19  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0529F08"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, TI-resistant, P-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.5%; Score 15.4; DB 1; Length 19;  
 Best Local Similarity 94.1%; Pred. No. 86;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTT 1881

Db 1 TTTTATTTTTTTTT 17

## RESULT 128

CF301151

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

ORyza sativa

ORyza sativa

ORyza sativa

ORyza sativa

ORyza sativa

ORyza sativa

ORyza sativa

ORyza sativa

ORyza sativa

ORyza sativa

ORyza sativa

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ORyza sativa

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ORyza sativa

ORyza sativa

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ORyza sativa

ORyza sativa

ORyza sativa

CF301151

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

ORyza sativa

ORyza sativa

ORyza sativa

ORyza sativa

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## FEATURES

source

1...18

/organism="Oryza sativa"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:4530"

/clone="HD-11-E22"

/tissue\_type="callus"

/dev\_stage="proliferated callus on 2N6 media for 2 weeks"

/lab\_host="E.coli DH10B"

/clone\_lib="OSHDAC1-overexpressing transgenic rice plasmid"

cDNA library (HD)"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was"

treated with ABA(20um) for 1hr. Oligo-capped mRNA was"

reverse transcribed and then used for PCR. mRNA was"

derived from rice Histone Deacetylase overexpression"

line."

Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

1864

CTTTTATTTTTTTT 1881

Db

1

CTTTTATTTTTTTT 18

RESULT 130

AZ799396

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus

Mus musculus

Mus musculus

Mus musculus

Mus musculus

Mus musculus

Mus musculus

Mus musculus

Mus musculus

Mus musculus

Mus musculus

Mus musculus

Mus musculus

Mus musculus

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Mus musculus

Mus musculus

Mus musculus

Mus musculus

Mus musculus

Mus musculus

Mus musculus

Mus musculus

Mus musculus

Mus musculus

Mus musculus

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnam@bio.com, bhnam@bio.myongji.ac.kr.

Location/Qualifiers

1...18

/organism="Oryza sativa"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:4530"

/clone="HD-11-E22"

/tissue\_type="callus"

/dev\_stage="proliferated callus on 2N6 media for 2 weeks"

/lab\_host="E.coli DH10B"

/clone\_lib="OSHDAC1-overexpressing transgenic rice plasmid"

cDNA library (HD)"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was"

treated with ABA(20um) for 1hr. Oligo-capped mRNA was"

reverse transcribed and then used for PCR. mRNA was"

derived from rice Histone Deacetylase overexpression"

line."

Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

1.4%; Score 14.8; DB 1; Length 18;

88.9%; Pred. No. 93;

16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

AZ799396

2M0056N18R Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC2M0056N18 R, genomic survey sequence.

AZ799396

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AZ799396

AZ799396

AZ799396

AZ799396

AZ799396

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Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnam@bio.com, bhnam@bio.myongji.ac.kr.

Location/Qualifiers

1...18

/organism="Oryza sativa"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:4530"

/clone="HD-11-E22"

/tissue\_type="callus"

/dev\_stage="proliferated callus on 2N6 media for 2 weeks"

/lab\_host="E.coli DH10B"

/clone\_lib="OSHDAC1-overexpressing transgenic rice plasmid"

cDNA library (HD)"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was"

treated with ABA(20um) for 1hr. Oligo-capped mRNA was"

reverse transcribed and then used for PCR. mRNA was"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: pW42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pW42 (G1/432114|9b|Ari29072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

Query Match 1.4%; Score 14.8; DB 1; Length 19;  
 Best Local Similarity 88.9%; Pred. No. 96;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1814 ATATATATATATATGAC 1831  
 |||||  
 Db 2 ATATATATATATACATAC 19

RESULT 131  
 N41929/c  
 LOCUS  
 DEFINITION Y707502.r1 Soares melanocyte 2NDHM Homo sapiens CDNA clone  
 IMAGE:270507 5' similar to 9b:M92934 CONNECTIVE TISSUE GROWTH  
 FACTOR PRECURSOR (HUMAN); mRNA sequence.

ACCESSION N41929  
 VERSION N41929.1 GI:1165960  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 35)  
 AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,  
 Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,  
 Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,  
 Trevisan, E., Waterston, R., Williamson, A., Wohlmann, P. and  
 Wilson, R.

TITLE The WashU-Merck EST Project  
 JOURNAL Unpublished (1995)  
 COMMENT Contact: Wilson RK  
 Washington University School of Medicine  
 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 High quality sequence starts: 1  
 High quality sequence stops: 1  
 Source: IMAGE Consortium LLNL

This clone is available royalty-free through LLNL; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
 Trace considered overall poor quality  
 Seq primer: T7

High quality sequence stop: 1.  
 Location/Qualifiers  
 1..35  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="GDB:3880149"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:270507"

FEATURES  
 source

/sex="Male"  
 /tissue\_type="melanocyte"  
 /lab\_host="DH10B (ampicillin resistant)"  
 /clone\_lib="Soares melanocyte 2NDHM"  
 /note="Vector: p7773D (Pharmacia) with a modified  
 polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA  
 was primed with a Not I - oligo(dT) primer [5',  
 TGTTACCAATCTGAAGTGGAGCGCGAGTGTGTTTTTTTTTTT 3'],  
 double-stranded cDNA was size selected, ligated to Eco RI  
 adaptors (Pharmacia), digested with Not I and cloned into  
 the Not I and Eco RI sites of a modified p7773 vector  
 (Pharmacia). Library constructed by Bento Soares and  
 M. Fatima Bonaldo. RNA from normal foreskin melanocytes  
 (FS374) was kindly provided by Dr. Anthony P. Albino."

Query Match 1.4%; Score 14.8; DB 1; Length 35;  
 Best Local Similarity 80.0%; Pred. No. 1.2e+02;  
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1813 TATATATATATATGAC 1832  
 |||||  
 Db 35 TATATATATATATACACA 16

RESULT 132  
 N4247165  
 LOCUS  
 DEFINITION AW247165 17 bp mRNA linear EST 07-JAN-2000  
 IMAGE:2819675 3prime NIH\_MGC\_7 Homo sapiens CDNA clone IMAGE:2819675 3',  
 mRNA sequence.

ACCESSION N4247165  
 VERSION AW247165.1 GI:6590158  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 17)  
 AUTHORS NIH-MGC http://mgs.nci.nih.gov/  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Other ESTs: 2819675.5prime  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgs@bbs-rmail.nih.gov

Tissue Procurement: DCTD/BTP cDNA Library Preparation: Ling  
 Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.  
 Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing  
 project Clone distribution: MGC clone distribution information can  
 be found through the I.M.A.G.E. Consortium/LLNL at:  
 www.biol.llnl.gov/bbrp/image/image.html Base Calling / Quality  
 Scores: PHRED from University of Washington Genome Center  
 Trimming: cross match from University of Washington Genome Center  
 PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley  
 Drosophila Genome Project. University of Washington Genome Center:  
 http://www.genome.washington.edu Low Quality sequence: 17  
 contiguous PHRED high quality bases following vector sequence. Very  
 Low Quality Sequence: Trace file contained 17 contiguous distinct  
 peaks following vector sequence.  
 Plate: LCM2 row: D column: 12  
 High quality sequence stop: 17.  
 Location/Qualifiers  
 1..17

FEATURES  
 source

/organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2819675"  
 /tissue\_type="small cell carcinoma"  
 /cell\_line="MGC3"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH\_MGC\_7"  
 /note="Organ: lung; Vector: pOT37; Site 1: XhoI; Site 2:  
 EcoRI; cDNA made by oligo-dT priming. Directionally  
 cloned into EcoRI/XhoI sites using the following 5'  
 adaptor: GGCACGAG(G). Size-selected >500bp for average

insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 1.4%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 96;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1866 TTTTATTTTGTGTTTT 1881

DB 2 TTTTATTTTGTGTTTT 17

RESULT 133  
AW248574  
LOCUS  
DEFINITION  
AW248574  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

AW248574 17 bp mRNA linear EST 07-JAN-2000  
2821096.3prime NIH\_MGC\_7 Homo sapiens cDNA IMAGE:2821096 3',  
RNA sequence.  
AW248574  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 17)  
NIH-MGC http://mgs.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Other ESTs: 2821096.5prime  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs@mail.nih.gov  
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling  
Hong/Rubin laboratory cDNA library Arrayed by: The I.M.A.G.E.  
Consortium (ILMM) DNA sequencing by: Berkeley MGC sequencing  
Project Clone distribution: MGC clone distribution information can  
be found through the I.M.A.G.E. Consortium/ILMM at:  
www-bio.llnl.gov/bbr/image/image.html Base Calling / Quality  
Scores: PHRED from University of Washington Genome Center. Vector  
Trimming: cross match from University of Washington Genome Center. Vector  
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley  
Drosophila Genome Project. University of Washington Genome Center:  
http://www.genome.washington.edu Low Quality Sequence: 8 contiguous  
PHRED high quality bases following vector sequence. Very low  
Quality Sequence: Trace file contained 17 contiguous distinct peaks  
following vector sequence. Polyadenylation: Based upon the presence  
of a XhoI site followed by a run of 14 or more T residues at the  
beginning of the sequence, this cDNA insert was polyadenylated.  
Plate: L10MS row: 0 column: 17  
High quality sequence stop: 8.  
Location/Qualifiers

FEATURES  
source  
1..17  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clones="IMAGE:2821096"  
/tissue\_type="small cell carcinoma"  
/cell\_line="MGC3"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_7"  
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCACGAG(G). Size-selected >500bp for average  
insert size 1.8kb. Library constructed by Ling Hong in  
the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."

Query Match 1.4%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 96;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1866 TTTTATTTTGTGTTTT 1881  
DB 1 TTTTATTTTGTGTTTT 16

RESULT 134

AZ579599/c

LOCUS

DEFINITION

AZ579599

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: dgunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0367 row: P column: 06

Seq primer: CGTGTAAACGACGCGCAGT

Class: plasmid ends

High quality sequence stop: 21.

Location/Qualifiers

1..21

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clones="UUGC1M0367P06"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: pMD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pMD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

Query Match 1.4%; Score 14.2; DB 1; Length 21;

Best Local Similarity 84.2%; Pred No. 1.1e+02;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

AZ579599 21 bp DNA linear GSS 13-DEC-2000  
1M0367P06f Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0367P06 F, genomic survey sequence.

AZ579599

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

1 (bases 1 to 21)

Dunn, D., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Islam, H., Rose, M., Rose, R., Stokes, R., Ringey, A., von

Niederhauser, A. and Wright, D., Weiss, R.,

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: dgunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0367 row: P column: 06

Seq primer: CGTGTAAACGACGCGCAGT

Class: plasmid ends

High quality sequence stop: 21.

Location/Qualifiers

1..21

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clones="UUGC1M0367P06"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: pMD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pMD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

```

QY 1814 ATATATATATATATGAC 1932
DB 20 AGATATATATATATAC 2

RESULT 135
BQ590128
LOCUS
DEFINITION
  E012843-024-019-E19-T7 MP1Z-ADIS-024-storage root Beta vulgaris
  cDNA clone 024-019-E19 3-PRIME, mRNA sequence.
ACCESSION
  BQ590128
VERSION
  BQ590128.1 GI:26119711
KEYWORDS
  EST.
SOURCE
  Beta vulgaris
  ORGANISM
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
    Caryophyllales; Amaranthaceae; Beta.
REFERENCE
  1 (bases 1 to 17)
  Herwig, R., Schulz, B., Weisshaar, B., Hennig, S., Steinfath, M.,
  Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H.
  and Radelof, U.
  Construction of a 'unigene' cDNA clone set by oligonucleotide
  fingerprinting allows access to 25 000 potential sugar beet genes
  Plant J. 32 (5), 845-857 (2002)
JOURNAL
  22362189
MEDLINE
  12472698
PUBMED
  12472698
COMMENT
  Contact: Weisshaar B
  ADIS DNA core facility at MP1Z
  Max-Planck-Institute for Plant Breeding Research
  Carl-von-Linne Weg 10, 50829 Koeln, Germany
  Fax: 00492215062851
  Email: weisshaar@mpiz-koeln.mpg.de
  Insert Length: 17 Std Error: 0.00
  Plate: 19 row: B column: 19
  Seq primer: T7; GTAATACGACTCATATAGGCG.
  Location/Qualifiers
    1..17
    /organism="Beta vulgaris"
    /mol_type="mRNA"
    /cultivar="KWS2320 (double haploid, monogerm breeding
    line)"
    /db_xref="GABI:189986"
    /db_xref="taxon:161934"
    /clone="024-019-E19"
    /tissue_type="storage root"
    /lab_host="EMDH10B"
    /clone_lib="MP1Z-ADIS-024-storage root"
    /notes="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
    cDNA library from sugar beet library provided by KWS
    Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
    b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
    orientation:
    SP6-Sali-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
    Sequencing granted in the context of the GABI-Beet
    project, local PI: Dr. Katharina Schneider, coordinator:
    Prof. Christian Jung; Sequence submission managed by
    RZPD/GABI-Primary database: http://gabi.rzpd.de"
  Query Match 1.3%; Score 13.8; DB 1; Length 17;
  Best Local Similarity 88.2%; Pred. No. 1.1e+02;
  Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1866 TTTTATTTTGTGTTTA 1882
DB 1 TTTTATTTTGTGTTTA 17

RESULT 136
BQ590687/c
LOCUS
DEFINITION
  S013717-024-018-B24-T7 MP1Z-ADIS-024-storage root Beta vulgaris
  cDNA clone 024-018-B24 3-PRIME, mRNA sequence.
  17 bp mRNA linear EST 06-DEC-2002
BQ590687
LOCUS
DEFINITION
  E012715-024-017-B22-T7 MP1Z-ADIS-024-storage root Beta vulgaris
  cDNA clone 024-017-B22 3-PRIME, mRNA sequence.
ACCESSION
  BQ591177
VERSION
  BQ591177.1 GI:26120760
KEYWORDS
  EST.
SOURCE
  Beta vulgaris
  ORGANISM
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
    Caryophyllales; Amaranthaceae; Beta.
REFERENCE
  1 (bases 1 to 17)
  Herwig, R., Schulz, B., Weisshaar, B., Hennig, S., Steinfath, M.,
  Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H.
  and Radelof, U.
  Construction of a 'unigene' cDNA clone set by oligonucleotide
  fingerprinting allows access to 25 000 potential sugar beet genes
  Plant J. 32 (5), 845-857 (2002)
JOURNAL
  22362189
MEDLINE
  12472698
PUBMED
  12472698
COMMENT
  Contact: Weisshaar B
  ADIS DNA core facility at MP1Z
  Max-Planck-Institute for Plant Breeding Research
  Carl-von-Linne Weg 10, 50829 Koeln, Germany
  Fax: 00492215062851
  Email: weisshaar@mpiz-koeln.mpg.de
  Insert Length: 17 Std Error: 0.00
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    /notes="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
    cDNA library from sugar beet library provided by KWS
    Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
    b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
    orientation:
    SP6-Sali-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
    Sequencing granted in the context of the GABI-Beet
    project, local PI: Dr. Katharina Schneider, coordinator:
    Prof. Christian Jung; Sequence submission managed by
    RZPD/GABI-Primary database: http://gabi.rzpd.de"
  Query Match 1.3%; Score 13.8; DB 1; Length 17;
  Best Local Similarity 88.2%; Pred. No. 1.1e+02;
  Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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VERSION
  BQ590687.1 GI:26120270
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SOURCE
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    Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
    Caryophyllales; Amaranthaceae; Beta.
REFERENCE
  1 (bases 1 to 17)
  Herwig, R., Schulz, B., Weisshaar, B., Hennig, S., Steinfath, M.,
  Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H.
  and Radelof, U.
  Construction of a 'unigene' cDNA clone set by oligonucleotide
  fingerprinting allows access to 25 000 potential sugar beet genes
  Plant J. 32 (5), 845-857 (2002)
JOURNAL
  22362189
MEDLINE
  12472698
PUBMED
  12472698
COMMENT
  Contact: Weisshaar B
  ADIS DNA core facility at MP1Z
  Max-Planck-Institute for Plant Breeding Research
  Carl-von-Linne Weg 10, 50829 Koeln, Germany
  Fax: 00492215062851
  Email: weisshaar@mpiz-koeln.mpg.de
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    line)"
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    Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
    b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
    orientation:
    SP6-Sali-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
    Sequencing granted in the context of the GABI-Beet
    project, local PI: Dr. Katharina Schneider, coordinator:
    Prof. Christian Jung; Sequence submission managed by
    RZPD/GABI-Primary database: http://gabi.rzpd.de"
  Query Match 1.3%; Score 13.8; DB 1; Length 17;
  Best Local Similarity 88.2%; Pred. No. 1.1e+02;
  Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTT 1881
DB 17 TTTTATTTTGTGTTT 1

RESULT 137
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DEFINITION
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  cDNA clone 024-017-B22 3-PRIME, mRNA sequence.
ACCESSION
  BQ591177
VERSION
  BQ591177.1 GI:26120760
KEYWORDS
  EST.
SOURCE
  Beta vulgaris
  ORGANISM
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
    Caryophyllales; Amaranthaceae; Beta.
REFERENCE
  1 (bases 1 to 17)
  Herwig, R., Schulz, B., Weisshaar, B., Hennig, S., Steinfath, M.,
  Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H.
  and Radelof, U.
  Construction of a 'unigene' cDNA clone set by oligonucleotide
  fingerprinting allows access to 25 000 potential sugar beet genes
  Plant J. 32 (5), 845-857 (2002)
JOURNAL
  22362189
MEDLINE
  12472698
PUBMED
  12472698
COMMENT
  Contact: Weisshaar B
  ADIS DNA core facility at MP1Z
  Max-Planck-Institute for Plant Breeding Research
  Carl-von-Linne Weg 10, 50829 Koeln, Germany
  Fax: 00492215062851
  Email: weisshaar@mpiz-koeln.mpg.de
  Insert Length: 17 Std Error: 0.00
  Plate: 18 row: B column: 24
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    /clone="024-018-B24"
    /tissue_type="storage root"
    /lab_host="EMDH10B"
    /clone_lib="MP1Z-ADIS-024-storage root"
    /notes="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
    cDNA library from sugar beet library provided by KWS
    Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
    b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
    orientation:
    SP6-Sali-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
    Sequencing granted in the context of the GABI-Beet
    project, local PI: Dr. Katharina Schneider, coordinator:
    Prof. Christian Jung; Sequence submission managed by
    RZPD/GABI-Primary database: http://gabi.rzpd.de"
  Query Match 1.3%; Score 13.8; DB 1; Length 17;
  Best Local Similarity 88.2%; Pred. No. 1.1e+02;
  Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lebrach, H. and Radelof, U.  
 Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes  
 Plant J 32 (5), 845-857 (2002)  
 22342189  
 MEDLINE  
 12472698  
 PUBMED  
 COMMENT  
 Contact: Weishaar B  
 ADIS DNA core facility at MPIZ  
 Max-Planck-Institute for Plant Breeding Research  
 Carl-von-Linne Weg 10, 50829 Koeln, Germany  
 Fax: 00492215062851  
 Email: weishaar@piz-koeln.mpg.de  
 Insert Length: 17 Std Error: 0.00  
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 /clone="024-017-B22"  
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 /notes="Vector: PCWSPORT6; Site 1: SalI; Site 2: NotI; cDNA library from sugar beet, library provided by XMS Kleinwanzlebener Saatucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:  
 SP6-SalI-CCAGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet Project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

FEATURES

source  
 Query Match 1.3%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 1.1e+02;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Qy 1865 TTTTATTTTGTGTTTT 1881  
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 Db 1 TTTTATTTTGTGTTTT 17

RESULT 138

CF290854  
 LOCUS  
 DEFINITION 14ROOT--01-A21.b1 Rice root plasmid cDNA library (14ROOT) Oryza sativa cDNA clone 14ROOT--01-A21, mRNA sequence.  
 CF290854  
 VERSION  
 CF290854.1 GI:33659887  
 KEYWORDS  
 EST.  
 SOURCE  
 Oryza sativa  
 Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.  
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 /clone\_lib="Rice leaf plasmid cDNA library I (30DGS)"  
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."  
 AUTHORS  
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
 TITLE  
 Large-scale Sequencing Analysis of Rice ESTs  
 JOURNAL  
 Unpublished (2003)  
 COMMENT  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
 Yongin, Gyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES

source  
 Location/Qualifiers  
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 /mol\_type="mRNA"  
 /cultivar="Nackdong"  
 /db\_xref="taxon:4530"  
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 /tissue\_type="root"  
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 /lab\_host="E.coli DH10B"  
 /clone\_lib="Rice root plasmid cDNA library (14ROOT)"  
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."  
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 Best Local Similarity 88.2%; Pred. No. 1.1e+02;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Qy 1865 TTTTATTTTGTGTTTT 1881  
 |||||  
 Db 1 TTTTATTTTGTGTTTT 17

FEATURES

source  
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 /tissue\_type="leaf"  
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 /lab\_host="E.coli DH10B"  
 /clone\_lib="Rice leaf plasmid cDNA library I (30DGS)"  
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 Best Local Similarity 88.2%; Pred. No. 1.1e+02;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Qy 1866 TTTTATTTTGTGTTTTA 1882  
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 Db 1 TTTTATTTTGTGTTTTA 17

## RESULT 140

CF295988

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CF295988 17 bp mRNA linear EST 14-AUG-2003  
 30DGS--06-C17.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza  
 sativa cDNA clone 30DGS--06-C17, mRNA sequence.

CF295988  
 CF295988.1 GI:33665021  
 EST.

Oryza sativa  
 Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 17)  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)

Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

Location/Qualifiers

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/lab\_host="E.coli DH108"

/clone\_lib="Rice leaf plasmid cDNA library I (30DGS)"

/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped  
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 RT-PCR."

RT-PCR."

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 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1866 TTTTATTTTGTGTTTTA 1882

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1 TTTTATTTTGTGTTTTA 17

Db

RESULT 141

CF298589

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CF298589 17 bp mRNA linear EST 15-AUG-2003  
 7LEAF--02-A18.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
 sativa cDNA clone 7LEAF--02-A18, mRNA sequence.

CF298589  
 CF298589.1 GI:33670350  
 EST.

Oryza sativa  
 Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 17)  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)

Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355

Location/Qualifiers

1. 17

/organism="Oryza sativa"

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/cultivar="Nackdong"

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/dev\_stage="14 days after germination"

/lab\_host="E.coli DH108"

/clone\_lib="ABF3-overexpressing transgenic rice plasmid  
 cDNA library (ABF)"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried  
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 then used for PCR. mRNA was prepared from ABA-responsive  
 element binding transcription factor 3 overexpression  
 line."

Query Match 1.3%; Score 13.8; DB 1; Length 17;  
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 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1865 TTTTATTTTGTGTTTT 1881

|||||

1 TTTTATTTTGTGTTTT 17

Db

Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES

source

Location/Qualifiers

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/organism="Oryza sativa"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:4530"

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/clone\_lib="Rice leaf plasmid cDNA library II (7LEAF)"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped  
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RT-PCR."

Query Match 1.3%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 1.1e+02;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1865 TTTTATTTTGTGTTTT 1881

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1 TTTTATTTTGTGTTTT 17

Db

RESULT 142

CF310219

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CF310219 17 bp mRNA linear EST 15-AUG-2003  
 ABF--04-M02.g1 ABF3-overexpressing transgenic rice plasmid cDNA  
 library (ABF) Oryza sativa cDNA clone ABF--04-M02, mRNA sequence.

CF310219  
 CF310219.1 GI:33681980  
 EST.

Oryza sativa  
 Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 17)  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)

Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

Location/Qualifiers

1. 17

/organism="Oryza sativa"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:4530"

/clone="ABF--04-M02"

/tissue\_type="leaf"

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/lab\_host="E.coli DH108"

/clone\_lib="ABF3-overexpressing transgenic rice plasmid  
 cDNA library (ABF)"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried  
 for 2hrs. Oligo-capped mRNA was reverse transcribed and  
 then used for PCR. mRNA was prepared from ABA-responsive  
 element binding transcription factor 3 overexpression  
 line."

Query Match 1.3%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 1.1e+02;  
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Qy 1865 TTTTATTTTGTGTTTT 1881

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1 TTTTATTTTGTGTTTT 17

Db



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Db      1  TTTT TTTT TTTT TTTT 17

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LOCUS      JMT--03-013.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
DEFINITION      library (JMT) Oryza sativa cDNA clone JMT--03-013, mRNA sequence.
ACCESSION      CF334566
VERSION
KEYWORDS
SOURCE
ORGANISM      Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 17)
AUTHORS      Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

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/notes="vector: PCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
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prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

Query Match      1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity      88.2%; Pred. No. 1.1e+02;
Matches      15; Conservative      0; Mismatches      2; Indels      0; Gaps      0;

Qy      1865  TTTT TTTT TTTT TTTT 1881
Db      1  TTTT TTTT TTTT TTTT 17

RESULT 144
CF336950      17 bp  mRNA  linear  EST 18-AUG-2003
LOCUS      JMT--07-D04.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
DEFINITION      library (JMT) Oryza sativa cDNA clone JMT--07-D04, mRNA sequence.
ACCESSION      CF336950
VERSION
KEYWORDS
SOURCE
ORGANISM      Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 17)
AUTHORS      Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
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/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="JMT--03-013"
/tissue_type="leaf"
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cDNA library (JMT)"
/notes="vector: PCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
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prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

Query Match      1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity      88.2%; Pred. No. 1.1e+02;
Matches      15; Conservative      0; Mismatches      2; Indels      0; Gaps      0;

Qy      1865  TTTT TTTT TTTT TTTT 1881
Db      1  TTTT TTTT TTTT TTTT 17

RESULT 145
CF334566      16 bp  mRNA  linear  EST 09-MAR-1999
LOCUS      tf51h06.x1 NCI CGAP Brn23 Homo sapiens cDNA clone IMAGE:2102843 3'
DEFINITION      similar to TR:Q69565 Q69566 ;, mRNA sequence.
ACCESSION      AI424037
VERSION      AI424037.1 GI:4269968
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 16)
AUTHORS      NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE      National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BTGP), Tumor Gene Index
JOURNAL      Unpublished (1998)
COMMENT      Contact: Robert Straubeberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldi, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Seq primer: -40UP from Gibco
High quality sequence stop: 1.

FEATURES
Location/Qualifiers
1..16
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2102843"
/tissue_type="glicblastoma (pooled)"

```

```

COMMENT      Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
Location/Qualifiers
1..17
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="JMT--07-D04"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
/notes="vector: PCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

Query Match      1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity      88.2%; Pred. No. 1.1e+02;
Matches      15; Conservative      0; Mismatches      2; Indels      0; Gaps      0;

Qy      1866  TTTT TTTT TTTT TTTT 1882
Db      1  TTTT TTTT TTTT TTTT 17

RESULT 145
CF334566      16 bp  mRNA  linear  EST 09-MAR-1999
LOCUS      tf51h06.x1 NCI CGAP Brn23 Homo sapiens cDNA clone IMAGE:2102843 3'
DEFINITION      similar to TR:Q69565 Q69566 ;, mRNA sequence.
ACCESSION      AI424037
VERSION      AI424037.1 GI:4269968
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 16)
AUTHORS      NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE      National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BTGP), Tumor Gene Index
JOURNAL      Unpublished (1998)
COMMENT      Contact: Robert Straubeberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldi, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Seq primer: -40UP from Gibco
High quality sequence stop: 1.

FEATURES
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:2102843"
/tissue_type="glicblastoma (pooled)"

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RESULT 148
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LOCUS
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  cDNA clone 024-019-M04 3-PRIME, mRNA sequence.
ACCESSION
  BQ590507
VERSION
  BQ590507.1 GI:26120090
KEYWORDS
  EST.
SOURCE
  Beta vulgaris
  Beta vulgaris
ORGANISM
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
  Caryophyllales; Amaranthaceae; Beta.
REFERENCE
  1 (bases 1 to 16)
  Herwig, R., Schulz, B., Weishaar, B., Hennig, S., Steinfath, M.,
  Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H.
  and Radelof, U.
  Construction of a 'unigene' cDNA clone set by oligonucleotide
  fingerprinting allows access to 25 000 potential sugar beet genes
  Plant J. 32 (5), 845-857 (2002)
JOURNAL
  MEDLINE
  PUBMED
  12472698
COMMENT
  Contact: Weishaar B
  ADIS DNA core facility at MP1Z
  Max-Planck-Institute for Plant Breeding Research
  Carl-von-Linne Weg 10, 50829 Koeln, Germany
  Fax: 00492215062851
  Email: weishaar@piz-koeln.mpg.de
  Insert Length: 16 Std Error: 0.00
  Plate: 19 row: M column: 04
  Seq primer: T7; GTAATACGACTCACTATAGGCG.
FEATURES
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  /db_xref="taxon:161934"
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  /tissue_type="storage root"
  /lab_host="EMDH10B"
  /clone_lib="MP1Z-ADIS-024-storage root"
  /notes="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
  cDNA library from sugar beet. Library provided by KWS
  Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
  b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
  orientation:
  SP6-Sali-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
  Sequencing granted in the context of the GABI-Beet
  project, local PI: Dr. Katharina Schneider, coordinator:
  Prof. Christian Jung; Sequence submission managed by
  RZPD/GABI-Primary database: http://gabi.rzpd.de"
  Query Match 1.2%; Score 12.8; DB 1; Length 16;
  Best Local Similarity 87.5%; Pred. No. 1.2e+02;
  Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1867 TTTTATTTTGTGTTT 1882
Db 1 TTTTATTTTGTGTTT 16

RESULT 149
BQ592600/c
LOCUS
DEFINITION
  S013686-024-028-F08-SP6R-MP1Z-ADIS-024-developing root Beta
  vulgaris cDNA clone 024-028-F08 5-PRIME, mRNA sequence.
ACCESSION
  BQ592600
VERSION
  BQ592600.1 GI:26122183
KEYWORDS
  EST.
SOURCE
  Beta vulgaris
  Beta vulgaris
ORGANISM
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
  Caryophyllales; Amaranthaceae; Beta.
REFERENCE
  1 (bases 1 to 16)
  Herwig, R., Schulz, B., Weishaar, B., Hennig, S., Steinfath, M.,
  Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H.
  and Radelof, U.
  Construction of a 'unigene' cDNA clone set by oligonucleotide
  fingerprinting allows access to 25 000 potential sugar beet genes
  Plant J. 32 (5), 845-857 (2002)
JOURNAL
  MEDLINE
  PUBMED
  12472698
COMMENT
  Contact: Weishaar B
  ADIS DNA core facility at MP1Z
  Max-Planck-Institute for Plant Breeding Research
  Carl-von-Linne Weg 10, 50829 Koeln, Germany
  Fax: 00492215062851
  Email: weishaar@piz-koeln.mpg.de
  Insert Length: 16 Std Error: 0.00
  Plate: 19 row: M column: 04
  Seq primer: T7; GTAATACGACTCACTATAGGCG.
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  /mol_type="mRNA"
  /cultivar="KWS2320 (double haploid, monogerm breeding
  line)"
  /db_xref="GABI:189608"
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  /clone="024-019-M04"
  /tissue_type="storage root"
  /lab_host="EMDH10B"
  /clone_lib="MP1Z-ADIS-024-storage root"
  /notes="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
  cDNA library from sugar beet. Library provided by KWS
  Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
  b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
  orientation:
  SP6-Sali-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
  Sequencing granted in the context of the GABI-Beet
  project, local PI: Dr. Katharina Schneider, coordinator:
  Prof. Christian Jung; Sequence submission managed by
  RZPD/GABI-Primary database: http://gabi.rzpd.de"
  Query Match 1.2%; Score 12.8; DB 1; Length 16;
  Best Local Similarity 87.5%; Pred. No. 1.2e+02;
  Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTT 1880
Db 16 TTTTATTTTGTGTTT 1

RESULT 150
BQ592965
LOCUS
DEFINITION
  S013324-024-028-A01-T7 MP1Z-ADIS-024-developing root Beta vulgaris
  cDNA clone 024-028-A01 3-PRIME, mRNA sequence.
ACCESSION
  BQ592965
VERSION
  BQ592965.1 GI:26122548
KEYWORDS
  EST.
SOURCE
  Beta vulgaris
  Beta vulgaris
ORGANISM
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
  Caryophyllales; Amaranthaceae; Beta.
REFERENCE
  1 (bases 1 to 16)
  Herwig, R., Schulz, B., Weishaar, B., Hennig, S., Steinfath, M.,
  Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H.
  and Radelof, U.
  Construction of a 'unigene' cDNA clone set by oligonucleotide
  fingerprinting allows access to 25 000 potential sugar beet genes
  Plant J. 32 (5), 845-857 (2002)
JOURNAL
  MEDLINE
  PUBMED
  12472698
COMMENT
  Contact: Weishaar B
  ADIS DNA core facility at MP1Z
  Max-Planck-Institute for Plant Breeding Research
  Carl-von-Linne Weg 10, 50829 Koeln, Germany
  Fax: 00492215062851
  Email: weishaar@piz-koeln.mpg.de
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  Seq primer: SP6R; ATTAGTGACACTATAGAGA.
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  /clone="024-028-F08"
  /tissue_type="developing root"
  /lab_host="EMDH10B"
  /clone_lib="MP1Z-ADIS-024-developing root"
  /notes="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
  cDNA library from sugar beet. Library provided by KWS
  Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
  b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
  orientation:
  SP6-Sali-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
  Sequencing granted in the context of the GABI-Beet
  project, local PI: Dr. Katharina Schneider, coordinator:
  Prof. Christian Jung; Sequence submission managed by
  RZPD/GABI-Primary database: http://gabi.rzpd.de"
  Query Match 1.2%; Score 12.8; DB 1; Length 16;
  Best Local Similarity 87.5%; Pred. No. 1.2e+02;
  Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTT 1880
Db 16 TTTTATTTTGTGTTT 1

```

```

22362189 MEDLINE
12472698 PUBMED
Contact: Weisshaar B
ADIS DNA core facility at MPiZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
Insert Length: 16 Std Error: 0.00
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Seq primer: T7; GTAATACGACTCACTATAGGCG.
Location/Qualifiers
1. .16
/organism="Beta vulgaris"
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line)"
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cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"
Query Match 1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTT 1880
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Db 1 TTTTATTTTGTGTTT 16

RESULT 151
BQ595369 16 bp mRNA linear EST 06-DEC-2002
LOCUS
DEFINITION
cDNA clone 024-022-P02-T7 MPiZ-ADIS-024-developing root Beta vulgaris
ACCESSION
BQ595369.1 GI:26124952
VERSION
BQ595369.1
KEYWORDS
EST.
SOURCE
Beta vulgaris
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE
1 (bases 1 to 16)
AUTHORS
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
TITLE
Construction of a 'unigenes' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL
Plant J. 32 (5), 845-857 (2002)
MEDLINE
22362189
PUBMED
12472698
COMMENT
Contact: Weisshaar B
ADIS DNA core facility at MPiZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
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/clone="024-022-P02"
/tissue_type="developing root"
/lab_host="EMDH10B"
/clone_lib="MPiZ-ADIS-024-developing root"
/notes="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"
Query Match 1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTT 1880
|||||
Db 1 TTTTATTTTGTGTTT 16

RESULT 151
BQ595369 16 bp mRNA linear EST 06-DEC-2002
LOCUS
DEFINITION
cDNA clone 024-022-P02-T7 MPiZ-ADIS-024-developing root Beta vulgaris
ACCESSION
BQ595369.1 GI:26124952
VERSION
BQ595369.1
KEYWORDS
EST.
SOURCE
Beta vulgaris
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE
1 (bases 1 to 16)
AUTHORS
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
TITLE
Construction of a 'unigenes' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL
Plant J. 32 (5), 845-857 (2002)
MEDLINE
22362189
PUBMED
12472698
COMMENT
Contact: Weisshaar B
ADIS DNA core facility at MPiZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
Insert Length: 16 Std Error: 0.00
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FEATURES
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/clone="024-022-P02"
/tissue_type="developing root"
/lab_host="EMDH10B"
/clone_lib="MPiZ-ADIS-024-developing root"
/notes="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"
Query Match 1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1867 TTTTATTTTGTGTTT 1882
|||||
Db 1 TTTTATTTTGTGTTT 16

RESULT 152
BQ595717 16 bp mRNA linear EST 06-DEC-2002
LOCUS
DEFINITION
cDNA clone 024-022-H07-SP6 MPiZ-ADIS-024-developing root Beta vulgaris
ACCESSION
BQ595717.1 GI:26125300
VERSION
BQ595717.1
KEYWORDS
EST.
SOURCE
Beta vulgaris
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE
1 (bases 1 to 16)
AUTHORS
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
TITLE
Construction of a 'unigenes' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL
Plant J. 32 (5), 845-857 (2002)
MEDLINE
22362189
PUBMED
12472698
COMMENT
Contact: Weisshaar B
ADIS DNA core facility at MPiZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
Insert Length: 16 Std Error: 0.00
Plate: 22 row: H column: 07
Seq primer: SP6; CATACGATTTAGTGACACTATAG.
Location/Qualifiers
1. .16
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/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:191134"
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/clone="024-022-H07"

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/issue_type="developing root"
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/notes="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
b.schulz@kws.de, cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGGCTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
Project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match      1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTT 1880
Db 16 TTTTATTTTGTGTTT 1

RESULT 153
CF279325
LOCUS
DEFINITION
Oryza sativa cDNA clone 14ETL-05-J09, mRNA sequence.
ACCESSION
CF279325.1 GI:33656711
VERSION
EST.
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 16)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..16
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="14ETL-05-J09"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library
(14ETL)"
/notes="vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
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Query Match      1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTT 1880
Db 16 TTTTATTTTGTGTTT 16

RESULT 155
CF279325
LOCUS
DEFINITION
Oryza sativa cDNA clone 14ETL-05-J09, mRNA sequence.
ACCESSION
CF279325.1 GI:33656711
VERSION
EST.
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 16)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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/clone_lib="Rice etiolated leaf plasmid cDNA library
(14ETL)"
/notes="vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTT 1880
Db 1 TTTTATTTTGTGTTT 16

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RESULT 154
CF296130
LOCUS
DEFINITION
Oryza sativa cDNA clone 30DGS--06-F22, mRNA sequence.
ACCESSION
CF296130.1 GI:33665163
VERSION
EST.
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 16)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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/db_xref="taxon:4530"
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/tissue_type="leaf"
/dev_stage="30 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
/notes="vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      1.2%; Score 12.8; DB 1; Length 16;
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QY 1867 TTTTATTTTGTGTTT 1882
Db 1 TTTTATTTTGTGTTT 16

RESULT 155
CF311057
LOCUS
DEFINITION
ABF-06-C03.g1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa cDNA clone ABF--06-C03, mRNA sequence.
ACCESSION
CF311057
VERSION
EST.
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 16)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355

```

Email: bhnam@bio.com, bhnam@bio.myongji.ac.kr.

FEATURES

source

Location/Qualifiers  
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/organism="Oryza sativa"  
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/lab\_host="E.coli DH10B"  
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/note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 1.2%; Score 12.8; DB 1; Length 16;  
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Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTT 1880

Db 1 TTTTATTTTGTGTTT 16

RESULT 156  
CF314013  
LOCUS  
DEFINITION  
HD--02-G01.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--02-G01, mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE  
AUTHORS  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
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Unpublished (2003)  
Contact: Nahm B.H.  
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Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnam@bio.com, bhnam@bio.myongji.ac.kr.

FEATURES

source

Location/Qualifiers  
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Query Match 1.2%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 1.2e+02;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1867 TTTTATTTTGTGTTT 1882

Db 1 TTTTATTTTGTGTTT 16

RESULT 157

CF314377  
LOCUS  
DEFINITION  
HD--02-G01.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--02-G01, mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE  
AUTHORS  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
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Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnam@bio.com, bhnam@bio.myongji.ac.kr.

FEATURES

source

Location/Qualifiers  
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/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 1.2%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 1.2e+02;  
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QY 1865 TTTTATTTTGTGTTT 1880

Db 1 TTTTATTTTGTGTTT 16

RESULT 158

CF315789  
LOCUS  
DEFINITION  
HD--04-N10.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--04-N10, mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE  
1 (bases 1 to 16)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES source  
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derived from rice Histone Deacetylase overexpression  
line."

Query Match 1.2%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 1.2e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTT 1880  
Db 1 TTTTATTTTGTGTTT 16

RESULT 159  
CF316056  
LOCUS  
DEFINITION HD--05-D07.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA  
library (HD) Oryza sativa cDNA clone HD--05-D07, mRNA sequence.  
ACCESSION CF316056.1 GI:33687817  
VERSION  
KEYWORDS EST.  
SOURCE  
ORGANISM  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Eriartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 16)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES source  
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Best Local Similarity 87.5%; Pred. No. 1.2e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTT 1880  
Db 1 TTTTATTTTGTGTTT 16

RESULT 159  
CF316056  
LOCUS  
DEFINITION HD--05-D07.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA  
library (HD) Oryza sativa cDNA clone HD--05-D07, mRNA sequence.  
ACCESSION CF316056.1 GI:33687817  
VERSION  
KEYWORDS EST.  
SOURCE  
ORGANISM  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Eriartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 16)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES source  
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QY 1865 TTTTATTTTGTGTTT 1880  
Db 1 TTTTATTTTGTGTTT 16

RESULT 160  
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library (HD) Oryza sativa cDNA clone HD--07-I05, mRNA sequence.  
ACCESSION CF317718.1 GI:33689479  
VERSION  
KEYWORDS EST.  
SOURCE  
ORGANISM  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Eriartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 16)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES source  
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derived from rice Histone Deacetylase overexpression  
line."

Query Match 1.2%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 1.2e+02;  
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QY 1865 TTTTATTTTGTGTTT 1880  
Db 1 TTTTATTTTGTGTTT 16

RESULT 161  
CF320356  
LOCUS  
DEFINITION HD--11-D14.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA  
library (HD) Oryza sativa cDNA clone HD--11-D14, mRNA sequence.

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library (HD) Oryza sativa cDNA clone HD--11-D14, mRNA sequence.
ACCESSION CF320356
VERSION CF320356.1 GI:33692117
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
TITLE Ehrhartoidae; Oryzaceae; Oryza.
JOURNAL 1 (bases 1 to 16)
COMMENT Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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Query Match 1.2%; Score 12.8; DB 1; Length 16;
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Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTATTTGTTT 1880
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      1 TTTTATTATTTT 16

Db

RESULT 162
CF327722
LOCUS NACL--02-F06, b1 Rice callus plasmid cDNA library (NACL) Oryza
DEFINITION sativa cDNA clone NACL--02-F06, mRNA sequence.
ACCESSION CF327722
VERSION CF327722.1 GI:33803695
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
TITLE Ehrhartoidae; Oryzaceae; Oryza.
JOURNAL 1 (bases 1 to 16)
COMMENT Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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FEATURES
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Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTATTTGTTT 1880
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      1 TTTTATTATTTT 16

Db

RESULT 163
CF329320
LOCUS NACL--04-J17, b1 Rice callus plasmid cDNA library (NACL) Oryza
DEFINITION sativa cDNA clone NACL--04-J17, mRNA sequence.
ACCESSION CF329320
VERSION CF329320.1 GI:33806877
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
TITLE Ehrhartoidae; Oryzaceae; Oryza.
JOURNAL 1 (bases 1 to 16)
COMMENT Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Unpublished (2003)
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
        source
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Query Match 1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1867 TTTTATTATTTGTTT 1882
      |||||
      1 TTTTATTATTTT 16

Db

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```

University of Glasgow, Joseph Black Building, Glasgow G12 8QQ, UK
COMMENT bases 40 to 60 (SL to QR).
FEATURES Location/Qualifiers
1..21
    /organism="Plasmodium chabaudi"
    /mol_type="Genomic DNA"
    /db_xref="taxon:5825"
    /clone="PC4c11.plc"

Query Match      1.1%; Score 12; DB 1; Length 21;
Best Local Similarity 75.0%; Pred.No.1.6e-02;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      1772 TAAATTTTATTGTAATAA 1791
DB      1 TAAATATAAATTTTAAAA 20

RESULT 166
R06912
LOCUS       R06912             37 bp mRNA linear EST 05-APR-1995
DEFINITION Yfi2g95.gi Soares fetal liver spleen INFLS Homo sapiens cDNA clone
IMAGE12680 3' similar to gb:M92934 CONNECTIVE TISSUE GROWTH
FACTOR PRECURSOR (HUMAN), mRNA sequence.
ACCESSION   R06912
VERSION     R06912.1 GI:758835
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE   1 (bases 1 to 37)
AUTHORS     Hillier,L., Clark,M., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Travaskis,E., Waterston,R., Williamson,A., Woldmann,P. and
Wilson,R.
TITLE       The WashU-Merck EST Project
JOURNAL     Unpublished (1995)
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel.: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            Insert Size: 1597
            High quality sequence starts: 1 High quality sequence stops: 1
            Source: IMAGE Consortium, LLNL This clone is available royalty-free
            through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov)
            for further information. Trace considered overall poor quality
            Insert length: 1597 Std Error: 0.00
            Seq primer: -21ml3
            High quality sequence stop: 1.
            Location/Qualifiers
                1..37
                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="CDS:478841"
                    /db_xref="taxon:9606"
                    /clone="IMAGS:12680"
                    /sex="male"
                    /dev_stage="20 week-post conception fetus"
                    /lab_host="DH10B (ampicillin resistant)"
                    /clone_lib="Soares fetal liver spleen INFLS"
                    /note="Organ: Liver and Spleen; Vector: pTZ19 (Pharmacia)
with a modified polylinker; Site 1: Pac I; Site 2: Eco RI;
1st strand cDNA was primed with a Pac I - oligo(dT) primer
15' AACTGGAGCATTAATTAAGATCTTTTTTTTTTTTTTTT 3'',
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Pac I and cloned into the Pac I
and Eco RI sites of the modified pTZ19 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M.Patima Bonaldo."
FEATURES source

```



with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 1.1%; Score 11.4; DB 1; Length 14;  
Best Local Similarity 92.3%; Pred. No. 1.5e+02;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1764 AGATTTTAAAAA 1776  
|||||  
Db 2 AGAATTTTAAAAA 14

RESULT 170  
CF328966/c  
LOCUS 14 bp mRNA linear EST 18-AUG-2003  
DEFINITION NACL--04-B19.g1 Rice callus plasmid cDNA library (NACL) Oryza  
sativa cDNA clone NACL--04-B19, mRNA sequence.

ACCESSION CF328966  
VERSION  
KEYWORDS

SOURCE Oryza sativa  
ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 14)  
Kim J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)  
Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193  
Fax: 82 31 321 6355

Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES  
source

1. 14  
Location/Qualifiers  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="NACL-04-B19"  
/tissue\_type="callus"  
/dev\_stage="proliferated callus on 2N6 media for 30 days"  
/lab\_host="E.coli DH10B"  
/clone\_lib="Rice callus plasmid cDNA library (NACL)"  
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 1.1%; Score 11.4; DB 1; Length 14;  
Best Local Similarity 92.3%; Pred. No. 1.5e+02;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1767 TTTTAAAAATTT 1779  
|||||  
Db 14 TTTTAAAAATTT 2

RESULT 171  
CF299360/c  
LOCUS 11 bp mRNA linear EST 15-AUG-2003  
DEFINITION 7LEAF--03-F15.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
sativa cDNA clone 7LEAF--03-F15, mRNA sequence.

ACCESSION CF299360  
VERSION  
KEYWORDS

SOURCE Oryza sativa  
ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 11)  
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193  
Fax: 82 31 321 6355

Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES  
source

1. 11  
Location/Qualifiers  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="7LEAF--03-F15"  
/tissue\_type="leaf"  
/dev\_stage="7 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_lib="Rice leaf plasmid cDNA library II (7LEAF)"  
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 1.0%; Score 11; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1768 TTTTAAAAATTT 1778  
|||||  
Db 11 TTTTAAAAATTT 1

RESULT 172  
CF291168/c

LOCUS 13 bp mRNA linear EST 14-AUG-2003  
DEFINITION 14ROOT--01-H20.g1 Rice root plasmid cDNA library (14ROOT) Oryza  
sativa cDNA clone 14ROOT--01-H20, mRNA sequence.

ACCESSION CF291168  
VERSION  
KEYWORDS

SOURCE Oryza sativa  
ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 13)  
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)  
Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193  
Fax: 82 31 321 6355

Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES  
source

1. 13  
Location/Qualifiers  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="14ROOT--01-H20"  
/tissue\_type="root"  
/dev\_stage="14 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_lib="Rice root plasmid cDNA library (14ROOT)"

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/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      1.0%; Score 11; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1865 TTTTATATTTT 1875
DB 11 TTTTATATTTT 1

RESULT 173
CF300273/c
LOCUS      12 bp      mRNA      linear      EST 15-AUG-2003
DEFINITION 7LEAF--04-J19.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--04-J19, mRNA sequence.
ACCESSION  CF300273
VERSION     CF300273.1 GI:33672034
KEYWORDS   EST.
SOURCE     Oryza sativa
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE  1 (bases 1 to 12)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             source
    source
    1..12
    /organism="Oryza sativa"
    /mol_type="mRNA"
    /cultivar="Nackdong"
    /db_xref="taxon:4530"
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    /tissue_type="leaf"
    /dev_stage="7 days after germination"
    /lab_host="E.coli DH10B"
    /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
    /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      1.0%; Score 10.4; DB 1; Length 12;
Best Local Similarity 91.7%; Pred. No. 1.6e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2262 TGATATATTTT 2273
DB 12 TTTATATTTT 1

RESULT 174
CF328670/c
LOCUS      12 bp      mRNA      linear      EST 18-AUG-2003
DEFINITION NACL--03-K23.g1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--03-K23, mRNA sequence.
ACCESSION  CF328670
VERSION     CF328670.1 GI:33805589
KEYWORDS   EST.
SOURCE     Oryza sativa
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

```

```

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 12)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             source
    source
    1..12
    /organism="Oryza sativa"
    /mol_type="mRNA"
    /cultivar="Nackdong"
    /db_xref="taxon:4530"
    /clone="NACL--03-K23"
    /tissue_type="callus"
    /dev_stage="proliferated callus on 2N6 media for 30 days"
    /lab_host="E.coli DH10B"
    /clone_lib="Rice callus plasmid cDNA library (NACL)"
    /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      1.0%; Score 10.4; DB 1; Length 12;
Best Local Similarity 91.7%; Pred. No. 1.6e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1767 TTTTATAAATT 1778
DB 12 TTTTATAAATT 1

RESULT 175
CF329947/c
LOCUS      12 bp      mRNA      linear      EST 18-AUG-2003
DEFINITION NACL--05-H12.g1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--05-H12, mRNA sequence.
ACCESSION  CF329947
VERSION     CF329947.1 GI:33808116
KEYWORDS   EST.
SOURCE     Oryza sativa
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 12)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             source
    source
    1..12
    /organism="Oryza sativa"
    /mol_type="mRNA"
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    /clone="NACL--05-H12"
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    /dev_stage="proliferated callus on 2N6 media for 30 days"
    /lab_host="E.coli DH10B"

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/clone lib="Rice callus plasmid cDNA library (NACL)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      1.0%; Score 10.4; DB 1; Length 12;
Best Local Similarity 91.7%; Pred. No. 1.6e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1767 TTTTAAATTT 1778
Db 12 TTTTAAATTT 1

RESULT 176
AI744941/c
LOCUS AI744941 13 bp mRNA linear EST 21-JUN-1999
DEFINITION tr17603.x1 NCI CGAP Ov23 Homo sapiens cDNA clone IMAGE:2218588 3',
similar to TR:Q33563 Q33563 BATRO 164 KINETOPLAST ;, mRNA sequence.
ACCESSION AI744941
VERSION AI744941.1 GI:5113229
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 13)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapdb@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Greg Lennon, Ph.D.
cDNA Library Arrayed by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Seq primer: -40Up from Gibco
High quality sequence stop: 1.
Location/Qualifiers
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1. .13
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/tissue_type="tumor, 5 pooled (see description)"
/lab_host="DH10B"
/clone_lib="NCI-CGAP_Ov23"
/notes="Organ: ovary; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.35 kb. Tumor types include: mixed
Mullerian tumor, papillary serous, clear cell, spindle
cell. All are primary tumors, metastasis positive. Life
Technologies catalog #: 11534-013"

Query Match      1.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 1.7e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1869 TATTTTGTGTTT 1880
Db 13 TATTTTGTGTTT 2

RESULT 177
CF299938/c
LOCUS CF299938 13 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--04-C12.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--04-C12, mRNA sequence.
ACCESSION CF299938
VERSION CF299938.1 GI:33671699
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnaahm@bio.com, bhnaahm@bio.myongji.ac.kr.
Location/Qualifiers
source
1. .13
/organism="Oryza sativa"
/mol_type="mRNA"
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/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      1.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 1.7e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2262 TGTATATTTT 2273
Db 13 TTTATATTTT 2

RESULT 178
CF300659/c
LOCUS CF300659 13 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--05-D14.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--05-D14, mRNA sequence.
ACCESSION CF300659
VERSION CF300659.1 GI:33672420
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnaahm@bio.com, bhnaahm@bio.myongji.ac.kr.
Location/Qualifiers
source
1. .13

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/organism="Oryza sativa"  
/mol_type="mRNA"  
/cultivar="Nackdong"  
/db_xref="taxon:4530"  
/clone="7LEAF-05-D14"  
/tissue_type="leaf"  
/dev_stage="7 days after germination"  
/lab_host="E.coli DH10B"  
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."
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Query Match      1.0%; Score 10.4; DB 1; Length 13;  
Best Local Similarity 91.7%; Pred.No. 1.7e+02;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 1768 TTTTAAATTT 1779  
    |||||  
Db 13 TTTTAAATTT 2
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Search completed: April 2, 2004, 14:41:27  
Job time : 4 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 2, 2004, 14:34:08 ; Search time 2 Seconds

(without alignments)

4.085 Million cell updates/sec

Title: us-10-006-191-19

Perfect score: 1049

Sequence: 1 ttgaactgattcacatctca.....gtgtatatattttctataaa 1049

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 0.5

Searched: 232 seqs, 3894 residues

Total number of hits satisfying chosen parameters: 464

Minimum DB seq length: 8

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 254 summaries

Database : rni.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	32	3.1	32	1	US-08-859-998-400
C 2	32	3.1	32	1	US-09-225-928-400
C 3	32	3.1	32	1	US-09-225-201B-400
C 4	25	2.4	25	1	US-09-292-036-9
C 5	23.4	2.2	25	1	US-09-292-036-10
C 6	23	2.2	24	1	US-08-849-021-87
C 7	22.2	2.1	27	1	US-08-222-177A-143
C 8	22	2.1	22	1	US-08-849-021-88
C 9	21.8	2.1	25	1	US-08-222-177A-146
C 10	21.8	2.1	27	1	US-08-455-627-23
C 11	21.8	2.1	27	1	US-08-689-856-23
C 12	21.8	2.1	27	1	US-08-787-321-23
C 13	21.4	2.0	23	1	US-08-222-177A-454
C 14	21.4	2.0	24	1	US-08-222-177A-445
C 15	21.2	2.0	26	1	PCT-US92-1072A-445
C 16	21	2.0	21	1	US-08-222-177A-160
C 17	21	2.0	22	1	US-08-222-177A-125
C 18	21	2.0	23	1	US-08-787-321-22
C 19	20	1.9	20	1	US-08-849-021-89
C 20	20	1.9	20	1	US-08-863-639A-32
C 21	20	1.9	20	1	US-09-407-675-5
C 22	20	1.9	20	1	US-09-488-671-88
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C 24	20	1.9	21	1	US-08-529-878B-9
C 25	19.4	1.8	21	1	US-08-136-118-10
C 26	19	1.8	19	1	US-08-222-177A-742
C 27	19	1.8	19	1	US-08-849-021-74
C 28	19	1.8	19	1	US-08-915-609-3
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C 31	19	1.8	21	1	US-09-314-246-2
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C 33	18	1.7	18	1	US-08-734-973-5

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1	US-08-976-427-28	18	1.7	36	Sequence 28, Appli
1	US-09-648-312-28	18	1.7	37	Sequence 28, Appli
1	US-09-488-671-120	20	1.7	38	Sequence 120, App
1	US-09-496-694B-235	20	1.7	39	Sequence 235, App
1	US-08-222-177A-448	17	1.6	40	Sequence 448, App
1	US-08-885-126-9	17	1.6	41	Sequence 9, Appli
1	US-08-960-111-11	17	1.6	42	Sequence 11, Appli
1	US-09-490-774-11	17	1.6	43	Sequence 11, Appli
1	US-09-958-221A-16	17	1.6	44	Sequence 16, Appli
1	US-08-734-973-1	18	1.6	45	Sequence 1, Appli
1	US-08-734-973-3	18	1.6	46	Sequence 3, Appli
1	US-08-734-973-28	18	1.6	47	Sequence 28, Appli
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1	US-08-734-973-31	18	1.6	49	Sequence 31, Appli
1	US-08-734-973-32	18	1.6	50	Sequence 32, Appli
1	US-09-475-947A-337	17	1.6	51	Sequence 337, App
1	US-08-849-021-87	24	1.6	52	Sequence 87, Appli
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1	US-08-734-973-8	18	1.6	54	Sequence 8, Appli
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1	US-08-734-973-33	18	1.6	56	Sequence 33, Appli
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1	US-08-734-973-37	18	1.6	58	Sequence 37, Appli
1	US-08-734-973-38	18	1.6	59	Sequence 38, Appli
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1	US-08-153-051B-58	16	1.4	87	Sequence 58, Appli
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1	US-08-151-477A-58	16	1.4	89	Sequence 80, Appli
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1	US-08-464-011B-57	16	1.4	91	Sequence 57, Appli
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1	US-08-709-209-235	17	1.4	95	Sequence 235, App
1	US-08-458-101-235	17	1.4	96	Sequence 235, App
1	US-08-435-628-1058	17	1.4	97	Sequence 1058, Ap
1	US-08-486-969-52	17	1.4	98	Sequence 52, Appli
1	US-08-584-040-4159	17	1.4	99	Sequence 4159, Ap
1	US-09-321-005A-13	17	1.4	100	Sequence 13, Appli
1	US-09-371-772B-1926	17	1.4	101	Sequence 1926, Ap
1	US-09-371-772B-6656	17	1.4	102	Sequence 6656, Ap
1	US-09-496-694B-235	20	1.4	103	Sequence 235, App
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1	US-09-913-514-27	14	1.3	106	Sequence 27, Appli

c 107	14	1.3	14	1	US-09-913-514-27	Sequence 27, Appl	180	1.2	16	1	US-09-507-345A-2	Sequence 2, Appl
c 108	14	1.3	15	1	PCT-US92-00282-27	Sequence 27, Appl	c 181	1.2	16	1	US-09-619-103-22	Sequence 22, Appl
c 109	14	1.3	15	1	PCT-US92-00282-27	Sequence 27, Appl	c 182	1.2	16	1	US-09-739-928-2	Sequence 2, Appl
c 110	14	1.3	16	1	US-09-479-005A-336	Sequence 336, Appl	c 183	1.2	16	1	US-09-371-772B-6072	Sequence 6072, Ap
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c 115	14	1.3	17	1	US-08-373-124A-1859	Sequence 1859, Ap	c 188	1.2	14	1	US-08-153-051B-57	Sequence 57, Appl
c 116	14	1.3	17	1	US-08-373-124A-1861	Sequence 1861, Ap	c 189	1.2	14	1	US-08-060-953C-56	Sequence 56, Appl
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c 118	14	1.3	17	1	US-08-435-628-1060	Sequence 1060, Ap	c 191	1.2	14	1	US-08-819-867-78	Sequence 78, Appl
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c 122	13.8	1.3	17	1	US-08-373-124A-874	Sequence 874, App	c 195	1.2	14	1	US-09-378-535-78	Sequence 78, Appl
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c 125	13.8	1.3	17	1	US-08-851-843A-132	Sequence 132, App	c 198	1.2	15	1	US-08-334-847-335	Sequence 335, App
c 126	13.8	1.3	17	1	US-09-071-845-1988	Sequence 1988, App	c 199	1.2	15	1	US-08-292-620A-331	Sequence 331, App
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c 128	13.8	1.3	17	1	US-08-854-075-5	Sequence 5, Appl	c 201	1.2	15	1	US-08-832-021-64	Sequence 64, Appl
c 129	13.8	1.3	17	1	US-09-430-323-132	Sequence 132, App	c 202	1.2	15	1	US-09-071-845-331	Sequence 331, App
c 130	13.8	1.3	17	1	US-08-584-040-2550	Sequence 2550, Ap	c 203	1.2	15	1	US-08-444-818-203	Sequence 203, App
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c 134	13.8	1.3	17	1	US-09-726-096A-5	Sequence 5, Appl	c 207	1.2	15	1	US-09-164-249B-2	Sequence 2, Appl
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c 138	13.8	1.3	17	1	US-09-827-998-384	Sequence 384, App	c 211	1.2	15	1	US-08-291-932A-309	Sequence 309, App
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c 140	13.8	1.3	17	1	US-09-827-998-386	Sequence 386, App	c 213	1.2	15	1	US-08-334-847-32	Sequence 32, Appl
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c 143	13.8	1.3	17	1	US-09-827-998-389	Sequence 389, App	c 216	1.2	15	1	US-08-849-021-88	Sequence 88, Appl
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c 149	13.4	1.3	15	1	US-09-475-947A-83	Sequence 83, Appl	c 222	1.2	13	1	US-08-938-534-2	Sequence 2, Appl
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c 154	13.4	1.3	17	1	US-08-435-628-1060	Sequence 1060, Ap	c 227	1.2	13	1	US-09-922-445-35	Sequence 35, Appl
c 155	13	1.2	13	1	US-08-849-021-13	Sequence 13, Appl	c 228	1.2	13	1	US-09-378-535-77	Sequence 77, Appl
c 156	13	1.2	13	1	US-09-479-005A-117	Sequence 117, App	c 229	1.2	13	1	US-09-377-497-56	Sequence 56, Appl
c 157	13	1.2	13	1	US-09-393-783A-41	Sequence 41, Appl	c 230	1.2	14	1	US-08-268-799-6	Sequence 6, Appl
c 158	13	1.2	13	1	US-09-151-890B-41	Sequence 41, Appl	c 231	1.2	14	1	US-08-465-500-28	Sequence 28, Appl
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c 160	13	1.2	15	1	US-08-291-932A-121	Sequence 121, App	c 233	1.2	14	1	US-08-672-564-11	Sequence 11, Appl
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c 162	13	1.2	15	1	US-08-291-932A-310	Sequence 310, App	c 235	1.2	14	1	US-08-346-126-28	Sequence 28, Appl
c 163	13	1.2	15	1	US-08-812-951B-2	Sequence 2, Appl	c 236	1.2	14	1	US-08-346-126-28	Sequence 28, Appl
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c 168	13	1.2	15	1	US-09-409-778-9	Sequence 9, Appl	c 241	1.2	14	1	US-08-682-847-8	Sequence 8, Appl
c 169	13	1.2	16	1	US-07-971-978-36	Sequence 36, Appl	c 242	1.2	14	1	US-08-832-021-5	Sequence 5, Appl
c 170	12.8	1.2	16	1	US-07-971-978-42	Sequence 42, Appl	c 243	1.2	14	1	US-08-832-021-5	Sequence 5, Appl
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c 175	12.8	1.2	16	1	US-09-141-764-2	Sequence 2, Appl	c 248	1.2	14	1	US-08-893-614-1	Sequence 1, Appl
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c 177	12.8	1.2	16	1	US-08-851-843A-131	Sequence 131, App	c 250	1.2	14	1	US-08-893-614-1	Sequence 1, Appl
c 178	12.8	1.2	16	1	US-08-854-050-131	Sequence 131, App	c 251	1.2	14	1	US-08-893-614-1	Sequence 1, Appl
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; APPLICATION NUMBER: US/09/225,201B
; FILING DATE: 05-Jan-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/859,998
; FILING DATE: 21-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Field, Bret E.
; REGISTRATION NUMBER: 37,620
; REFERENCE/DOCKET NUMBER: 09096/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-322-5070
; TELEFAX: 415-854-0875
; INFORMATION FOR SEQ ID NO: 400:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; OTHER INFORMATION: oligonucleotide primer
; SEQUENCE DESCRIPTION: SEQ ID NO: 400:
US-09-225-201B-400

Query Match          3.1%; Score 32; DB 1; Length 32;
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Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 32 CTTGTGGCAAGTGAATTCCTGTACACAGCC 1

RESULT 4
US-09-292-036-9/c
; Sequence 9, Application US/09292036
; Patent No. 6358741
; GENERAL INFORMATION:
; APPLICANT: FIBROGEN, INC
; APPLICANT: SCHMIDT, Brian
; APPLICANT: ALLEN, Margaret
; APPLICANT: SVERDRUP, Fran
; APPLICANT: CARMICHAEL, David
; TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR (CTGF) AND METHODS OF USE
; FILE REFERENCE: FIB01100-1
; CURRENT APPLICATION NUMBER: US/09/292,036
; CURRENT FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: US 09/292,036
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: US 09/187,478
; PRIOR FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 9
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Antisense CTGF oligonucleotide
US-09-292-036-9

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Best Local Similarity 100.0%; Pred. No. 9;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1718 ATTAGACTGCACAGCTTGCGCAAG 1742
Db 25 ATTAGACTGCACAGCTTGCGCAAG 1

RESULT 5
US-09-292-036-10/c
; Sequence 10, Application US/09292036
; Patent No. 6358741
; GENERAL INFORMATION:
; APPLICANT: FIBROGEN, INC
; APPLICANT: SCHMIDT, Brian
; APPLICANT: ALLEN, Margaret
; APPLICANT: SVERDRUP, Fran
; APPLICANT: CARMICHAEL, David
; TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR (CTGF) AND METHODS OF USE
; FILE REFERENCE: FIB01100-1
; CURRENT APPLICATION NUMBER: US/09/292,036
; CURRENT FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: US 09/292,036
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: US 09/187,478
; PRIOR FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 10
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Antisense CTGF oligonucleotide
US-09-292-036-10

Query Match          2.2%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 14;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 25 GTGAATTCCTGTACACAGCCAGA 1

RESULT 6
US-08-849-021-87/c
; Sequence 87, Application US/08849021
; Patent No. 5955276
; GENERAL INFORMATION:
; APPLICANT: MORGANTE, MICHELE
; APPLICANT: VOGEL, JULIE M.
; TITLE OF INVENTION: COMPOUND MICROSATELLITE
; TITLE OF INVENTION: PRIMERS FOR THE
; TITLE OF INVENTION: DETECTION OF GENETIC
; TITLE OF INVENTION: POLYMORPHISMS
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: U.S.A.
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PATENT IN RELEASE #1.0, VERSION 1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/849,021
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/346,456
; FILING DATE: 28 NOVEMBER 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: FLOYD, LINDA AXAMETHY
; REGISTRATION NUMBER: 33,692
; REFERENCE/DOCKET NUMBER: BB-1064-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-892-8112
```

```
TELEFAX: 302-992-7949
; INFORMATION FOR SEQ ID NO: 87:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-849-021-87

Query Match 2.2%; Score 23; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1805 TGTGTGTGTATATATATATAT 1827
Db 24 TGTGTGTGTATATATATATAT 2

RESULT 7
US-08-222-177A-143/C
; Sequence 143, Application US/08222177A
; Patent No. 5582979
; GENERAL INFORMATION:
; APPLICANT: Weber, James L.
; TITLE OF INVENTION: LENGTH POLYMORPHISMS IN
; TITLE OF INVENTION: (dc-da)n.(dg-dt)n SEQUENCES AND METHODS OF USING SAME
; NUMBER OF SEQUENCES: 460
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dewitt Ross & Stevens, S.C.
; STREET: 8000 Excelsior Drive, Suite 401
; CITY: Madison
; STATE: Wisconsin
; COUNTRY: U.S.A.
; ZIP: 53717-1914
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/222,177A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/341,562
; FILING DATE: 21-APR-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Sara, Charles S.
; REGISTRATION NUMBER: 30,492
; REFERENCE/DOCKET NUMBER: 09865.601
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 831-2100
; TELEFAX: (608) 831-2106
; TELEX:
; INFORMATION FOR SEQ ID NO: 143:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; IMMEDIATE SOURCE:
; CLONE: mfd312s
US-08-222-177A-143

Query Match 2.1%; Score 22.2; DB 1; Length 27;
Best Local Similarity 88.9%; Pred. No. 22;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTATATAT 1819
Db 27 TGTGTGTGTGTGTGTGTGTGTGTGT 1
```

```
RESULT 8
US-08-849-021-88/C
; Sequence 88, Application US/08849021
; Patent No. 5953276
; GENERAL INFORMATION:
; APPLICANT: MORGANTE, MICHELE
; APPLICANT: VOGEL, JULIE M.
; TITLE OF INVENTION: COMPOUND MICROSATELLITE
; TITLE OF INVENTION: PRIMERS FOR THE
; TITLE OF INVENTION: DETECTION OF GENETIC
; TITLE OF INVENTION: POLYMORPHISMS
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND
; COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: U.S.A.
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PATENT IN RELEASE #1.0, VERSION 1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/849,021
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/346,456
; FILING DATE: 28 NOVEMBER 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: FLOYD, LINDA AXAMETHY
; REGISTRATION NUMBER: 33,692
; REFERENCE/DOCKET NUMBER: BB-1064-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-892-8112
; TELEFAX: 302-992-7949
; INFORMATION FOR SEQ ID NO: 88:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-849-021-88

Query Match 2.1%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1801 TGTGTGTGTGTATATATATAT 1822
Db 22 TGTGTGTGTGTATATATATAT 1

RESULT 9
US-08-222-177A-146/C
; Sequence 146, Application US/08222177A
; Patent No. 5582979
; GENERAL INFORMATION:
; APPLICANT: Weber, James L.
; TITLE OF INVENTION: LENGTH POLYMORPHISMS IN
; TITLE OF INVENTION: (dc-da)n.(dg-dt)n SEQUENCES AND METHODS OF USING SAME
; NUMBER OF SEQUENCES: 460
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dewitt Ross & Stevens, S.C.
; STREET: 8000 Excelsior Drive, Suite 401
; CITY: Madison
; STATE: Wisconsin
```

```

; COUNTRY: USA
; ZIP: 53717-1914
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/222,177A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/341,562
; FILING DATE: 21-APR-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Sara, Charles S.
; REGISTRATION NUMBER: 30,492
; REFERENCE/DOCKET NUMBER: 09865.601
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 831-2100
; TELEFAX: (608) 831-2106
; TELEX:
; INFORMATION FOR SEQ ID NO: 146:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; IMMEDIATE SOURCE:
; CLONE: mfd32rs
;
US-08-222-177A-146
Query Match 2.1%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 22;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTAT 1817
Db 25 TGTGTGTGTGTGTGTGTGTGT 1

RESULT 10
US-08-455-627-23/c
; Sequence 23, Application US/08455627
; Patent No. 5571677
; GENERAL INFORMATION:
; APPLICANT: Sergei M. Gryaznov
; TITLE OF INVENTION: Convergent Synthesis of Branched and Multiply
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward LLP
; STREET: Five Palo Alto Square, 3000 El Camino Real
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,627
; FILING DATE: 31-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,627
; FILING DATE: 31-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Nakamura, Jackie N.
; REGISTRATION NUMBER: 35,966
; REFERENCE/DOCKET NUMBER: LYNX-003/01 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5000
; TELEFAX: 415-857-0663
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
;
US-08-455-627-23
Query Match 2.1%; Score 21.8; DB 1; Length 27;
Best Local Similarity 92.0%; Pred. No. 25;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTAT 1817
Db 26 TGTGTGTGTGTGTGTGTGTGT 2

RESULT 12
US-08-455-627-23/c
; Sequence 23, Application US/08689856
; Patent No. 5830658
; GENERAL INFORMATION:
; APPLICANT: Sergei M. Gryaznov
; TITLE OF INVENTION: Convergent Synthesis of Branched and Multiply
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward LLP
; STREET: Five Palo Alto Square, 3000 El Camino Real
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/689,856
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,627
; FILING DATE: 31-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Nakamura, Jackie N.
; REGISTRATION NUMBER: 35,966
; REFERENCE/DOCKET NUMBER: LYNX-003/01 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5000
; TELEFAX: 415-857-0663
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
;
US-08-689-856-23
Query Match 2.1%; Score 21.8; DB 1; Length 27;
Best Local Similarity 92.0%; Pred. No. 25;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTAT 1817
Db 26 TGTGTGTGTGTGTGTGTGTGT 2

RESULT 11
US-08-689-856-23/c
; Sequence 23, Application US/08689856
; Patent No. 5830658
; GENERAL INFORMATION:
; APPLICANT: Sergei M. Gryaznov
; TITLE OF INVENTION: Convergent Synthesis of Branched and Multiply
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward LLP
; STREET: Five Palo Alto Square, 3000 El Camino Real
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/689,856
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,627
; FILING DATE: 31-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Nakamura, Jackie N.
; REGISTRATION NUMBER: 35,966
; REFERENCE/DOCKET NUMBER: LYNX-003/01 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5000
; TELEFAX: 415-857-0663
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
;
US-08-689-856-23
Query Match 2.1%; Score 21.8; DB 1; Length 27;
Best Local Similarity 92.0%; Pred. No. 25;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTAT 1817
Db 26 TGTGTGTGTGTGTGTGTGTGT 2
```

```

; TELEFAX: 415-857-0663
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
;
US-08-455-627-23
Query Match 2.1%; Score 21.8; DB 1; Length 27;
Best Local Similarity 92.0%; Pred. No. 25;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTAT 1817
Db 26 TGTGTGTGTGTGTGTGTGTGT 2

RESULT 11
US-08-689-856-23/c
; Sequence 23, Application US/08689856
; Patent No. 5830658
; GENERAL INFORMATION:
; APPLICANT: Sergei M. Gryaznov
; TITLE OF INVENTION: Convergent Synthesis of Branched and Multiply
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward LLP
; STREET: Five Palo Alto Square, 3000 El Camino Real
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/689,856
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,627
; FILING DATE: 31-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Nakamura, Jackie N.
; REGISTRATION NUMBER: 35,966
; REFERENCE/DOCKET NUMBER: LYNX-003/01 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5000
; TELEFAX: 415-857-0663
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
;
US-08-689-856-23
Query Match 2.1%; Score 21.8; DB 1; Length 27;
Best Local Similarity 92.0%; Pred. No. 25;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTAT 1817
Db 26 TGTGTGTGTGTGTGTGTGTGT 2

RESULT 12
US-08-689-856-23/c
; Sequence 23, Application US/08689856
; Patent No. 5830658
; GENERAL INFORMATION:
; APPLICANT: Sergei M. Gryaznov
; TITLE OF INVENTION: Convergent Synthesis of Branched and Multiply
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward LLP
; STREET: Five Palo Alto Square, 3000 El Camino Real
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/689,856
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,627
; FILING DATE: 31-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Nakamura, Jackie N.
; REGISTRATION NUMBER: 35,966
; REFERENCE/DOCKET NUMBER: LYNX-003/01 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5000
; TELEFAX: 415-857-0663
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
;
US-08-689-856-23
Query Match 2.1%; Score 21.8; DB 1; Length 27;
Best Local Similarity 92.0%; Pred. No. 25;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTAT 1817
Db 26 TGTGTGTGTGTGTGTGTGTGT 2
```

```
US-08-787-321-23/c
; Sequence 23, Application US/08787321A
; Patent No. 6180777
; GENERAL INFORMATION:
; APPLICANT: Horn, Thomas
; TITLE OF INVENTION: SYNTHESIS OF BRANCHED NUCLEIC ACIDS
; FILE REFERENCE: (1300)-1199.002
; CURRENT APPLICATION NUMBER: US/08/787,321A
; CURRENT FILING DATE: 1997-01-03
; EARLIER APPLICATION NUMBER: US PROV 60/009,918
; EARLIER FILING DATE: 1996-01-12
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: oligonucleotide
US-08-787-321-23

Query Match      2.1%; Score 21.8; DB 1; Length 27;
Best Local Similarity 92.0%; Pred. No. 25;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTAT 1817
      |||||
Db 26 TGTGTGTGTGTGTGTGTGTGT 2

RESULT 13
US-08-222-177A-454/c
; Sequence 454, Application US/08222177A
; Patent No. 5582979
; GENERAL INFORMATION:
; APPLICANT: Weber, James L.
; TITLE OF INVENTION: LENGTH POLYMORPHISMS IN
; TITLE OF INVENTION: (dC-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING SAME
; NUMBER OF SEQUENCES: 460
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dewitt Ross & Stevens, S.C.
; STREET: 8000 Excelsior Drive, Suite 401
; CITY: Madison
; STATE: Wisconsin
; COUNTRY: USA
; ZIP: 53717-1914
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/222,177A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/341,562
; FILING DATE: 21-APR-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Sara, Charles S.
; REGISTRATION NUMBER: 30,492
; REFERENCE/DOCKET NUMBER: 09865.601
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 831-2100
; TELEFAX: (608) 831-2106
; TELEX:
; INFORMATION FOR SEQ ID NO: 454:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-222-177A-445

Query Match      2.0%; Score 21.4; DB 1; Length 24;
Best Local Similarity 95.7%; Pred. No. 23;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTAT 1815
      |||||
Db 24 TGTGTGTGTGTGTGTGTGT 2

RESULT 14
US-08-222-177A-445/c
; Sequence 445, Application US/08222177A
; Patent No. 5582979
; GENERAL INFORMATION:
; APPLICANT: Weber, James L.
; TITLE OF INVENTION: LENGTH POLYMORPHISMS IN
; TITLE OF INVENTION: (dC-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING SAME
; NUMBER OF SEQUENCES: 460
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dewitt Ross & Stevens, S.C.
; STREET: 8000 Excelsior Drive, Suite 401
; CITY: Madison
; STATE: Wisconsin
; COUNTRY: USA
; ZIP: 53717-1914
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/222,177A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/341,562
; FILING DATE: 21-APR-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Sara, Charles S.
; REGISTRATION NUMBER: 30,492
; REFERENCE/DOCKET NUMBER: 09865.601
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 831-2100
; TELEFAX: (608) 831-2106
; TELEX:
; INFORMATION FOR SEQ ID NO: 445:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-222-177A-454

Query Match      2.0%; Score 21.4; DB 1; Length 24;
Best Local Similarity 95.7%; Pred. No. 23;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTAT 1815
      |||||
Db 24 TGTGTGTGTGTGTGTGTGT 2

RESULT 15
PCT-US92-10792-44
; Sequence 44, Application PC/TUS9210792
; GENERAL INFORMATION:
; APPLICANT: Jayasena, Sumedha D.
; APPLICANT: Johnston, Brian H.
; TITLE OF INVENTION: Triple Helix Formation at
```



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; LENGTH: 22 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; IMMEDIATE SOURCE:
; CLONE: mfg251s
US-08-222-177A-125

Query Match          2.0%; Score 21; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTGT 1813
DB 21 TGTGTGTGTGTGTGTGTGTGT 1

RESULT 18
US-08-787-321-22/c
; Sequence 22, Application US/08787321A
; Patent No. 6180777
; GENERAL INFORMATION:
; APPLICANT: Horn, Thomas
; TITLE OF INVENTION: SYNTHESIS OF BRANCHED NUCLEIC ACIDS
; FILE REFERENCE: (1300)-1199.002
; CURRENT APPLICATION NUMBER: US/08/787,321A
; CURRENT FILING DATE: 1997-01-03
; EARLIER APPLICATION NUMBER: US PROV 60/009,918
; EARLIER FILING DATE: 1996-01-12
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 22
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: oligonucleotide
US-08-787-321-22

Query Match          2.0%; Score 21; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTGT 1813
DB 22 TGTGTGTGTGTGTGTGTGTGT 2

RESULT 19
US-08-849-021-89/c
; Sequence 89, Application US/08849021
; Patent No. 595276
; GENERAL INFORMATION:
; APPLICANT: MORGANTE, MICHELE
; APPLICANT: VOGEL, JULIE M.
; TITLE OF INVENTION: COMPOUND MICROSATELLITE
; TITLE OF INVENTION: PRIMERS FOR THE
; TITLE OF INVENTION: DETECTION OF GENETIC
; TITLE OF INVENTION: POLYMORPHISMS
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND
; ADDRESSEE: COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: U.S.A.
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PATENT IN RELEASE #1.0, VERSION 1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/849,021
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/346,456
; FILING DATE: 28 NOVEMBER 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: FLOYD, LINDA AXAMETHY
; REGISTRATION NUMBER: 33,692
; REFERENCE/DOCKET NUMBER: BB-1064-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-892-8112
; TELEFAX: 302-992-7949
; INFORMATION FOR SEQ ID NO: 89:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-849-021-89

Query Match          1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1799 TGTGTGTGTGTGTGTATATA 1818
DB 20 TGTGTGTGTGTGTGTATATA 1

RESULT 20
US-08-863-639A-32/c
; Sequence 32, Application US/08863639A
; Patent No. 5981185
; GENERAL INFORMATION:
; APPLICANT: Matson, Robert S.
; APPLICANT: Coassin, Peter J.
; APPLICANT: Rampal, Jang B.
; APPLICANT: Caskey, C. T.
; TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheldon & Mak
; STREET: 225 South Lake Avenue, 9th Floor
; CITY: Pasadena
; STATE: CA
; COUNTRY: USA
; ZIP: 91101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Corel Wordperfect 8 version
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/863,639A
; FILING DATE: May 28, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph E. Mueth
; REGISTRATION NUMBER: 20,532
; REFERENCE/DOCKET NUMBER: 11859-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (626) 796-4000
; TELEFAX: (626) 795-6321
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
```

```

; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
US-08-863-639A-32

Query Match 1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTGT 1813
DB 20 GTGTGTGTGTGTGTGTGT 1

RESULT 21
US-09-407-675-5/C
; Sequence 5, Application US/09407675
; Patent No. 6169176
; GENERAL INFORMATION:
; APPLICANT: Bruice, Thomas C.
; TITLE OF INVENTION: DEOXYNUCLEIC ALKYL THIUREA COMPOUNDS AND USES THEREOF
; FILE REFERENCE: 30448.65US02
; CURRENT APPLICATION NUMBER: US/09/407,675
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: 09/347,443
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091,481
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/111,800
; PRIOR FILING DATE: 1998-12-11
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 5
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Oligo 5
US-09-407-675-5

Query Match 1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGT 1812
DB 20 TGTGTGTGTGTGTGTGTGT 1

RESULT 22
US-09-488-671-88/C
; Sequence 88, Application US/09488671A
; Patent No. 6187545
; GENERAL INFORMATION:
; APPLICANT: Robert McKay
; APPLICANT: Madeline M. Butler
; APPLICANT: Jacqueline Wyatt
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF PEPCK-CYTOSOLIC EXPRESSION
; FILE REFERENCE: RT8-0123
; CURRENT APPLICATION NUMBER: US/09/488,671A
; CURRENT FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 177
; SEQ ID NO 88
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-488-671-88

Query Match 1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;

US-09-180-903-8
; Sequence 8, Application US/09180903
; Patent No. 6316190
; GENERAL INFORMATION:
; APPLICANT: Rein, Alan
; APPLICANT: Casas-Finet, Jose
; APPLICANT: Fisher, Robert
; APPLICANT: Fivash, Matthew
; APPLICANT: Henderson, Louis E.
; TITLE OF INVENTION: Oligonucleotides Which Specifically Bind
; RETROVIRAL NUCLEOCAPSID PROTEINS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/180,903
; FILING DATE: 12-JUL-1999
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/017,128
; FILING DATE: 20-MAY-1996
; APPLICATION NUMBER: WO PCT/US97/08936
; FILING DATE: 19-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Choi, Kathleen L.
; REGISTRATION NUMBER: 43,433
; REFERENCE/DOCKET NUMBER: 015280-279100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-180-903-8

Query Match 1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGT 1812
DB 1 TGTGTGTGTGTGTGTGTGT 20

RESULT 24
US-08-529-878B-9
; Sequence 9, Application US/08529878B
; Patent No. 5932556
; GENERAL INFORMATION:
; APPLICANT: Tam, Robert C.

```



;; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR  
;; TITLE OF INVENTION: REGULATION OF CD28 EXPRESSION  
;; NUMBER OF SEQUENCES: 48  
;; CORRESPONDENCE ADDRESSES:  
;; ADDRESSEE: Crockett & Fish  
;; STREET: 3000 S. Augusta Court  
;; CITY: La Habra  
;; STATE: California  
;; COUNTRY: United States of America  
;; ZIP: 90631  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: WordPerfect 6.1  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/529,878B  
;; FILING DATE: 13-SEP-1995  
;; CLASSIFICATION: 424  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Fish, Robert D.  
;; REGISTRATION NUMBER: 33,880  
;; REFERENCE/DOCKET NUMBER: 213/003  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 714-525-3433  
;; TELEFAX: 714-525-3303  
;; TELEX:  
;; INFORMATION FOR SEQ ID NO: 9:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 21 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: unknown  
;; TOPOLOGY: unknown  
;; MOLECULE TYPE: DNA (genomic)  
US-08-529-878B-9  
Query Match 1.9%; Score 20; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1794 GTGTGTGTGTGTGTGTGTGT 1813  
DB 1 GTGTGTGTGTGTGTGTGTGT 20  
RESULT 25  
US-08-136-118-10/c  
; Sequence 10, Application US/08136118  
; Patent No. 5580969  
; GENERAL INFORMATION:  
; APPLICANT: HOKE, Glenn D  
; APPLICANT: BRADLEY, Matthews O  
; APPLICANT: WILLIAMS, Taify J  
; APPLICANT: LEE, Che-Hung  
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES DIRECTED  
; TITLE OF INVENTION: AGAINST HUMAN ICAM-1  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Naval Medical Res. & Dev. Cmd.  
; STREET: 8901 Wisconsin Ave.  
; CITY: Bethesda  
; STATE: Maryland  
; COUNTRY: USA  
; ZIP: 20889-5606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/136,118  
; FILING DATE:  
; CLASSIFICATION: 514

;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/918,259  
;; FILING DATE: 24-JUL-1992  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Spavack, A. David  
;; REGISTRATION NUMBER: 24,743  
;; REFERENCE/DOCKET NUMBER: N.C. 75,776  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (202) 295-6759  
;; TELEFAX: (202) 295-1022  
;; INFORMATION FOR SEQ ID NO: 10:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 21 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; HYPOTHETICAL: NO  
;; ANTI-SENSE: YES  
US-08-136-118-10  
Query Match 1.8%; Score 19.4; DB 1; Length 21;  
Best Local Similarity 95.2%; Pred. No. 33;  
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1793 TGTGTGTGTGTGTGTGTGTGT 1813  
DB 21 TGTGTGTGTGTGTGTGTGTGT 1  
RESULT 26  
US-08-222-177A-442/c  
; Sequence 442, Application US/08222177A  
; Patent No. 5582979  
; GENERAL INFORMATION:  
; APPLICANT: Weber, James L.  
; TITLE OF INVENTION: LENGTH POLYMORPHISMS IN  
; TITLE OF INVENTION: (dc-ca)n.(gg-ct)n SEQUENCES AND METHODS OF USING SAME  
; NUMBER OF SEQUENCES: 460  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dewitt Ross & Stevens, S.C.  
; STREET: 8000 Excelsior Drive, Suite 401  
; CITY: Madison  
; STATE: Wisconsin  
; COUNTRY: USA  
; ZIP: 53717-1914  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/222,177A  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/341,562  
; FILING DATE: 21-APR-1989  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sara, Charles S.  
; REGISTRATION NUMBER: 30,492  
; REFERENCE/DOCKET NUMBER: 09865.601  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (608) 831-2100  
; TELEFAX: (608) 831-2106  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 442:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 19 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-222-177A-442

Query Match 1.8%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 32;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGT 1811  
|||||  
Db 19 TGTGTGTGTGTGTGTGT 1

## RESULT 27

US-08-849-021-74  
; Sequence 74, Application US/08849021  
; Patent No. 5955276  
; GENERAL INFORMATION:  
; APPLICANT: MORGANTE, MICHELE  
; APPLICANT: VOGEL, JULIE M.  
; TITLE OF INVENTION: COMPOUND MICROSATELLITE  
; TITLE OF INVENTION: PRIMERS FOR THE  
; TITLE OF INVENTION: DETECTION OF GENETIC  
; TITLE OF INVENTION: POLYMORPHISMS  
; NUMBER OF SEQUENCES: 89  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND  
; ADDRESSEE: COMPANY  
; STREET: 1007 MARKET STREET  
; CITY: WILMINGTON  
; STATE: DELAWARE  
; COUNTRY: U.S.A.  
; ZIP: 19898  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: FLOPPY DISK  
; COMPUTER: IBM PC COMPATIBLE  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PATENT IN RELEASE #1.0, VERSION 1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/849,021  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/346,456  
; FILING DATE: 28 NOVEMBER 1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: FLOYD, LINDA AXWETHY  
; REGISTRATION NUMBER: 33,692  
; REFERENCE/DOCKET NUMBER: BB-1064-A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 302-892-8112  
; TELEFAX: 302-992-7949  
; INFORMATION FOR SEQ ID NO: 74:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 19 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)

US-08-849-021-74  
Query Match 1.8%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 32;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1799 TGTGTGTGTGTGTATAT 1817  
|||||  
Db 1 TGTGTGTGTGTGTATAT 19

## RESULT 28

US-08-915-609-3/c  
; Sequence 3, Application US/08915609  
; Patent No. 6054300  
; GENERAL INFORMATION:  
; APPLICANT: McKendree Jr., William L.

; TITLE OF INVENTION: Single-Site Amplification (SSA) Method for Accelerated  
; FILE REFERENCE: 0115.97  
; CURRENT APPLICATION NUMBER: US/08/915,609  
; CURRENT FILING DATE: 1997-08-21  
; EARLIER APPLICATION NUMBER: 60/028,775  
; EARLIER FILING DATE: 1996-08-23  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: Patentin Ver. 2.0 - beta  
; SEQ ID NO 3  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: primer  
; FEATURE:  
; NAME/KEY: primer\_bind  
; LOCATION: (1)..(19)  
; FEATURE:  
; NAME/KEY: primer\_bind  
; LOCATION: (1)..(19)  
; US-08-915-609-3

Query Match 1.8%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 32;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTG 1812  
|||||  
Db 19 GTGTGTGTGTGTGTGTG 1

## RESULT 29

US-08-915-609-4  
; Sequence 4, Application US/08915609  
; Patent No. 6054300  
; GENERAL INFORMATION:  
; APPLICANT: McKendree Jr., William L.  
; TITLE OF INVENTION: Single-Site Amplification (SSA) Method for Accelerated  
; FILE REFERENCE: 0115.97  
; CURRENT APPLICATION NUMBER: US/08/915,609  
; CURRENT FILING DATE: 1997-08-21  
; EARLIER APPLICATION NUMBER: 60/028,775  
; EARLIER FILING DATE: 1996-08-23  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: Patentin Ver. 2.0 - beta  
; SEQ ID NO 4  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: primer  
; FEATURE:  
; NAME/KEY: primer\_bind  
; LOCATION: (1)..(19)  
; FEATURE:  
; NAME/KEY: primer\_bind  
; LOCATION: (1)..(19)  
; US-08-915-609-4

Query Match 1.8%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 32;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTG 1812  
|||||  
Db 1 GTGTGTGTGTGTGTGTG 19

## RESULT 30

US-09-314-246-1  
; Sequence 1, Application US/09314246

Patent No. 6180349  
GENERAL INFORMATION:  
APPLICANT: Ginzinger, David G.  
APPLICANT: Godfrey, Tony E.  
APPLICANT: Jensen, Ronald H.  
APPLICANT: Gray, Joe W.  
APPLICANT: The Regents of the University of California  
TITLE OF INVENTION: A Quantitative PCR Method to Enumerate DNA Copy Number  
FILE REFERENCE: 2307AA-096200US  
CURRENT APPLICATION NUMBER: US/09/314,246  
CURRENT FILING DATE: 1999-05-18  
NUMBER OF SEQ ID NOS: 2  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 1  
LENGTH: 21  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: TM-TaqMan  
OTHER INFORMATION: dual-labeled fluorogenic oligonucleotide probe  
OTHER INFORMATION: complementary to amplification products of  
OTHER INFORMATION: CA-repeat  
NAME/KEY: modified\_base  
LOCATION: (1)  
OTHER INFORMATION: 5'-t attached to 6-carboxy fluorescein (FAM)  
NAME/KEY: modified\_base  
LOCATION: (21)  
OTHER INFORMATION: 3'-t attached to 6-carboxy tetramethyl rhodamine  
OTHER INFORMATION: (TAMRA)  
US-09-314-246-1

Query Match 1.8%; Score 19; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTG 1812  
Db 2 GTGTGTGTGTGTGTGTG 20

RESULT 31  
US-09-314-246-2  
Sequence 2, Application US/09314246  
Patent No. 6180349  
GENERAL INFORMATION:  
APPLICANT: Ginzinger, David G.  
APPLICANT: Godfrey, Tony E.  
APPLICANT: Jensen, Ronald H.  
APPLICANT: Gray, Joe W.  
APPLICANT: The Regents of the University of California  
TITLE OF INVENTION: A Quantitative PCR Method to Enumerate DNA Copy Number  
FILE REFERENCE: 2307AA-096200US  
CURRENT APPLICATION NUMBER: US/09/314,246  
CURRENT FILING DATE: 1999-05-18  
NUMBER OF SEQ ID NOS: 2  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 21  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: TM-TaqMan  
OTHER INFORMATION: dual-labeled fluorogenic oligonucleotide probe  
OTHER INFORMATION: complementary to amplification products of  
OTHER INFORMATION: CA-repeat  
NAME/KEY: modified\_base  
LOCATION: (1)  
OTHER INFORMATION: 5'-t attached to reporter dye  
NAME/KEY: modified\_base  
LOCATION: (21)  
OTHER INFORMATION: 3'-t attached to quenching dye  
US-09-314-246-2

Query Match 1.8%; Score 19; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1794 GTGTGTGTGTGTGTGTG 1812  
Db 2 GTGTGTGTGTGTGTGTG 20

RESULT 32  
US-08-734-973-4/c  
Sequence 4, Application US/08734973  
Patent No. 5912147  
GENERAL INFORMATION:  
APPLICANT: Stoler, Daniel L.  
APPLICANT: Basik, Mark  
APPLICANT: Anderson, Garth R.  
TITLE OF INVENTION: A Rapid Means For Quantitating  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear  
STREET: 1800 One Mt Plaza  
CITY: Buffalo  
STATE: New York  
COUNTRY: United States  
ZIP: 14203-2391  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS/ Microsoft Windows  
SOFTWARE: Wordperfect for Windows  
CURRENT APPLICATION DATA: US/08/734,973  
APPLICATION NUMBER: US/08/734,973  
FILING DATE: October 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Nelson, M. Bud  
REGISTRATION NUMBER: 35,300  
REFERENCE/DOCKET NUMBER: 03551.0021  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (716) 856-4000  
TELEFAX: (716) 849-0349  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single-stranded  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
HYPOTHETICAL: No  
US-08-734-973-4  
Query Match 1.7%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 39;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1791 ATTGTGTGTGTGTGTG 1808  
Db 18 ATTGTGTGTGTGTGTG 1  
RESULT 33  
US-08-734-973-5/c  
Sequence 5, Application US/08734973  
Patent No. 5912147  
GENERAL INFORMATION:  
APPLICANT: Stoler, Daniel L.  
APPLICANT: Basik, Mark  
APPLICANT: Anderson, Garth R.  
TITLE OF INVENTION: A Rapid Means For Quantitating  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear  
STREET: 1800 One M&T Plaza  
CITY: Buffalo  
STATE: New York  
COUNTRY: United States  
ZIP: 14203-2391  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS/ Microsoft Windows  
SOFTWARE: Wordperfect for Windows  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/734,973  
FILING DATE: October 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Nelson, M. Bud  
REGISTRATION NUMBER: 35,300  
REFERENCE/DOCKET NUMBER: 03551.0021  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (716) 856-4000  
TELEFAX: (716) 849-0349  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single-stranded  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
HYPOTHETICAL: NO  
US-08-734-973-5

Query Match 1.7%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 39;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1791 ATTGTGTGTGTGTGTGTGT 1808  
Db 18 ATTGTGTGTGTGTGTGTGT 1

RESULT 34  
US-08-700-530-1/c  
; Sequence 1, Application US/08700530  
; Patent No. 6316186  
; GENERAL INFORMATION:  
; APPLICANT: EKINS, Roger P  
; TITLE OF INVENTION: Binding assay using binding agents with tail groups  
; FILE REFERENCE: 0380-P01180US0  
; CURRENT APPLICATION NUMBER: US/08/700,530  
; CURRENT FILING DATE: 1996-10-23  
; PRIOR APPLICATION NUMBER: PCT/GB95/00521  
; PRIOR FILING DATE: 1995-03-10  
; PRIOR APPLICATION NUMBER: GB 9404709.9  
; PRIOR FILING DATE: 1994-03-11  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:  
; OTHER INFORMATION: Oligonucleotide  
US-08-700-530-1

Query Match 1.7%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 39;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTGTGTGTGT 1810  
Db 18 TGTGTGTGTGTGTGTGTGT 1

RESULT 35  
US-08-700-530-2  
; Sequence 2, Application US/08700530  
; Patent No. 6316186  
; GENERAL INFORMATION:  
; APPLICANT: EKINS, Roger P  
; TITLE OF INVENTION: Binding assay using binding agents with tail groups  
; FILE REFERENCE: 0380-P01180US0  
; CURRENT APPLICATION NUMBER: US/08/700,530  
; CURRENT FILING DATE: 1996-10-23  
; PRIOR APPLICATION NUMBER: PCT/GB95/00521  
; PRIOR FILING DATE: 1995-03-10  
; PRIOR APPLICATION NUMBER: GB 9404709.9  
; PRIOR FILING DATE: 1994-03-11  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:  
; OTHER INFORMATION: Oligonucleotide  
US-08-700-530-2

Query Match 1.7%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 39;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1794 GTGTGTGTGTGTGTGTGT 1811  
Db 1 GTGTGTGTGTGTGTGTGT 18

RESULT 36  
US-08-976-427-28  
; Sequence 28, Application US/08976427A  
; Patent No. 6322968  
; GENERAL INFORMATION:  
; APPLICANT: Head, Steven R.  
; APPLICANT: Geolet, Philip  
; APPLICANT: Karn, Jonathan  
; APPLICANT: Boyce-Jacino, Michael  
; TITLE OF INVENTION: De No. 5322968 or "Universal" Sequencing Array  
; FILE REFERENCE: 04990.0049  
; CURRENT APPLICATION NUMBER: US/08/976,427A  
; CURRENT FILING DATE: 1997-11-21  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 28  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic primer  
US-08-976-427-28

Query Match 1.7%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 39;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTGTGTGTGT 1810  
Db 1 TGTGTGTGTGTGTGTGTGT 18

RESULT 37  
US-09-648-312-28  
; Sequence 28, Application US/09648312  
; Patent No. 6337188  
; GENERAL INFORMATION:  
; APPLICANT: Head, Steven R.

APPLICANT: Goelet, Philip  
APPLICANT: Karn, Jonathan  
APPLICANT: Boyce-Jacino, Michael  
TITLE OF INVENTION: De No. 63371880 or "Universal" Sequencing Array  
FILE REFERENCE: 04990.0049  
CURRENT APPLICATION NUMBER: US/09/648,312  
CURRENT FILING DATE: 2000-08-25  
NUMBER OF SEQ ID NOS: 31  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 28  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic primer  
US-09-648-312-28

Query Match 1.7%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 39;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTG 1810  
DB 1 TGTGTGTGTGTGTGTGTG 18

RESULT 38  
US-09-488-671-120  
Sequence 120, Application US/09488671A  
Patent No. 6187545  
GENERAL INFORMATION:  
APPLICANT: Robert McKay  
APPLICANT: Madeline M. Butler  
APPLICANT: Jacqueline Wyatt  
APPLICANT: Lex M. Cowsett  
TITLE OF INVENTION: ANTISENSE MODULATION OF PEPC-CYTOSOLIC EXPRESSION  
FILE REFERENCE: RTS-0123  
CURRENT APPLICATION NUMBER: US/09/488,671A  
CURRENT FILING DATE: 2000-01-21  
NUMBER OF SEQ ID NOS: 177  
SEQ ID NO 120  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Antisense Oligonucleotide  
US-09-488-671-120

Query Match 1.7%; Score 17.4; DB 1; Length 20;  
Best Local Similarity 94.7%; Pred. No. 53;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTGTG 1812  
DB 1 GTGTGTGTGTGTGTGTGTG 19

RESULT 39  
US-09-496-694B-235/c  
Sequence 235, Application US/09496694B  
Patent No. 6335194  
GENERAL INFORMATION:  
APPLICANT: C. Frank Bennett  
APPLICANT: Elizabeth J. Ackermann  
APPLICANT: Eric B. Swayze  
APPLICANT: Lex M. Cowsett  
TITLE OF INVENTION: ANTISENSE MODULATION OF SURVIVIN EXPRESSION  
FILE REFERENCE: ISPH-0439  
CURRENT APPLICATION NUMBER: US/09/496,694B  
CURRENT FILING DATE: 2000-02-02  
PRIOR APPLICATION NUMBER: 09/286,407  
PRIOR FILING DATE: 1999-04-05  
PRIOR APPLICATION NUMBER: 09/163,162

PRIOR FILING DATE: 1998-09-29  
NUMBER OF SEQ ID NOS: 249  
SEQ ID NO 235  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Antisense Oligonucleotide  
US-09-496-694B-235

Query Match 1.7%; Score 17.4; DB 1; Length 20;  
Best Local Similarity 94.7%; Pred. No. 53;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1811 TGTATATATATATATGT 1829  
DB 19 TGTATATATATATGT 1

RESULT 40  
US-08-222-177A-448/c  
Sequence 448, Application US/08222177A  
Patent No. 5582979  
GENERAL INFORMATION:  
APPLICANT: Weber, James L.  
TITLE OF INVENTION: LENGTH POLYMORPHISMS IN  
TITLE OF INVENTION: (dc-da)n.(dg-dt)n SEQUENCES AND METHODS OF USING SAME  
NUMBER OF SEQUENCES: 460  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dewitt Ross & Stevens, S.C.  
STREET: 8000 Excelsior Drive, Suite 401  
CITY: Madison  
STATE: Wisconsin  
COUNTRY: USA  
ZIP: 53717-1914  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/222,177A  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/341,562  
FILING DATE: 21-APR-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Sara, Charles S.  
REGISTRATION NUMBER: 30,492  
REFERENCE/DOCKET NUMBER: 09865.601  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (608) 831-2100  
TELEFAX: (608) 831-2106  
TELEX:  
INFORMATION FOR SEQ ID NO: 448:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-222-177A-448

Query Match 1.6%; Score 17; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 47;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGT 1809  
DB 17 TGTGTGTGTGTGTGTGT 1

RESULT 41  
US-08-885-126-9  
; Sequence 9, Application US/08885126A  
; Patent No. 595597  
; GENERAL INFORMATION:  
; APPLICANT: Arnold, Lyle J.  
; APPLICANT: Riley, Timothy A.  
; APPLICANT: Reynolds, Mark A.  
; APPLICANT: Schwartz, David A.  
; TITLE OF INVENTION: CHIRALLY ENRICHED SYNTHETIC PHOSPHATE  
; TITLE OF INVENTION: OLIGOMERS  
; FILE REFERENCE: GENTA.020FW2  
; CURRENT APPLICATION NUMBER: US/08/885,126A  
; CURRENT FILING DATE: 1997-06-30  
; EARLIER APPLICATION NUMBER: 08/343,018  
; EARLIER FILING DATE: 1994-11-21  
; EARLIER APPLICATION NUMBER: 08/154,013  
; EARLIER FILING DATE: 1993-11-16  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 9  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Chemically synthesized oligomer  
US-08-885-126-9

Query Match 1.6%; Score 17; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 47;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1798 GTGTGTGTGTGTGTA 1814  
Db 1 GTGTGTGTGTGTGTA 17

RESULT 42  
US-08-960-111-11  
; Sequence 11, Application US/08960111  
; Patent No. 6060456  
; GENERAL INFORMATION:  
; APPLICANT: Arnold Jr., Lyle J.  
; APPLICANT: Reynolds, Mark A.  
; APPLICANT: Giachetti, Christina  
; TITLE OF INVENTION: Chimeric Oligonucleoside Compounds  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 611 West Sixth St.  
; CITY: Los Angeles  
; STATE: CA  
; COUNTRY: U.S.A.  
; ZIP: 90017  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/960,111  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/238,177  
; FILING DATE: 04-MAY-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meier, Paul H.  
; REGISTRATION NUMBER: 32,274  
; REFERENCE/DOCKET NUMBER: 207/174  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 213/489-1600  
; TELEFAX: 213/955-0440

TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; HYPOTHETICAL: no  
; ANTI-SENSE: yes  
; FEATURE:  
; NAME/KEY: GT oligomers 2517-1, 2516-1  
; IDENTIFICATION METHOD: synthesis experiments  
; OTHER INFORMATION: complementary to synthetic RNA  
; OTHER INFORMATION: target  
US-08-960-111-11

Query Match 1.6%; Score 17; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 47;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1798 GTGTGTGTGTGTGTA 1814  
Db 1 GTGTGTGTGTGTGTA 17

RESULT 43  
US-09-490-774-11  
; Sequence 11, Application US/09490774  
; Patent No. 6262036  
; GENERAL INFORMATION:  
; APPLICANT: Arnold Jr., Lyle J.  
; APPLICANT: Reynolds, Mark A.  
; APPLICANT: Giachetti, Christina  
; TITLE OF INVENTION: Chimeric Oligonucleoside Compounds  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 611 West Sixth St.  
; CITY: Los Angeles  
; STATE: CA  
; COUNTRY: U.S.A.  
; ZIP: 90017  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/490,774  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/960,111  
; FILING DATE:  
; APPLICATION NUMBER: US/08/238,177  
; FILING DATE: 04-MAY-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meier, Paul H.  
; REGISTRATION NUMBER: 32,274  
; REFERENCE/DOCKET NUMBER: 207/174  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 213/489-1600  
; TELEFAX: 213/955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; HYPOTHETICAL: no



Query Match 1.6%; Score 17; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 51;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1792 TTGTGTGTGTGTGTG 1808  
DB 17 TTGTGTGTGTGTGTG 1

RESULT 47  
US-08-734-973-28/c  
; Sequence 28, Application US/08734973  
; Patent No. 5912147  
; GENERAL INFORMATION:  
; APPLICANT: Stoler, Daniel L.  
; APPLICANT: Basic, Mark  
; APPLICANT: Anderson, Garth R.  
; TITLE OF INVENTION: A Rapid Means For Quantitating  
; TITLE OF INVENTION: Genomic Instability  
; NUMBER OF SEQUENCES: 38  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear  
; STREET: 1800 One M&T Plaza  
; CITY: Buffalo  
; STATE: New York  
; COUNTRY: United States  
; ZIP: 14203-2391  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.5 inch  
; OPERATING SYSTEM: MS-DOS/ Microsoft Windows  
; SOFTWARE: Wordperfect for Windows  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/734,973  
; FILING DATE: October 1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Nelson, M. Bud  
; REGISTRATION NUMBER: 35,300  
; REFERENCE/DOCKET NUMBER: 03551.0021  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (716) 856-4000  
; TELEFAX: (716) 849-0349  
; INFORMATION FOR SEQ ID NO: 30 :  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 nucleotides  
; TYPE: nucleic acid  
; STRANDEDNESS: single-stranded  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
; HYPOTHETICAL: No  
US-08-734-973-30

Query Match 1.6%; Score 17; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 51;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTG 1810  
DB 17 GTGTGTGTGTGTGTG 1

RESULT 49  
US-08-734-973-31/c  
; Sequence 31, Application US/08734973  
; Patent No. 5912147  
; GENERAL INFORMATION:  
; APPLICANT: Stoler, Daniel L.  
; APPLICANT: Basic, Mark  
; APPLICANT: Anderson, Garth R.  
; TITLE OF INVENTION: A Rapid Means For Quantitating  
; TITLE OF INVENTION: Genomic Instability  
; NUMBER OF SEQUENCES: 38  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear  
; STREET: 1800 One M&T Plaza  
; CITY: Buffalo  
; STATE: New York  
; COUNTRY: United States  
; ZIP: 14203-2391  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.5 inch  
; OPERATING SYSTEM: MS-DOS/ Microsoft Windows  
; SOFTWARE: Wordperfect for Windows  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/734,973  
; FILING DATE: October 1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Nelson, M. Bud  
; REGISTRATION NUMBER: 35,300  
; REFERENCE/DOCKET NUMBER: 03551.0021  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (716) 856-4000  
; TELEFAX: (716) 849-0349  
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear  
STREET: 1800 One M&T Plaza  
CITY: Buffalo  
STATE: New York  
COUNTRY: United States  
ZIP: 14203-2391  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch  
OPERATING SYSTEM: MS-DOS/ Microsoft Windows  
SOFTWARE: Wordperfect for Windows  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/734,973  
FILING DATE: October 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Nelson, M. Bud  
REGISTRATION NUMBER: 35,300  
REFERENCE/DOCKET NUMBER: 03551.0021  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (716) 856-4000  
TELEFAX: (716) 849-0349  
INFORMATION FOR SEQ ID NO: 30 :  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single-stranded  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
HYPOTHETICAL: No  
US-08-734-973-30

Query Match 1.6%; Score 17; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 51;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTG 1810  
DB 17 GTGTGTGTGTGTGTG 1

RESULT 49  
US-08-734-973-31/c  
; Sequence 31, Application US/08734973  
; Patent No. 5912147  
; GENERAL INFORMATION:  
; APPLICANT: Stoler, Daniel L.  
; APPLICANT: Basic, Mark  
; APPLICANT: Anderson, Garth R.  
; TITLE OF INVENTION: A Rapid Means For Quantitating  
; TITLE OF INVENTION: Genomic Instability  
; NUMBER OF SEQUENCES: 38  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear  
; STREET: 1800 One M&T Plaza  
; CITY: Buffalo  
; STATE: New York  
; COUNTRY: United States  
; ZIP: 14203-2391  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.5 inch  
; OPERATING SYSTEM: MS-DOS/ Microsoft Windows  
; SOFTWARE: Wordperfect for Windows  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/734,973  
; FILING DATE: October 1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Nelson, M. Bud  
; REGISTRATION NUMBER: 35,300  
; REFERENCE/DOCKET NUMBER: 03551.0021  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (716) 856-4000  
; TELEFAX: (716) 849-0349  
; CORRESPONDENCE ADDRESS:



; INFORMATION FOR SEQ ID NO: 31 :  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 nucleotides  
; TYPE: nucleic acid  
; STRANDEDNESS: single-stranded  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
; HYPOTHETICAL: NO  
US-08-734-973-31

Query Match 1.6%; Score 17; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 51;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1794 GTGTGTGTGTGTGTG 1810  
Db 17 GTGTGTGTGTGTGTG 1

RESULT 50  
US-08-734-973-32/c

; Sequence 32, Application US/08734973  
; Patent No. 5912147  
; GENERAL INFORMATION:  
; APPLICANT: Stoler, Daniel L.  
; APPLICANT: Basik, Mark  
; APPLICANT: Anderson, Garth R.  
; TITLE OF INVENTION: A Rapid Means For Quantitating  
; TITLE OF INVENTION: Genomic Instability  
; NUMBER OF SEQUENCES: 38  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear  
; STREET: 1800 One M&T Plaza  
; CITY: Buffalo  
; STATE: New York  
; COUNTRY: United States  
; ZIP: 14203-2391  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.5 inch  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: MS-DOS/ Microsoft Windows  
; SOFTWARE: Wordperfect for Windows  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/734,973  
; FILING DATE: October 1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Nelson, M. Bud  
; REGISTRATION NUMBER: 35,300  
; REFERENCE/DOCKET NUMBER: 03551.0021  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (716) 856-4000  
; TELEFAX: (716) 849-0349  
; INFORMATION FOR SEQ ID NO: 32 :  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 nucleotides  
; TYPE: nucleic acid  
; STRANDEDNESS: single-stranded  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
; HYPOTHETICAL: NO  
US-08-734-973-32

Query Match 1.6%; Score 17; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 51;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1794 GTGTGTGTGTGTGTG 1810  
Db 17 GTGTGTGTGTGTGTG 1

RESULT 51  
US-09-475-947A-337/c

; Sequence 337, Application US/09475947A  
; Patent No. 6472154  
; GENERAL INFORMATION:  
; APPLICANT: Garner, Harold R.  
; APPLICANT: Wren, Jonathan D.  
; APPLICANT: Minna, John D.  
; TITLE OF INVENTION: Polymorphic Repeats in Human Genes  
; FILE REFERENCE: UTSD0667  
; CURRENT APPLICATION NUMBER: US/09/475,947A  
; CURRENT FILING DATE: 1999-12-31  
; NUMBER OF SEQ ID NOS: 346  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 337  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: human  
US-09-475-947A-337

Query Match 1.6%; Score 16.8; DB 1; Length 20;  
Best Local Similarity 90.0%; Pred. No. 82;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1792 TTGTGTGTGTGTGTGTGT 1811  
Db 20 TCGGGTGTGTGTGTGTGT 1

RESULT 52

US-08-849-021-87  
; Sequence 87, Application US/08849021  
; Patent No. 5955276  
; GENERAL INFORMATION:  
; APPLICANT: MORGANTE, MICHELE  
; APPLICANT: VOGEL, JULIE M.  
; TITLE OF INVENTION: COMPOUND MICROSATELLITE  
; TITLE OF INVENTION: PRIMERS FOR THE  
; TITLE OF INVENTION: DETECTION OF GENETIC  
; TITLE OF INVENTION: POLYMORPHISMS  
; NUMBER OF SEQUENCES: 89  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND  
; ADDRESSEE: COMPANY  
; STREET: 1007 MARKET STREET  
; CITY: WILMINGTON  
; STATE: DELAWARE  
; COUNTRY: U.S.A.  
; ZIP: 19898  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: FLOPPY DISK  
; COMPUTER: IBM PC COMPATIBLE  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PATENT IN RELEASE #1.0, VERSION 1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/849,021  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/346,456  
; FILING DATE: 28 NOVEMBER 1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: FLOYD, LINDA AXAMETHY  
; REGISTRATION NUMBER: 33,692  
; REFERENCE/DOCKET NUMBER: BB-1064-A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 302-892-8112  
; TELEFAX: 302-992-7949  
; INFORMATION FOR SEQ ID NO: 87:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 24 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)

```

US-08-849-021-87
Query Match 1.6%; Score 16.8; DB 1; Length 24;
Best Local Similarity 90.0%; Pred. No. 78;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1813 TATATATATATATATAC 1832
DB 1 TATATATATATATATAC 20

RESULT 53
US-08-734-973-7/c
; Sequence 7, Application US/08734973
; Patent No. 5912147
; GENERAL INFORMATION:
; APPLICANT: Stoler, Daniel L.
; APPLICANT: Basik, Mark
; APPLICANT: Anderson, Garth R.
; TITLE OF INVENTION: A Rapid Means For Quantitating
; TITLE OF INVENTION: Genomic Instability
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear
; STREET: 1800 One M&T Plaza
; CITY: Buffalo
; STATE: New York
; COUNTRY: United States
; ZIP: 14203-2391
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS/ Microsoft Windows
; SOFTWARE: Wordperfect for Windows
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/734,973
; FILING DATE: October 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Nelson, M. Bud
; REGISTRATION NUMBER: 35,300
; REFERENCE/DOCKET NUMBER: 03551.0021
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 856-4000
; TELEFAX: (716) 849-0349
; INFORMATION FOR SEQ ID NO: 8 :
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single-stranded
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; HYPOTHETICAL: NO
; US-08-734-973-8

Query Match 1.6%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 60;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1791 ATTGTGTGTGTGTGTG 1808
DB 18 ACTGTGTGTGTGTGTG 1

RESULT 55
US-08-734-973-29/c
; Sequence 29, Application US/08734973
; Patent No. 5912147
; GENERAL INFORMATION:
; APPLICANT: Stoler, Daniel L.
; APPLICANT: Basik, Mark
; APPLICANT: Anderson, Garth R.
; TITLE OF INVENTION: A Rapid Means For Quantitating
; TITLE OF INVENTION: Genomic Instability
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear
; STREET: 1800 One M&T Plaza
; CITY: Buffalo
; STATE: New York
; COUNTRY: United States
; ZIP: 14203-2391
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS/ Microsoft Windows
; SOFTWARE: Wordperfect for Windows
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/734,973
; FILING DATE: October 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Nelson, M. Bud
; REGISTRATION NUMBER: 35,300
; REFERENCE/DOCKET NUMBER: 03551.0021
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 856-4000
; TELEFAX: (716) 849-0349
; INFORMATION FOR SEQ ID NO: 7 :
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single-stranded
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; HYPOTHETICAL: NO
; US-08-734-973-7

Query Match 1.6%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 60;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1791 ATTGTGTGTGTGTGTG 1808
DB 18 ACTGTGTGTGTGTGTG 1

RESULT 54
US-08-734-973-8/c
; Sequence 8, Application US/08734973
; Patent No. 5912147
; GENERAL INFORMATION:
; APPLICANT: Stoler, Daniel L.
; APPLICANT: Basik, Mark
; APPLICANT: Anderson, Garth R.
; TITLE OF INVENTION: A Rapid Means For Quantitating
; TITLE OF INVENTION: Genomic Instability

```

TELEPHONE: (716) 856-4000  
TELEFAX: (716) 849-0349  
INFORMATION FOR SEQ ID NO: 29 :  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single-stranded  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
HYPOTHETICAL: NO  
US-08-734-973-29

Query Match 1.6%; Score 16.4; DB 1; Length 18;  
Best Local Similarity 94.4%; Pred. No. 60;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTG 1810  
Db 18 TCTGTGTGTGTGTGTG 1

RESULT 56  
US-08-734-973-33/c  
Sequence 33, Application US/08734973  
Patent No. 5912147  
GENERAL INFORMATION:  
APPLICANT: Stoler, Daniel L.  
APPLICANT: Basik, Mark  
APPLICANT: Anderson, Garth R.  
TITLE OF INVENTION: A Rapid Means For Quantitating  
TITLE OF INVENTION: Genomic Instability  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear  
STREET: 1800 One M&T Plaza  
CITY: Buffalo  
STATE: New York  
COUNTRY: United States  
ZIP: 14203-2391  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS/ Microsoft Windows  
SOFTWARE: Wordperfect for Windows  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/734,973  
FILING DATE: October 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Nelson, M. Bud  
REGISTRATION NUMBER: 35,300  
REFERENCE/DOCKET NUMBER: 03551.0021  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (716) 856-4000  
TELEFAX: (716) 849-0349  
INFORMATION FOR SEQ ID NO: 33 :  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single-stranded  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
HYPOTHETICAL: NO  
US-08-734-973-33

Query Match 1.6%; Score 16.4; DB 1; Length 18;  
Best Local Similarity 94.4%; Pred. No. 60;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1791 ATTGTGTGTGTGTGTG 1808  
Db 18 AATGTGTGTGTGTGTG 1

RESULT 57  
US-08-734-973-35/c  
Sequence 35, Application US/08734973  
Patent No. 5912147  
GENERAL INFORMATION:  
APPLICANT: Stoler, Daniel L.  
APPLICANT: Basik, Mark  
APPLICANT: Anderson, Garth R.  
TITLE OF INVENTION: A Rapid Means For Quantitating  
TITLE OF INVENTION: Genomic Instability  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear  
STREET: 1800 One M&T Plaza  
CITY: Buffalo  
STATE: New York  
COUNTRY: United States  
ZIP: 14203-2391  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS/ Microsoft Windows  
SOFTWARE: Wordperfect for Windows  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/734,973  
FILING DATE: October 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Nelson, M. Bud  
REGISTRATION NUMBER: 35,300  
REFERENCE/DOCKET NUMBER: 03551.0021  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (716) 856-4000  
TELEFAX: (716) 849-0349  
INFORMATION FOR SEQ ID NO: 35 :  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single-stranded  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
HYPOTHETICAL: NO  
US-08-734-973-35

Query Match 1.6%; Score 16.4; DB 1; Length 18;  
Best Local Similarity 94.4%; Pred. No. 60;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1791 ATTGTGTGTGTGTGTG 1808  
Db 18 AATGTGTGTGTGTGTG 1

RESULT 58  
US-08-734-973-37/c  
Sequence 37, Application US/08734973  
Patent No. 5912147  
GENERAL INFORMATION:  
APPLICANT: Stoler, Daniel L.  
APPLICANT: Basik, Mark  
APPLICANT: Anderson, Garth R.  
TITLE OF INVENTION: A Rapid Means For Quantitating  
TITLE OF INVENTION: Genomic Instability  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear  
STREET: 1800 One M&T Plaza  
CITY: Buffalo  
STATE: New York  
COUNTRY: United States  
ZIP: 14203-2391  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch  
COMPUTER: IBM Compatible

OPERATING SYSTEM: MS-DOS/ Microsoft Windows  
SOFTWARE: Wordperfect for Windows  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/734,973  
FILING DATE: October 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Nelson, M. Bud  
REGISTRATION NUMBER: 35,300  
REFERENCE/DOCKET NUMBER: 03551.0021  
TELEPHONE: (716) 856-4000  
TELEFAX: (716) 849-0349  
INFORMATION FOR SEQ ID NO: 37 :  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single-stranded  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
HYPOTHETICAL: NO  
US-08-734-973-37

Query Match 1.6%; Score 16.4; DB 1; Length 18;  
Best Local Similarity 94.4%; Pred. No. 60;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1791 ATTGTGTGTGTGTGTG 1808  
Db 18 AATGTGTGTGTGTGTG 1

RESULT 59  
US-08-734-973-38/c  
Sequence 38, Application US/08734973  
Patent No. 5912147  
GENERAL INFORMATION:  
APPLICANT: Stoller, Daniel L.  
APPLICANT: Basik, Mark  
APPLICANT: Anderson, Garth R.  
TITLE OF INVENTION: A Rapid Means For Quantitating  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear  
STREET: 1800 One M&T Plaza  
CITY: Buffalo  
STATE: New York  
COUNTRY: United States  
ZIP: 14203-2391  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS/ Microsoft Windows  
SOFTWARE: Wordperfect for Windows  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/734,973  
FILING DATE: October 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Nelson, M. Bud  
REGISTRATION NUMBER: 35,300  
REFERENCE/DOCKET NUMBER: 03551.0021  
TELEPHONE: (716) 856-4000  
TELEFAX: (716) 849-0349  
INFORMATION FOR SEQ ID NO: 38 :  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single-stranded  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
HYPOTHETICAL: NO  
US-08-734-973-38

Query Match 1.6%; Score 16.4; DB 1; Length 18;  
Best Local Similarity 94.4%; Pred. No. 60;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1791 ATTGTGTGTGTGTGTG 1808  
Db 18 AATGTGTGTGTGTGTG 1  
RESULT 60  
US-09-475-947A-104  
Sequence 104, Application US/09475947A  
Patent No. 6472154  
GENERAL INFORMATION:  
APPLICANT: Garner, Harold R.  
APPLICANT: Wren, Jonathan D.  
APPLICANT: Minna, John D.  
TITLE OF INVENTION: Polymorphic Repeats in Human Genes  
FILE REFERENCE: UTSD0667  
CURRENT APPLICATION NUMBER: US/09/475,947A  
CURRENT FILING DATE: 1999-12-31  
NUMBER OF SEQ ID NOS: 346  
SOFTWARE: Patent In Ver. 2.1  
SEQ ID NO 104  
LENGTH: 18  
TYPE: DNA  
ORGANISM: human  
US-09-475-947A-104

Query Match 1.6%; Score 16.4; DB 1; Length 18;  
Best Local Similarity 94.4%; Pred. No. 60;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1810 GTGTATATATATATATAT 1827  
Db 1 GTATATATATATATATAT 18

RESULT 61  
US-09-475-947A-104/c  
Sequence 104, Application US/09475947A  
Patent No. 6472154  
GENERAL INFORMATION:  
APPLICANT: Garner, Harold R.  
APPLICANT: Wren, Jonathan D.  
APPLICANT: Minna, John D.  
TITLE OF INVENTION: Polymorphic Repeats in Human Genes  
FILE REFERENCE: UTSD0667  
CURRENT APPLICATION NUMBER: US/09/475,947A  
CURRENT FILING DATE: 1999-12-31  
NUMBER OF SEQ ID NOS: 346  
SOFTWARE: Patent In Ver. 2.1  
SEQ ID NO 104  
LENGTH: 18  
TYPE: DNA  
ORGANISM: human  
US-09-475-947A-104

Query Match 1.6%; Score 16.4; DB 1; Length 18;  
Best Local Similarity 94.4%; Pred. No. 60;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1814 ATATATATATATATGTAC 1831  
Db 18 ATATATATATATATATAC 1

RESULT 62  
US-08-222-177A-439/c  
Sequence 439, Application US/08222177A  
Patent No. 5582979  
GENERAL INFORMATION:

APPLICANT: Weber, James L.  
 TITLE OF INVENTION: LENGTH POLYMORPHISMS IN  
 TITLE OF INVENTION: (GC-dA)n.(GG-dT)n SEQUENCES AND METHODS OF USING SAME  
 NUMBER OF SEQUENCES: 460  
 CORRESPONDENCE ADDRESS:  
 ADDRESSES: Demitt Ross & Stevens, S.C.  
 STREET: 8000 Excelsior Drive, Suite 401  
 CITY: Madison  
 STATE: Wisconsin  
 COUNTRY: USA  
 ZIP: 53717-1914  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/222,177A  
 FILING DATE:  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/341,562  
 FILING DATE: 21-APR-1989  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Sara, Charles S.  
 REGISTRATION NUMBER: 30,492  
 REFERENCE/DOCKET NUMBER: 09865.601  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (608) 831-2100  
 TELEFAX: (608) 831-2106  
 TELEX:  
 INFORMATION FOR SEQ ID NO: 439:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 16 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 US-08-222-177A-439

Query Match 1.5%; Score 16; DB 1; Length 16;  
 Best Local Similarity 100.0%; Pred.No. 57;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTGTGTG 1808  
 Db 16 TGTGTGTGTGTGTGTG 1

RESULT 63  
 US-09-371-772B-6069  
 ; Sequence 6069, Application US/09371772B  
 ; Patent No. 6566127  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
 ; APPLICANT: Pavco, Pam  
 ; APPLICANT: McSwigen, Jim  
 ; APPLICANT: Stancincomb, Dan  
 ; APPLICANT: Escobedo, Jaime  
 ; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
 ; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor  
 ; FILE REFERENCE: MBH00,876-J (237/198)  
 ; CURRENT APPLICATION NUMBER: US/09/371,772B  
 ; CURRENT FILING DATE: 1999-08-10  
 ; PRIOR APPLICATION NUMBER: US 60/005,974  
 ; PRIOR FILING DATE: 1995-10-26  
 ; PRIOR APPLICATION NUMBER: US 08/584,040  
 ; PRIOR FILING DATE: 1996-01-08  
 ; NUMBER OF SEQ ID NOS: 14225  
 ; SOFTWARE: Patent in version 3.0  
 ; SEQ ID NO 6069  
 ; LENGTH: 16  
 ; TYPE: RNA

; ORGANISM: Homo sapiens  
 ; US-09-371-772B-6069  
 Query Match 1.5%; Score 16; DB 1; Length 16;  
 Best Local Similarity 50.0%; Pred.No. 57;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1794 GTGTGTGTGTGTGTGTGT 1809  
 Db 1 GUGUGUGUGUGUGUGU 16

RESULT 64  
 US-09-958-221A-17  
 ; Sequence 17, Application US/09958221A  
 ; Patent No. 6686160  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Haeringen van, Willem A.  
 ; APPLICANT: Haeringen van, Hendrik  
 ; TITLE OF INVENTION: UNIVERSAL VARIABLE FRAGMENTS  
 ; FILE REFERENCE: 92750/64  
 ; CURRENT APPLICATION NUMBER: US/09/958,221A  
 ; CURRENT FILING DATE: 2001-10-03  
 ; PRIOR APPLICATION NUMBER: EP 00200757.3  
 ; PRIOR FILING DATE: 2000-03-03  
 ; PRIOR APPLICATION NUMBER: PCT/NL01/001177  
 ; PRIOR FILING DATE: 2001-03-05  
 ; NUMBER OF SEQ ID NOS: 27  
 ; SOFTWARE: Patent in Ver. 2.1  
 ; SEQ ID NO 17  
 ; LENGTH: 17  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: primer  
 ; US-09-958-221A-17

Query Match 1.5%; Score 16; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred.No. 62;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTGTGTGTG 1808  
 Db 2 TGTGTGTGTGTGTGTGTG 17

RESULT 65  
 US-09-958-221A-18  
 ; Sequence 18, Application US/09958221A  
 ; Patent No. 6686160  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Haeringen van, Willem A.  
 ; APPLICANT: Haeringen van, Hendrik  
 ; TITLE OF INVENTION: UNIVERSAL VARIABLE FRAGMENTS  
 ; FILE REFERENCE: 92750/64  
 ; CURRENT APPLICATION NUMBER: US/09/958,221A  
 ; CURRENT FILING DATE: 2001-10-03  
 ; PRIOR APPLICATION NUMBER: EP 00200757.3  
 ; PRIOR FILING DATE: 2000-03-03  
 ; PRIOR APPLICATION NUMBER: PCT/NL01/001177  
 ; PRIOR FILING DATE: 2001-03-05  
 ; NUMBER OF SEQ ID NOS: 27  
 ; SOFTWARE: Patent in Ver. 2.1  
 ; SEQ ID NO 18  
 ; LENGTH: 17  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: primer  
 ; US-09-958-221A-18

Query Match 1.5%; Score 16; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred.No. 62;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTGTGTG 1808  
Db 2 TGTGTGTGTGTGTGTG 17

RESULT 66  
US-09-958-221A-19/c  
; Sequence 19, Application US/09958221A  
; Patent No. 6686160  
; GENERAL INFORMATION:  
; APPLICANT: Haeringen van, Willem A.  
; TITLE OF INVENTION: UNIVERSAL VARIABLE FRAGMENTS  
; FILE REFERENCE: 92750/64  
; CURRENT APPLICATION NUMBER: US/09/958,221A  
; CURRENT FILING DATE: 2001-10-03  
; PRIOR APPLICATION NUMBER: EP 00200757.3  
; PRIOR FILING DATE: 2000-03-03  
; PRIOR APPLICATION NUMBER: PCT/NL01/00177  
; PRIOR FILING DATE: 2001-03-05  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 19  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: primer  
US-09-958-221A-19

Query Match 1.5%; Score 16; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 62;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTGTGTG 1808  
Db 17 TGTGTGTGTGTGTGTG 2

RESULT 67  
US-09-958-221A-20/c  
; Sequence 20, Application US/09958221A  
; Patent No. 6686160  
; GENERAL INFORMATION:  
; APPLICANT: Haeringen van, Willem A.  
; TITLE OF INVENTION: UNIVERSAL VARIABLE FRAGMENTS  
; FILE REFERENCE: 92750/64  
; CURRENT APPLICATION NUMBER: US/09/958,221A  
; CURRENT FILING DATE: 2001-10-03  
; PRIOR APPLICATION NUMBER: EP 00200757.3  
; PRIOR FILING DATE: 2000-03-03  
; PRIOR APPLICATION NUMBER: PCT/NL01/00177  
; PRIOR FILING DATE: 2001-03-05  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 20  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: primer  
US-09-958-221A-20

Query Match 1.5%; Score 16; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 62;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTGTGTG 1808  
Db 17 TGTGTGTGTGTGTGTG 2

RESULT 68  
US-09-958-221A-21/c  
; Sequence 21, Application US/09958221A  
; Patent No. 6686160  
; GENERAL INFORMATION:  
; APPLICANT: Haeringen van, Willem A.  
; TITLE OF INVENTION: UNIVERSAL VARIABLE FRAGMENTS  
; FILE REFERENCE: 92750/64  
; CURRENT APPLICATION NUMBER: US/09/958,221A  
; CURRENT FILING DATE: 2001-10-03  
; PRIOR APPLICATION NUMBER: EP 00200757.3  
; PRIOR FILING DATE: 2000-03-03  
; PRIOR APPLICATION NUMBER: PCT/NL01/00177  
; PRIOR FILING DATE: 2001-03-05  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 21  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: primer  
US-09-958-221A-21

Query Match 1.5%; Score 16; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 62;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTGTGTG 1808  
Db 17 TGTGTGTGTGTGTGTG 2

RESULT 69  
US-08-734-973-2/c  
; Sequence 2, Application US/08734973  
; Patent No. 5912147  
; GENERAL INFORMATION:  
; APPLICANT: Stoler, Daniel L.  
; APPLICANT: Basik, Mark  
; APPLICANT: Anderson, Garth R.  
; TITLE OF INVENTION: A Rapid Means For Quantitating  
; TITLE OF INVENTION: Genomic Instability  
; NUMBER OF SEQUENCES: 38  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear  
; STREET: 1800 One M&T Plaza  
; CITY: Buffalo  
; STATE: New York  
; COUNTRY: United States  
; ZIP: 14203-2391  
; MEDIUM TYPE: Diskette, 3.5 inch  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: MS-DOS/ Microsoft Windows  
; SOFTWARE: Wordperfect for Windows  
; CURRENT APPLICATION DATA: US/08/734,973  
; APPLICATION NUMBER: US/08/734,973  
; FILING DATE: October 1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Nelson, M. Bud  
; REGISTRATION NUMBER: 35,300  
; REFERENCE/DOCKET NUMBER: 03551.0021  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (716) 856-4000  
; TELEFAX: (716) 849-0349  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 nucleotides  
; TYPE: nucleic acid

Query Match 1.5%; Score 16; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 62;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTGTGTG 1808  
Db 17 TGTGTGTGTGTGTGTG 2

RESULT 70  
US-08-734-973-2/c  
; Sequence 2, Application US/08734973  
; Patent No. 5912147  
; GENERAL INFORMATION:  
; APPLICANT: Stoler, Daniel L.  
; APPLICANT: Basik, Mark  
; APPLICANT: Anderson, Garth R.  
; TITLE OF INVENTION: A Rapid Means For Quantitating  
; TITLE OF INVENTION: Genomic Instability  
; NUMBER OF SEQUENCES: 38  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear  
; STREET: 1800 One M&T Plaza  
; CITY: Buffalo  
; STATE: New York  
; COUNTRY: United States  
; ZIP: 14203-2391  
; MEDIUM TYPE: Diskette, 3.5 inch  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: MS-DOS/ Microsoft Windows  
; SOFTWARE: Wordperfect for Windows  
; CURRENT APPLICATION DATA: US/08/734,973  
; APPLICATION NUMBER: US/08/734,973  
; FILING DATE: October 1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Nelson, M. Bud  
; REGISTRATION NUMBER: 35,300  
; REFERENCE/DOCKET NUMBER: 03551.0021  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (716) 856-4000  
; TELEFAX: (716) 849-0349  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 nucleotides  
; TYPE: nucleic acid

Query Match 1.5%; Score 16; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 62;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTGTGTG 1808  
Db 17 TGTGTGTGTGTGTGTG 2

STRANDEDNESS: single-stranded  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
HYPOTHETICAL: NO  
US-08-734-973-2

Query Match 1.5%; Score 16; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 67;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTG 1808  
|||||  
DB 16 TGTGTGTGTGTGTG 1

## RESULT 70

US-08-734-973-6/c  
Sequence 6, Application US/08734973  
Patent No. 5912147

GENERAL INFORMATION:  
APPLICANT: Stoler, Daniel L.  
APPLICANT: Basik, Mark  
APPLICANT: Anderson, Garth R.  
TITLE OF INVENTION: A Rapid Means For Quantitating  
TITLE OF INVENTION: Genomic Instability  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear  
STREET: 1800 One M&T Plaza  
CITY: Buffalo  
STATE: New York  
COUNTRY: United States  
ZIP: 14203-2391  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS/ Microsoft Windows  
SOFTWARE: Wordperfect for Windows  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/734,973  
FILING DATE: October 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Nelson, M. Bud  
REGISTRATION NUMBER: 35,300  
REFERENCE/DOCKET NUMBER: 03551.0021  
TELEPHONE: (716) 856-4000  
TELEFAX: (716) 849-0349  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single-stranded  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
HYPOTHETICAL: NO

US-08-734-973-6

Query Match 1.5%; Score 16; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 67;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTG 1808  
|||||  
DB 16 TGTGTGTGTGTGTG 1

## RESULT 71

US-08-734-973-34/c  
Sequence 34, Application US/08734973  
Patent No. 5912147  
GENERAL INFORMATION:  
APPLICANT: Stoler, Daniel L.

APPLICANT: Basik, Mark  
APPLICANT: Anderson, Garth R.  
TITLE OF INVENTION: A Rapid Means For Quantitating  
TITLE OF INVENTION: Genomic Instability  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear  
STREET: 1800 One M&T Plaza  
CITY: Buffalo  
STATE: New York  
COUNTRY: United States  
ZIP: 14203-2391  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS/ Microsoft Windows  
SOFTWARE: Wordperfect for Windows  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/734,973  
FILING DATE: October 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Nelson, M. Bud  
REGISTRATION NUMBER: 35,300  
REFERENCE/DOCKET NUMBER: 03551.0021  
TELEPHONE: (716) 856-4000  
TELEFAX: (716) 849-0349  
INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single-stranded  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
HYPOTHETICAL: NO

US-08-734-973-34

Query Match 1.5%; Score 16; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 67;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTG 1808  
|||||  
DB 16 TGTGTGTGTGTGTG 1

US-08-734-973-36/c  
Sequence 36, Application US/08734973  
Patent No. 5912147  
GENERAL INFORMATION:  
APPLICANT: Stoler, Daniel L.  
APPLICANT: Basik, Mark  
APPLICANT: Anderson, Garth R.  
TITLE OF INVENTION: A Rapid Means For Quantitating  
TITLE OF INVENTION: Genomic Instability  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear  
STREET: 1800 One M&T Plaza  
CITY: Buffalo  
STATE: New York  
COUNTRY: United States  
ZIP: 14203-2391  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS/ Microsoft Windows  
SOFTWARE: Wordperfect for Windows  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/734,973  
FILING DATE: October 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Nelson, M. Bud  
REGISTRATION NUMBER: 35,300  
REFERENCE/DOCKET NUMBER: 03551.0021  
TELEPHONE: (716) 856-4000  
TELEFAX: (716) 849-0349  
INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single-stranded  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
HYPOTHETICAL: NO

US-08-734-973-34

Query Match 1.5%; Score 16; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 67;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTG 1808  
|||||  
DB 16 TGTGTGTGTGTGTG 1

US-08-734-973-36/c  
Sequence 36, Application US/08734973  
Patent No. 5912147  
GENERAL INFORMATION:  
APPLICANT: Stoler, Daniel L.  
APPLICANT: Basik, Mark  
APPLICANT: Anderson, Garth R.  
TITLE OF INVENTION: A Rapid Means For Quantitating  
TITLE OF INVENTION: Genomic Instability  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear  
STREET: 1800 One M&T Plaza  
CITY: Buffalo  
STATE: New York  
COUNTRY: United States  
ZIP: 14203-2391  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS/ Microsoft Windows  
SOFTWARE: Wordperfect for Windows  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/734,973  
FILING DATE: October 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Nelson, M. Bud  
REGISTRATION NUMBER: 35,300  
REFERENCE/DOCKET NUMBER: 03551.0021  
TELEPHONE: (716) 856-4000  
TELEFAX: (716) 849-0349  
INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single-stranded  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
HYPOTHETICAL: NO

US-08-734-973-34

Query Match 1.5%; Score 16; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 67;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTG 1808  
|||||  
DB 16 TGTGTGTGTGTGTG 1

US-08-734-973-36/c  
Sequence 36, Application US/08734973  
Patent No. 5912147  
GENERAL INFORMATION:  
APPLICANT: Stoler, Daniel L.  
APPLICANT: Basik, Mark  
APPLICANT: Anderson, Garth R.  
TITLE OF INVENTION: A Rapid Means For Quantitating  
TITLE OF INVENTION: Genomic Instability  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear  
STREET: 1800 One M&T Plaza  
CITY: Buffalo  
STATE: New York  
COUNTRY: United States  
ZIP: 14203-2391  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS/ Microsoft Windows  
SOFTWARE: Wordperfect for Windows  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/734,973  
FILING DATE: October 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Nelson, M. Bud  
REGISTRATION NUMBER: 35,300  
REFERENCE/DOCKET NUMBER: 03551.0021  
TELEPHONE: (716) 856-4000  
TELEFAX: (716) 849-0349  
INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single-stranded  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
HYPOTHETICAL: NO

US-08-734-973-34

Query Match 1.5%; Score 16; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 67;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTG 1808  
|||||  
DB 16 TGTGTGTGTGTGTG 1

US-08-734-973-36/c  
Sequence 36, Application US/08734973  
Patent No. 5912147  
GENERAL INFORMATION:  
APPLICANT: Stoler, Daniel L.  
APPLICANT: Basik, Mark  
APPLICANT: Anderson, Garth R.  
TITLE OF INVENTION: A Rapid Means For Quantitating  
TITLE OF INVENTION: Genomic Instability  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear  
STREET: 1800 One M&T Plaza  
CITY: Buffalo  
STATE: New York  
COUNTRY: United States  
ZIP: 14203-2391  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS/ Microsoft Windows  
SOFTWARE: Wordperfect for Windows  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/734,973  
FILING DATE: October 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Nelson, M. Bud  
REGISTRATION NUMBER: 35,300  
REFERENCE/DOCKET NUMBER: 03551.0021  
TELEPHONE: (716) 856-4000  
TELEFAX: (716) 849-0349  
INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single-stranded  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
HYPOTHETICAL: NO

US-08-734-973-34

Query Match 1.5%; Score 16; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 67;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTG 1808  
|||||  
DB 16 TGTGTGTGTGTGTG 1

US-08-734-973-34/c  
Sequence 34, Application US/08734973  
Patent No. 5912147  
GENERAL INFORMATION:  
APPLICANT: Stoler, Daniel L.

US-08-734-973-34/c

Query Match 1.5%; Score 16; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 67;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTG 1808  
|||||  
DB 16 TGTGTGTGTGTGTG 1

US-08-734-973-34/c  
Sequence 34, Application US/08734973  
Patent No. 5912147  
GENERAL INFORMATION:  
APPLICANT: Stoler, Daniel L.

NAME: Nelson, M. Bud  
REGISTRATION NUMBER: 35,300  
REFERENCE/DOCKET NUMBER: 03551.0021  
TELEPHONE: (716) 856-4000  
TELEFAX: (716) 849-0349  
INFORMATION FOR SEQ ID NO: 36 :  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single-stranded  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
HYPOTHETICAL: NO  
US-08-734-973-36

Query Match 1.5%; Score 16; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 67;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTG 1808  
|||  
Db 16 TGTGTGTGTGTGTG 1

RESULT 73  
US-08-849-021-7/c  
; Sequence 7, Application US/08849021  
; Patent No. 5955276  
; GENERAL INFORMATION:  
; APPLICANT: MORGANTE, MICHELE  
; APPLICANT: VOGEL, JULIE M.  
; TITLE OF INVENTION: COMPOUND MICROSATELLITE  
; TITLE OF INVENTION: PRIMERS FOR THE  
; TITLE OF INVENTION: DETECTION OF GENETIC  
; TITLE OF INVENTION: POLYMORPHISMS  
; NUMBER OF SEQUENCES: 89  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND  
; ADDRESSEE: COMPANY  
; STREET: 1007 MARKET STREET  
; CITY: WILMINGTON  
; STATE: DELAWARE  
; COUNTRY: U.S.A.  
; ZIP: 19898  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: FLOPPY DISK  
; COMPUTER: IBM PC COMPATIBLE  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PATENT IN RELEASE #1.0, VERSION 1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/849,021  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/346,456  
; FILING DATE: 28 NOVEMBER 1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: FLOYD, LINDA AXAMETHY  
; REGISTRATION NUMBER: 33,692  
; REFERENCE/DOCKET NUMBER: BB-1064-A  
; TELEPHONE: 302-992-8112  
; TELEFAX: 302-992-7949  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-849-021-7

Query Match 1.4%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 68;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTG 1807  
|||  
Db 15 TGTGTGTGTGTGTG 1

RESULT 74  
US-08-849-021-8/c  
; Sequence 8, Application US/08849021  
; Patent No. 5955276  
; GENERAL INFORMATION:  
; APPLICANT: MORGANTE, MICHELE  
; APPLICANT: VOGEL, JULIE M.  
; TITLE OF INVENTION: COMPOUND MICROSATELLITE  
; TITLE OF INVENTION: PRIMERS FOR THE  
; TITLE OF INVENTION: DETECTION OF GENETIC  
; TITLE OF INVENTION: POLYMORPHISMS  
; NUMBER OF SEQUENCES: 89  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND  
; ADDRESSEE: COMPANY  
; STREET: 1007 MARKET STREET  
; CITY: WILMINGTON  
; STATE: DELAWARE  
; COUNTRY: U.S.A.  
; ZIP: 19898  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: FLOPPY DISK  
; COMPUTER: IBM PC COMPATIBLE  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PATENT IN RELEASE #1.0, VERSION 1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/849,021  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/346,456  
; FILING DATE: 28 NOVEMBER 1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: FLOYD, LINDA AXAMETHY  
; REGISTRATION NUMBER: 33,692  
; REFERENCE/DOCKET NUMBER: BB-1064-A  
; TELEPHONE: 302-992-8112  
; TELEFAX: 302-992-7949  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-849-021-8

Query Match 1.4%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 68;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTG 1808  
|||  
Db 15 GTGTGTGTGTGTG 1

RESULT 75  
US-08-849-021-9  
; Sequence 9, Application US/08849021  
; Patent No. 5955276  
; GENERAL INFORMATION:  
; APPLICANT: MORGANTE, MICHELE  
; APPLICANT: VOGEL, JULIE M.



```

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PATENT IN RELEASE #1.0, VERSION 1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/849,021
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/346,456
; FILING DATE: 28 NOVEMBER 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: FLOYD, LINDA AXAMETHY
; REGISTRATION NUMBER: 33,692
; REFERENCE/DOCKET NUMBER: BB-1064-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-892-8112
; TELEFAX: 302-992-7949
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-849-021-10
;
Query Match 1.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTG 1808
Db 1 GTGTGTGTGTGTGTG 15

RESULT 77
US-08-787-321-24/c
; Sequence 24, Application US/08787321A
; Patent No. 6180777
; GENERAL INFORMATION:
; APPLICANT: Horn, Thomas
; TITLE OF INVENTION: SYNTHESIS OF BRANCHED NUCLEIC ACIDS
; FILE REFERENCE: (1300)-1199.002
; CURRENT APPLICATION NUMBER: US/08/787,321A
; CURRENT FILING DATE: 1997-01-03
; EARLIER APPLICATION NUMBER: US PROV 50/009,918
; EARLIER FILING DATE: 1996-01-12
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: oligonucleotide
US-08-787-321-24
;
Query Match 1.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTG 1808
Db 15 GTGTGTGTGTGTGTG 1

RESULT 78
US-09-081-646-733
; Sequence 733, Application US/09081646
; Patent No. 6333152
; GENERAL INFORMATION:
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Vogelstein, Bert

```

APPLICANT: Zhang, Lin  
APPLICANT: Zhou, Wei  
TITLE OF INVENTION: Gene Expression Profiles in No. 5333152mal and  
FILE REFERENCE: 01107.74664  
CURRENT APPLICATION NUMBER: US/09/081,646  
EARLIER FILING DATE: 1998-05-20  
EARLIER APPLICATION NUMBER: 60/047,352  
EARLIER FILING DATE: 1997-05-21  
NUMBER OF SEQ ID NOS: 871  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 733  
LENGTH: 15  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-081-646-733

Query Match 1.4%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 68;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2231 CATGTTTGACCTT 2245  
|||||  
Db 1 CATGTTTGACCTT 15

RESULT 79  
US-07-971-978-2  
Sequence 2, Application US/07971978  
Patent No. 5614617  
GENERAL INFORMATION:  
APPLICANT: Cook and Sanghvi  
TITLE OF INVENTION: Nuclease Resistant, Pyrimidine  
TITLE OF INVENTION: Modified Oligonucleotides that Detect and Modulate  
TITLE OF INVENTION: Gene Expression  
NUMBER OF SEQUENCES: 65  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and  
ADDRESSEE: No. 5614617ris  
STREET: One Liberty Place - 46th Floor  
CITY: Philadelphia  
STATE: PA  
COUNTRY: U.S.A.  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/971,978  
FILING DATE: February 18, 1993  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/558,806  
FILING DATE: July 27, 1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Joseph Lucci  
REGISTRATION NUMBER: 33,307  
REFERENCE/DOCKET NUMBER: ISIS-0333  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-568-3100  
TELEFAX: 215-568-3439  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 2

OTHER INFORMATION: 6-aza-thymidine substitution  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 4  
OTHER INFORMATION: 6-aza-thymidine substitution  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 6  
OTHER INFORMATION: 6-aza-thymidine substitution  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 8  
OTHER INFORMATION: 6-aza-thymidine substitution  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 10  
OTHER INFORMATION: 6-aza-thymidine substitution  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 12  
OTHER INFORMATION: 6-aza-thymidine substitution  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 14  
OTHER INFORMATION: 6-aza-thymidine substitution  
US-07-971-978-2

Query Match 1.4%; Score 15; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 74;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1813 TATATATATATAT 1827  
|||||  
Db 2 TATATATATATAT 16

RESULT 80  
US-07-971-978-2/c  
Sequence 2, Application US/07971978  
Patent No. 5614617  
GENERAL INFORMATION:  
APPLICANT: Cook and Sanghvi  
TITLE OF INVENTION: Nuclease Resistant, Pyrimidine  
TITLE OF INVENTION: Modified Oligonucleotides that Detect and Modulate  
TITLE OF INVENTION: Gene Expression  
NUMBER OF SEQUENCES: 65  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and  
ADDRESSEE: No. 5614617ris  
STREET: One Liberty Place - 46th Floor  
CITY: Philadelphia  
STATE: PA  
COUNTRY: U.S.A.  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/971,978  
FILING DATE: February 18, 1993  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/558,806  
FILING DATE: July 27, 1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Joseph Lucci  
REGISTRATION NUMBER: 33,307  
REFERENCE/DOCKET NUMBER: ISIS-0333  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-568-3100  
TELEFAX: 215-568-3439

INFORMATION FOR SEQ ID NO: 2;  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 2  
OTHER INFORMATION: 6-aza-thymidine substitution  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 4  
OTHER INFORMATION: 6-aza-thymidine substitution  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 6  
OTHER INFORMATION: 6-aza-thymidine substitution  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 8  
OTHER INFORMATION: 6-aza-thymidine substitution  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 10  
OTHER INFORMATION: 6-aza-thymidine substitution  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 12  
OTHER INFORMATION: 6-aza-thymidine substitution  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 14  
OTHER INFORMATION: 6-aza-thymidine substitution  
US-07-971-978-2

Query Match 1.4%; Score 15; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 74;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1813 TATATATATATATAT 1827  
DB 15 TATATATATATAT 1

RESULT 81  
US-09-371-772B-6068  
Sequence 6068, Application US/09371772B  
Patent No. 6566127  
GENERAL INFORMATION:  
APPLICANT: Ribozyne Pharmaceuticals, Inc.  
APPLICANT: Pavco, Pam  
APPLICANT: McSwiggen, Jim  
APPLICANT: Stinchcomb, Dan  
APPLICANT: Escobedo, Jaime  
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Relating to the Growth of Endothelial Cells  
FILE REFERENCE: MEH00,876-J (237/198)  
CURRENT FILING DATE: 1999-08-10  
PRIOR FILING DATE: 1995-10-26  
PRIOR APPLICATION NUMBER: US 60/005,974  
PRIOR FILING DATE: 1996-01-08  
NUMBER OF SEQ ID NOS: 14225  
SOFTWARE: Patent in version 3.0  
SEQ ID NO 6068  
LENGTH: 16  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-09-371-772B-6068

Query Match 1.4%; Score 15; DB 1; Length 16;  
Best Local Similarity 46.7%; Pred. No. 74;  
Matches 7; Conservative 8; Mismatches 0; Indels 0; Gaps 0;  
QY 1793 TGCTGTGTGTGTGT 1807  
DB 2 UGUGUGUGUGUGUGU 16  
RESULT 82  
US-09-371-772B-6070  
Sequence 6070, Application US/09371772B  
Patent No. 6566127  
GENERAL INFORMATION:  
APPLICANT: Ribozyne Pharmaceuticals, Inc.  
APPLICANT: Pavco, Pam  
APPLICANT: McSwiggen, Jim  
APPLICANT: Stinchcomb, Dan  
APPLICANT: Escobedo, Jaime  
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Relating to the Growth of Endothelial Cells  
FILE REFERENCE: MEH00,876-J (237/198)  
CURRENT FILING DATE: 1999-08-10  
PRIOR FILING DATE: 1995-10-26  
PRIOR APPLICATION NUMBER: US 60/005,974  
PRIOR FILING DATE: 1996-01-08  
NUMBER OF SEQ ID NOS: 14225  
SOFTWARE: Patent in version 3.0  
SEQ ID NO 6070  
LENGTH: 16  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-09-371-772B-6070

Query Match 1.4%; Score 15; DB 1; Length 16;  
Best Local Similarity 53.3%; Pred. No. 74;  
Matches 8; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGT 1808  
DB 1 GUGUGUGUGUGUGUG 15

RESULT 83  
US-08-853-998-400  
Sequence 400, Application US/08859998  
Patent No. 5994076  
GENERAL INFORMATION:  
APPLICANT: Chenchik, Alex  
APPLICANT: Jokhadze, George  
APPLICANT: Bibilashvili, Robert  
TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL EXPRESSION  
NUMBER OF SEQUENCES: 1375  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson, P.C.  
STREET: 2200 Sand Hill Road, Suite 100  
CITY: Menlo Park  
STATE: CA  
COUNTRY: US  
ZIP: 94025  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/859,998  
FILING DATE: 21-MAY-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:

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;
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Field, Bret E.
; REGISTRATION NUMBER: 37,620
; REFERENCE/DOCKET NUMBER: 09096/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-0875
; TELEFAX: 415-854-0875
; INFORMATION FOR SEQ ID NO: 400:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; OTHER INFORMATION: oligonucleotide primer
US-08-859-998-400

Query Match 1.4%; Score 15; DB 1; Length 32;
Best Local Similarity 67.7%; Pred. No. 1.5e+02;
Matches 21; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1731 GCTTGTGCGCAAGTGAATTGCTGTACAAG 1761
|||||
Db 2 GCTTGTACAGGCAAAATTCATTGCCACAAG 32

RESULT 84
US-09-225-928-400
; Sequence 400, Application US/09225928
; Patent No. 6352829
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; Jokhadze, George
; Bibilashvili, Robert
; TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
; EXPRESSION
; NUMBER OF SEQUENCES: 1375
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 2200 Sand Hill Road, Suite 100
; CITY: Menlo Park
; STATE: CA
; COUNTRY: US
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/225,928
; FILING DATE: 05-Jan-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/859,998
; FILING DATE: 21-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Field, Bret E.
; REGISTRATION NUMBER: 37,620
; REFERENCE/DOCKET NUMBER: 09096/002001
; TELEPHONE: 415-854-0875
; TELEFAX: 415-854-0875
; INFORMATION FOR SEQ ID NO: 400:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; OTHER INFORMATION: oligonucleotide primer
US-08-859-998-400

Query Match 1.4%; Score 15; DB 1; Length 32;
Best Local Similarity 67.7%; Pred. No. 1.5e+02;
Matches 21; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1731 GCTTGTGCGCAAGTGAATTGCTGTACAAG 1761
|||||
Db 2 GCTTGTACAGGCAAAATTCATTGCCACAAG 32

RESULT 85
US-09-225-201B-400
; Sequence 400, Application US/09225201B
; Patent No. 8489455
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; Jokhadze, George
; Bibilashvili, Robert
; TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
; EXPRESSION
; NUMBER OF SEQUENCES: 1375
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 2200 Sand Hill Road, Suite 100
; CITY: Menlo Park
; STATE: CA
; COUNTRY: US
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/225,201B
; FILING DATE: 05-Jan-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/859,998
; FILING DATE: 21-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Field, Bret E.
; REGISTRATION NUMBER: 37,620
; REFERENCE/DOCKET NUMBER: 09096/002001
; TELEPHONE: 415-322-5070
; TELEFAX: 415-854-0875
; INFORMATION FOR SEQ ID NO: 400:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; OTHER INFORMATION: oligonucleotide primer
US-09-225-201B-400

Query Match 1.4%; Score 15; DB 1; Length 32;
Best Local Similarity 67.7%; Pred. No. 1.5e+02;
Matches 21; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1731 GCTTGTGCGCAAGTGAATTGCTGTACAAG 1761
|||||
Db 2 GCTTGTACAGGCAAAATTCATTGCCACAAG 32

RESULT 86
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; FEATURE:
; OTHER INFORMATION: oligonucleotide primer
; SEQUENCE DESCRIPTION: SEQ ID NO: 400:
US-09-225-928-400

Query Match 1.4%; Score 15; DB 1; Length 32;
Best Local Similarity 67.7%; Pred. No. 1.5e+02;
Matches 21; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1731 GCTTGTGCGCAAGTGAATTGCTGTACAAG 1761
|||||
Db 2 GCTTGTACAGGCAAAATTCATTGCCACAAG 32

RESULT 85
US-09-225-201B-400
; Sequence 400, Application US/09225201B
; Patent No. 8489455
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; Jokhadze, George
; Bibilashvili, Robert
; TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
; EXPRESSION
; NUMBER OF SEQUENCES: 1375
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 2200 Sand Hill Road, Suite 100
; CITY: Menlo Park
; STATE: CA
; COUNTRY: US
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/225,201B
; FILING DATE: 05-Jan-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/859,998
; FILING DATE: 21-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Field, Bret E.
; REGISTRATION NUMBER: 37,620
; REFERENCE/DOCKET NUMBER: 09096/002001
; TELEPHONE: 415-322-5070
; TELEFAX: 415-854-0875
; INFORMATION FOR SEQ ID NO: 400:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; OTHER INFORMATION: oligonucleotide primer
US-09-225-201B-400

Query Match 1.4%; Score 15; DB 1; Length 32;
Best Local Similarity 67.7%; Pred. No. 1.5e+02;
Matches 21; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1731 GCTTGTGCGCAAGTGAATTGCTGTACAAG 1761
|||||
Db 2 GCTTGTACAGGCAAAATTCATTGCCACAAG 32

RESULT 86
```

US-09-344-520-40/c  
; Sequence 40, Application US/09344520  
; Patent No. 6037176  
; GENERAL INFORMATION:  
; APPLICANT: Frank Bennett  
; APPLICANT: Brett P. Monia  
; APPLICANT: Lex M. Cowser  
; TITLE OF INVENTION: ANTISENSE MODULATION OF integrin beta 3 EXPRESSION  
; FILE REFERENCE: RTS-0070  
; CURRENT APPLICATION NUMBER: US/09/344,520  
; CURRENT FILING DATE: 1999-06-25  
; NUMBER OF SEQ ID NOS: 47  
; SEQ ID NO 40  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-09-344-520-40

Query Match 1.4%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 91;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1794 GTGTGTGTGTGTGTGTGT 1811  
Db 18 GTGTGTGTGTGTGTGTGT 1

RESULT 87  
US-08-153-051B-58  
; Sequence 58, Application US/08153051B  
; Patent No. 5645986  
; GENERAL INFORMATION:  
; APPLICANT: Michael D. West  
; APPLICANT: Jerry W. Shay  
; APPLICANT: Woodring E. Wright  
; APPLICANT: Elizabeth Blackburn  
; APPLICANT: Nam Woo Kim  
; APPLICANT: Calvin B. Harley  
; APPLICANT: Scott L. Weinrich  
; APPLICANT: Catherine Strahl  
; APPLICANT: Michael J. McEachern  
; APPLICANT: Homayoun Vaziri  
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF  
; TITLE OF INVENTION: CONDITIONS RELATED TO TELOMERE  
; TITLE OF INVENTION: LENGTH AND/OR TELOMERASE ACTIVITY  
; NUMBER OF SEQUENCES: 58  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 MB  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/153,051B  
; FILING DATE: No. 5645986ember 12, 1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/038,766  
; FILING DATE: March 24, 1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 204/195  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 955-0440  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 58:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-153-051B-58

TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 58:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-153-051B-58  
Query Match 1.4%; Score 14.4; DB 1; Length 16;  
Best Local Similarity 93.8%; Pred. No. 87;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1793 TGTGTGTGTGTGTGTGT 1808  
Db 1 TGGGTGTGTGTGTGTGT 16  
RESULT 88  
US-08-060-952C-57  
; Sequence 57, Application US/08060952C  
; Patent No. 5695932  
; GENERAL INFORMATION:  
; APPLICANT: Michael D. West  
; APPLICANT: Jerry W. Shay  
; APPLICANT: Woodring E. Wright  
; APPLICANT: Elizabeth Blackburn  
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF CONDITIONS  
; TITLE OF INVENTION: RELATED TO TELOMERE LENGTH AND/OR  
; TITLE OF INVENTION: TELOMERASE ACTIVITY  
; NUMBER OF SEQUENCES: 57  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/060,952C  
; FILING DATE: May 13, 1993  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/882,438  
; FILING DATE: May 13, 1992  
; APPLICATION NUMBER: 08/038,766  
; FILING DATE: March 24, 1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard J.  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 202/045  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 57:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-060-952C-57  
Query Match 1.4%; Score 14.4; DB 1; Length 16;

Best Local Similarity 93.8%; Pred. No. 87;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTG 1808  
Db 1 TGGGTGTGTGTGTG 16

RESULT 89  
US-08-151-477A-58  
; Sequence 58, Application US/08151477A  
; Patent No. 5830644  
; GENERAL INFORMATION:  
; APPLICANT: Michael D. West  
; APPLICANT: Jerry W. Shay  
; APPLICANT: Woodring E. Wright  
; APPLICANT: Elizabeth Blackburn  
; APPLICANT: Nam Woo Kim  
; APPLICANT: Calvin B. Harley  
; APPLICANT: Scott L. Weinrich  
; APPLICANT: Catherine Strahl  
; APPLICANT: Michael J. McEachern  
; APPLICANT: Homayoun Vaziri  
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF  
; TITLE OF INVENTION: CONDITIONS RELATED TO TELOMERE  
; TITLE OF INVENTION: LENGTH AND/OR TELOMERASE ACTIVITY  
; NUMBER OF SEQUENCES: 58  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071

COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: FastSEQ Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/151,477A  
; FILING DATE: March 24, 1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/038,766  
; FILING DATE: March 24, 1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 202/189  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 58:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear

US-08-151-477A-58  
Query Match 1.4%; Score 14.4; DB 1; Length 16;  
Best Local Similarity 93.8%; Pred. No. 87;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTG 1808  
Db 1 TGGGTGTGTGTGTG 16

RESULT 90  
US-08-151-477A-58  
; Sequence 58, Application US/08151477A  
; Patent No. 5830644  
; GENERAL INFORMATION:  
; APPLICANT: Michael D. West  
; APPLICANT: Jerry W. Shay  
; APPLICANT: Woodring E. Wright  
; APPLICANT: Elizabeth Blackburn  
; APPLICANT: Nam Woo Kim  
; APPLICANT: Calvin B. Harley  
; APPLICANT: Scott L. Weinrich  
; APPLICANT: Catherine Strahl  
; APPLICANT: Michael J. McEachern  
; APPLICANT: Homayoun Vaziri  
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF  
; TITLE OF INVENTION: CONDITIONS RELATED TO TELOMERE  
; TITLE OF INVENTION: LENGTH AND/OR TELOMERASE ACTIVITY  
; NUMBER OF SEQUENCES: 58  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071

COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: FastSEQ Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/151,477A  
; FILING DATE: March 24, 1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/038,766  
; FILING DATE: March 24, 1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 202/189  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 58:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear

US-08-151-477A-58  
Query Match 1.4%; Score 14.4; DB 1; Length 16;  
Best Local Similarity 93.8%; Pred. No. 87;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTG 1808  
Db 1 TGGGTGTGTGTGTG 16

RESULT 91  
US-08-464-011B-57  
; Sequence 57, Application US/08464011B  
; Patent No. 6368789  
; GENERAL INFORMATION:  
; APPLICANT: Michael D. West

US-08-819-867-80  
; Sequence 80, Application US/08819867  
; Patent No. 6007989  
; GENERAL INFORMATION:  
; APPLICANT: Michael D. West  
; APPLICANT: Calvin B. Harley  
; APPLICANT: Scott L. Weinrich  
; APPLICANT: Catherine M. Strahl  
; APPLICANT: Michael J. McEachern  
; APPLICANT: Jerry Shay  
; APPLICANT: Woodring E. Wright  
; APPLICANT: Elizabeth H. Blackburn  
; APPLICANT: Nam Woo Kim  
; APPLICANT: Homayoun Vaziri  
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF  
; TITLE OF INVENTION: CONDITIONS RELATED TO  
; TITLE OF INVENTION: TELOMERE LENGTH AND/OR  
; TITLE OF INVENTION: TELOMERASE ACTIVITY  
; NUMBER OF SEQUENCES: 80  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066

COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: FastSEQ for Windows 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/819,867  
; FILING DATE: March 14, 1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/153,051  
; FILING DATE: NO. 6007989ember 12, 1993  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Chambers, Daniel M.  
; REGISTRATION NUMBER: 34,561  
; REFERENCE/DOCKET NUMBER: 224/232  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 80:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear

US-08-819-867-80  
Query Match 1.4%; Score 14.4; DB 1; Length 16;  
Best Local Similarity 93.8%; Pred. No. 87;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTG 1808  
Db 1 TGGGTGTGTGTGTG 16

RESULT 91  
US-08-464-011B-57  
; Sequence 57, Application US/08464011B  
; Patent No. 6368789  
; GENERAL INFORMATION:  
; APPLICANT: Michael D. West

Jerry W. Shay  
Woodring E. Wright  
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF CONDITIONS  
RELATED TO TELOMERE LENGTH AND/OR  
TELOMERASE ACTIVITY  
NUMBER OF SEQUENCES: 61  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
SUITE: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/464,011B  
FILING DATE: 05-Jun-1995  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/882,438  
FILING DATE: May 13, 1992  
APPLICATION NUMBER: 08/038,766  
FILING DATE: March 24, 1993  
APPLICATION NUMBER: 08/060,952  
FILING DATE: May 13, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 202/045  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 57:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 57:  
US-08-464-011B-57  
Query Match 1.4%; Score 14.4; DB 1; Length 16;  
Best Local Similarity 93.8%; Pred. No. 87;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1793 TGTGTGTGTGTGTGTG 1808  
DB 1 TGGGTGTGTGTGTGTG 16  
RESULT 92  
US-09-378-535-80  
Sequence 6071, Application US/09378535  
Patent No. 6551774  
GENERAL INFORMATION:  
APPLICANT: Michael D. West  
Calvin B. Harley  
Scott L. Wehrich  
Catherine M. Strahl  
Michael J. McEachern  
Jerry Shay  
Woodring E. Wright  
Elizabeth H. Blackburn  
Nam Woo Kim  
Homayoun Vaziri  
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF

CONDITIONS RELATED TO  
TELOMERE LENGTH AND/OR  
TELOMERASE ACTIVITY  
NUMBER OF SEQUENCES: 80  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
SUITE: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq for Windows 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/378,535  
FILING DATE: 20-Aug-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/819,867  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Chambers, Daniel M.  
REGISTRATION NUMBER: 34,561  
REFERENCE/DOCKET NUMBER: 224/232  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 80:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 80:  
US-09-378-535-80  
Query Match 1.4%; Score 14.4; DB 1; Length 16;  
Best Local Similarity 93.8%; Pred. No. 87;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1793 TGTGTGTGTGTGTGTG 1808  
DB 1 TGGGTGTGTGTGTGTG 16  
RESULT 93  
US-09-371-772B-6071  
Sequence 6071, Application US/09371772B  
Patent No. 6566127  
GENERAL INFORMATION:  
APPLICANT: Ribozyne Pharmaceuticals, Inc.  
APPLICANT: Pavco, Pam  
APPLICANT: McSwiggen, Jim  
APPLICANT: Stinchcomb, Dan  
APPLICANT: Escobedo, Jaime  
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel  
ated to Vascular Endothelial Growth Factor Receptor  
FILE REFERENCE: MEH00,876-J (237/198)  
CURRENT APPLICATION NUMBER: US/09/371,772B  
CURRENT FILING DATE: 1999-08-10  
PRIOR APPLICATION NUMBER: US 60/005,974  
PRIOR FILING DATE: 1995-10-26  
PRIOR APPLICATION NUMBER: US 08/584,040  
PRIOR FILING DATE: 1996-01-08  
NUMBER OF SEQ ID NOS: 14225  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 6071

APPLICANT:	Draper, Kenneth	APPLICANT:	McSwiggen, James
TITLE OF INVENTION:	TREATMENT OF RESTENOSIS AND CANCER USING RIBOZYMES	TITLE OF INVENTION:	GENETICALLY ENGINEERED VACCINE
TITLE OF INVENTION:	TREATMENT OF RESTENOSIS AND CANCER USING RIBOZYMES	TITLE OF INVENTION:	GENETICALLY ENGINEERED VACCINE
NUMBER OF SEQUENCES:	2627	NUMBER OF SEQUENCES:	462
CORRESPONDENCE ADDRESS:	2627	CORRESPONDENCE ADDRESS:	462
ADDRESSEE:	Lyon & Lyon	ADDRESSEE:	Curtis, Morris & Safford
STREET:	633 West Fifth Street	STREET:	c/o William S. Frommer
CITY:	Los Angeles	CITY:	530 Fifth Avenue
STATE:	California	STATE:	New York
COUNTRY:	U.S.A.	COUNTRY:	NY
ZIP:	90071	ZIP:	10036
COMPUTER READABLE FORM:	3.5" Diskette, 1.44 MB	COMPUTER READABLE FORM:	Floppy disk
MEDIUM TYPE:	storage	MEDIUM TYPE:	IBM PC compatible
COMPUTER:	IBM Compatible	COMPUTER:	IBM PC compatible
OPERATING SYSTEM:	IBM P.C. DOS 5.0	OPERATING SYSTEM:	PC-DOS/MS-DOS
SOFTWARE:	Word Perfect 5.1	SOFTWARE:	Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:		CURRENT APPLICATION DATA:	
APPLICATION NUMBER:	US/08/373,124A	APPLICATION NUMBER:	US/08/105,483
FILING DATE:	January 13, 1995	FILING DATE:	12-AUG-1993
PRIOR APPLICATION NUMBER:	08/245,466	PRIOR APPLICATION NUMBER:	424
APPLICATION NUMBER:	08/192,943	APPLICATION NUMBER:	US 07/847,951
FILING DATE:	May 18, 1994	FILING DATE:	08-MAR-1992
APPLICATION NUMBER:	07/987,132	APPLICATION NUMBER:	25,506
FILING DATE:	December 7, 1992	APPLICATION NUMBER:	454310-2400
APPLICATION NUMBER:	07/936,422	APPLICATION NUMBER:	454310-2400
FILING DATE:	August 26, 1992	APPLICATION NUMBER:	454310-2400
ATTORNEY/AGENT INFORMATION:		ATTORNEY/AGENT INFORMATION:	
NAME:	Warburg, Richard	NAME:	Frommer, William S.
REGISTRATION NUMBER:	32,327	REGISTRATION NUMBER:	25,506
REFERENCE/DOCKET NUMBER:	209/035	REFERENCE/DOCKET NUMBER:	454310-2400
TELECOMMUNICATION INFORMATION:		TELECOMMUNICATION INFORMATION:	
TELEPHONE:	(213) 489-1600	TELEPHONE:	(212) 840-3333
TELEFAX:	(213) 955-0440	TELEFAX:	(212) 840-0712
TELEX:	67-3510	TELEX:	840-0712
INFORMATION FOR SEQ ID NO:	1058:	INFORMATION FOR SEQ ID NO:	235:
SEQUENCE CHARACTERISTICS:		SEQUENCE CHARACTERISTICS:	
LENGTH:	17 base pairs	LENGTH:	17 base pairs
TYPE:	nucleic acid	TYPE:	nucleic acid
STRANDEDNESS:	single	STRANDEDNESS:	single
TOPOLOGY:	linear	TOPOLOGY:	linear
US-08-373-124A-1058		US-08-105-483-235	
Query Match	1.4%; Score 14.4; DB 1; Length 17;	Query Match	1.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity	93.8%; Pred. No. 94;	Best Local Similarity	93.8%; Pred. No. 94;
Matches	15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	Matches	15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	1811 TGTATATATATATATA 1826	QY	1777 TTTATATTGTAATAT 1792
Db	17 TGTATATATATATAA 2	Db	1 TTTATATTGTAATAT 16
RESULT 96		RESULT 95	
US-08-709-209-235		US-08-373-124A-1058/c	
Sequence 235, Application US/08709209		Sequence 1058, Application US/08373124A	
Patent No. 5762938		Patent No. 5646042	
GENERAL INFORMATION:		GENERAL INFORMATION:	
APPLICANT:	Paolotti, Enzo	APPLICANT:	Stinchcomb, Dan T.
TITLE OF INVENTION:	GENETICALLY ENGINEERED VACCINE	TITLE OF INVENTION:	STRAIN
TITLE OF INVENTION:	STRAIN	TITLE OF INVENTION:	STRAIN
NUMBER OF SEQUENCES:	462	NUMBER OF SEQUENCES:	462
CORRESPONDENCE ADDRESS:		CORRESPONDENCE ADDRESS:	
ADDRESSEE:	Curtis, Morris & Safford	ADDRESSEE:	Curtis, Morris & Safford
STREET:	530 Fifth Avenue	STREET:	530 Fifth Avenue
CITY:	New York	CITY:	New York
STATE:	NY	STATE:	NY
COUNTRY:	USA	COUNTRY:	USA
ZIP:	10036	ZIP:	10036
COMPUTER READABLE FORM:		COMPUTER READABLE FORM:	
MEDIUM TYPE:	Floppy disk	MEDIUM TYPE:	Floppy disk
COMPUTER:	IBM PC compatible	COMPUTER:	IBM PC compatible
OPERATING SYSTEM:	PC-DOS/MS-DOS	OPERATING SYSTEM:	PC-DOS/MS-DOS
SOFTWARE:	Patent in Release #1.0, Version #1.25	SOFTWARE:	Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:		CURRENT APPLICATION DATA:	
APPLICATION NUMBER:	US/08/105,483	APPLICATION NUMBER:	US/08/105,483
FILING DATE:	12-AUG-1993	FILING DATE:	12-AUG-1993
CLASSIFICATION:	424	CLASSIFICATION:	424
PRIOR APPLICATION DATA:		PRIOR APPLICATION DATA:	
APPLICATION NUMBER:	US 07/847,951	APPLICATION NUMBER:	US 07/847,951
FILING DATE:	08-MAR-1992	FILING DATE:	08-MAR-1992
ATTORNEY/AGENT INFORMATION:		ATTORNEY/AGENT INFORMATION:	
NAME:	Frommer, William S.	NAME:	Frommer, William S.
REGISTRATION NUMBER:	25,506	REGISTRATION NUMBER:	25,506
REFERENCE/DOCKET NUMBER:	454310-2400	REFERENCE/DOCKET NUMBER:	454310-2400
TELECOMMUNICATION INFORMATION:		TELECOMMUNICATION INFORMATION:	
TELEPHONE:	(212) 840-3333	TELEPHONE:	(212) 840-3333
TELEFAX:	(212) 840-0712	TELEFAX:	(212) 840-0712
INFORMATION FOR SEQ ID NO:	235:	INFORMATION FOR SEQ ID NO:	



COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/709,209  
FILING DATE: 21-AUG-1996  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/105,483  
FILING DATE: 12-AUG-1993  
APPLICATION NUMBER: US 07/847,951  
FILING DATE: 06-MAR-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Frommer, William S.  
REGISTRATION NUMBER: 25,506  
REFERENCE/DOCKET NUMBER: 454310-2400  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 840-3333  
TELEFAX: (212) 840-0712  
INFORMATION FOR SEQ ID NO: 235:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-709-209-235

Query Match 1.4%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 94;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1777 TTTATATTGTAATAT 1792  
|||||  
Db 1 TTTATATTGTAATAT 16

RESULT 97  
US-08-458-101-235  
Sequence 235, Application US/08458101  
Patent No. 5766599  
GENERAL INFORMATION:  
APPLICANT: Paolletti, Enzo  
APPLICANT: Perkus, Marion E.  
APPLICANT: Taylor, Jill  
APPLICANT: Tartaglia, James  
APPLICANT: No. 5766599ton, Elizabeth K.  
APPLICANT: Riviere, Michel  
APPLICANT: de Taisne, Charles  
APPLICANT: Limbach, Keith J.  
APPLICANT: Johnson, Gerard P.  
APPLICANT: Pincus, Steven E.  
APPLICANT: Cox, William I.  
APPLICANT: Audonnet, Jean-Christophe Francis  
APPLICANT: Gettig, Russell Robert  
TITLE OF INVENTION: GENETICALLY ENGINEERED VACCINE  
NUMBER OF SEQUENCES: 467  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Curtis, Morris & Safford  
ADDRESSEE: c/o William S. Frommer  
STREET: 530 Fifth Avenue  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/458,101  
FILING DATE: 01-JUN-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Frommer, William S.  
REGISTRATION NUMBER: 25,506  
REFERENCE/DOCKET NUMBER: 454310-2740  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 840-3333  
TELEFAX: (212) 840-0712  
INFORMATION FOR SEQ ID NO: 235:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-458-101-235

Query Match 1.4%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 94;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1777 TTTATATTGTAATAT 1792  
|||||  
Db 1 TTTATATTGTAATAT 16

RESULT 98  
US-08-435-628-1058/c  
Sequence 1058, Application US/08435628  
Patent No. 5817796  
GENERAL INFORMATION:  
APPLICANT: Stinchcomb, Dan T.  
APPLICANT: Draper, Kenneth  
APPLICANT: McSwiggen, James  
APPLICANT: Jarvis, Thale  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR  
TREATMENT OF RESTENOSIS AND  
CANCER USING RIBOZYMES  
NUMBER OF SEQUENCES: 2627  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/435,628  
FILING DATE: 05-MAY-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/373,124  
FILING DATE: January 13, 1995  
APPLICATION NUMBER: 08/245,466  
FILING DATE: May 18, 1994  
APPLICATION NUMBER: 08/192,943  
FILING DATE: February 7, 1994  
APPLICATION NUMBER: 07/987,132  
FILING DATE: December 7, 1992  
APPLICATION NUMBER: 07/936,422  
FILING DATE: August 26, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard

```

; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 209/035
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1058:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-435-628-1058

Query Match 1.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 94;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1811 TGTATATATATATATA 1826
Db 17 TGTATATATATATAA 2

RESULT 99
US-08-486-969-52
; Sequence 52, Application US/08486969
; Patent No. 5843456
; GENERAL INFORMATION:
; APPLICANT: Paoletti, Enzo
; APPLICANT: Maki, Joanne
; TITLE OF INVENTION: RECOMBINANT POXVIRUS - RABIES
; TITLE OF INVENTION: COMPOSITIONS AND COMBINATION COMPOSITIONS AND USES
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford, P.C.
; STREET: 530 Fifth Avenue, 25th Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,969
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454310-2600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-486-969-52

Query Match 1.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 94;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1777 TTTATATTGTAATAT 1792
Db 1 TTTATATTGTAATAT 16
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```

RESULT 100
US-08-584-040-4159
; Sequence 4159, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 4159:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-584-040-4159

Query Match 1.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 75.0%; Pred. No. 94;
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1749 TGCTGTAAACGA 1764
Db 2 UGCCUGAACCAAGCA 17

RESULT 101
US-09-321-005A-i3/c
; Sequence 13, Application US/09321005A
; Patent No. 6503710
; GENERAL INFORMATION:
; APPLICANT: Gut, Ivo
; TITLE OF INVENTION: Mutation Analysis Using Mass Spectrometry
; FILE REFERENCE: B0004/7065
; CURRENT APPLICATION NUMBER: US/09/321,005A
; CURRENT FILING DATE: 1999-05-27
; NUMBER OF SEQ ID NOS: 17
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; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Hypothetical Sequence for Exemplary Purposes
; Patent No. 6503710
US-09-321-005A-13
```

```
Query Match 1.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 94;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 1891 ATATTTCATGTTAGC 1906
|||:|||||
Db 16 ATATTTCATGTCAGC 1
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RESULT 102
US-09-371-772B-1926
; Sequence 1926, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MEH800.876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1926
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-1926
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Query Match 1.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 75.0%; Pred. No. 94;
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
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QY 1749 TGCTGTAAACAGCCA 1764
|||:|||||
Db 2 UGCCUGUACCAAGCCA 17
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RESULT 103
US-09-371-772B-6656
; Sequence 6656, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MEH800.876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
```

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; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6656
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-6656
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```
Query Match 1.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 94;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1750 GCTGTAAACAGCCA 1765
|||:|||||
Db 1 GCCUGUACCAAGCCA 16
```

```
RESULT 104
US-09-496-694B-235
; Sequence 235, Application US/09496694B
; Patent No. 6335194
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Elizabeth J. Ackermann
; APPLICANT: Eric S. Swayze
; APPLICANT: Lex M. Cowbert
; TITLE OF INVENTION: ANTISENSE MODULATION OF SURVIVIN EXPRESSION
; FILE REFERENCE: ISPH-0439
; CURRENT APPLICATION NUMBER: US/09/496,694B
; CURRENT FILING DATE: 2000-02-02
; PRIOR APPLICATION NUMBER: 09/286,407
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: 09/163,162
; PRIOR FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 249
; SEQ ID NO 235
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-496-694B-235
```

```
Query Match 1.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1814 ATATATATATATGTACA 1832
|||:|||||
Db 1 ACATATATATATAACA 19
```

```
RESULT 105
US-08-222-177A-436/C
; Sequence 436, Application US/08222177A
; Patent No. 5582379
; GENERAL INFORMATION:
; APPLICANT: Weber, James L.
; TITLE OF INVENTION: LENGTH POLYMORPHISMS IN
; TITLE OF INVENTION: (dC-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING SAME
; NUMBER OF SEQUENCES: 460
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dewitt Ross & Stevens, S.C.
; STREET: 8000 Excelsior Drive, Suite 401
; CITY: Madison
; STATE: Wisconsin
; COUNTRY: USA
; ZIP: 53717-1914
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
```

SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/222,177A  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION NUMBER: US 07/341,562  
FILING DATE: 21-APR-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Sara, Charles S.  
REGISTRATION NUMBER: 30,492  
REFERENCE/DOCKET NUMBER: 09865.601  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (608) 831-2100  
TELEFAX: (608) 831-2106  
TELEX:  
INFORMATION FOR SEQ ID NO: 436:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-222-177A-436

Query Match 1.3%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 81;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGT 1807

DB 14 GTGTGTGTGTGT 1

RESULT 106  
US-09-913-514-27  
Sequence 27, Application US/09913514  
Patent No. 6653069  
GENERAL INFORMATION:  
APPLICANT: GOMI, Yasuyuki  
APPLICANT: SUNAMACHI, Hiroki  
APPLICANT: TAKAHASHI, Michiaki  
APPLICANT: YAMANISHI, Koichi  
TITLE OF INVENTION: Method for Quality Control of an Attenuated Varicella Live Vaccine  
FILE REFERENCE: 0216-0454P  
CURRENT FILING DATE: 2001-12-07  
PRIOR APPLICATION NUMBER: PCT/JP01/00678  
PRIOR FILING DATE: 2001-01-31  
PRIOR APPLICATION NUMBER: JP 2000-62734  
PRIOR FILING DATE: 2000-01-31  
NUMBER OF SEQ ID NOS: 42  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 27  
LENGTH: 14  
TYPE: DNA  
ORGANISM: Varicella virus  
US-09-913-514-27

Query Match 1.3%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 81;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1813 TATATATATATATA 1826

DB 1 TATATATATATATA 14

RESULT 107  
US-09-913-514-27/c  
Sequence 27, Application US/09913514  
Patent No. 6653069  
GENERAL INFORMATION:

APPLICANT: GOMI, Yasuyuki  
APPLICANT: SUNAMACHI, Hiroki  
APPLICANT: TAKAHASHI, Michiaki  
APPLICANT: YAMANISHI, Koichi  
TITLE OF INVENTION: Method for Quality Control of an Attenuated Varicella Live Vaccine  
FILE REFERENCE: 0216-0454P  
CURRENT APPLICATION NUMBER: US/09/913,514  
CURRENT FILING DATE: 2001-12-07  
PRIOR APPLICATION NUMBER: PCT/JP01/00678  
PRIOR FILING DATE: 2001-01-31  
PRIOR APPLICATION NUMBER: JP 2000-62734  
PRIOR FILING DATE: 2000-01-31  
NUMBER OF SEQ ID NOS: 42  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 27  
LENGTH: 14  
TYPE: DNA  
ORGANISM: Varicella virus  
US-09-913-514-27

Query Match 1.3%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 81;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1813 TATATATATATATA 1826

DB 14 TATATATATATATA 1

RESULT 108  
PCT-US92-00282-27  
Sequence 27, Application PC/TUS9200282  
GENERAL INFORMATION:  
APPLICANT: OWENS, IDA S.  
APPLICANT: RITTER, JOSEPH K.  
TITLE OF INVENTION: THE GENETIC LOCUS UGT1 AND A MUTATION THEREIN.  
NUMBER OF SEQUENCES: 40  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CUSHMAN DABY & CUSHMAN  
STREET: 1615 L STREET, N.W.  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20036-5601  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/00282  
FILING DATE: 19920110  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: SCOTT, WATSON T.  
REGISTRATION NUMBER: 26581  
REFERENCE/DOCKET NUMBER: 91532-PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-861-3000  
TELEFAX: 202-822-0944  
TELEX: 6714627 CUSH  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
PCT-US92-00282-27

Query Match 1.3%; Score 14; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 89;

```
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1813 TATATATATATATA 1826
Db 1 TATATATATATATA 14

RESULT 109
PCT-US92-00282-27/c
; Sequence 27, Application PC/TUS9200282
; GENERAL INFORMATION:
; APPLICANT: OWENS, IDA S.
; APPLICANT: RITTER, JOSEPH K.
; TITLE OF INVENTION: THE GENETIC LOCUS UGT1 AND A MUTATION
; TITLE OF INVENTION: THEREIN.
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARBAY & CUSHMAN
; STREET: 1615 L STREET, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20036-5601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/00282
; FILING DATE: 19920110
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: SCOTT, WATSON T.
; REGISTRATION NUMBER: 26581
; REFERENCE/DOCKET NUMBER: 91532-PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
PCT-US92-00282-27

Query Match 1.3%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1813 TATATATATATATA 1826
Db 14 TATATATATATATA 1

RESULT 110
US-09-479-005A-336
; Sequence 336, Application US/09479005A
; Patent No. 6656731
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity
; FILE REFERENCE: MEH000-884-C
; CURRENT APPLICATION NUMBER: US/09/479,005A
; CURRENT FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/444,209
; PRIOR FILING DATE: 1999-11-19
; PRIOR APPLICATION NUMBER: US 09/159,274
; PRIOR FILING DATE: 1998-09-22
; PRIOR APPLICATION NUMBER: US 60/059,473
```

```
; PRIOR FILING DATE: 1997-09-22
; NUMBER OF SEQ ID NOS: 1208
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 336
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-479-005A-336

Query Match 1.3%; Score 14; DB 1; Length 16;
Best Local Similarity 71.4%; Pred. No. 96;
Matches 10; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 1392 GTTAAGACTTGACA 1405
Db 1 GUUAGACUUGACA 14

RESULT 111
US-08-373-124A-1060/c
; Sequence 1060, Application US/08373124A
; Patent No. 5646042
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth
; APPLICANT: McSwiggen, James
; APPLICANT: Jarvis, Thale
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
; TITLE OF INVENTION: CANCER USING RIBOZYMES
; NUMBER OF SEQUENCES: 2627
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/373,124A
; FILING DATE: January 13, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/245,466
; FILING DATE: May 18, 1994
; APPLICATION NUMBER: 08/192,943
; FILING DATE: February 7, 1994
; APPLICATION NUMBER: 07/987,132
; FILING DATE: December 7, 1992
; APPLICATION NUMBER: 07/936,422
; FILING DATE: August 26, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 209/035
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1060:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-373-124A-1060
```

Query Match 1.3%; Score 14; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1811 TGTATATATATATA 1824  
DB 15 TGTATATATATATA 2

RESULT 112  
US-08-373-124A-1855  
; Sequence 1855, Application US/08373124A  
; Patent No. 5646042  
; GENERAL INFORMATION:  
; APPLICANT: Stinchcomb, Dan T.  
; APPLICANT: Draper, Kenneth  
; APPLICANT: McSwiggen, James  
; APPLICANT: Jarvis, Thale  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR  
; TREATMENT OF RESTENOSIS AND  
; CANCER USING RIBOZYMES  
; NUMBER OF SEQUENCES: 2627  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/373,124A  
; FILING DATE: January 13, 1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/245,466  
; FILING DATE: May 18, 1994  
; APPLICATION NUMBER: 08/192,943  
; FILING DATE: February 7, 1994  
; APPLICATION NUMBER: 07/987,132  
; FILING DATE: December 7, 1992  
; APPLICATION NUMBER: 07/936,422  
; FILING DATE: August 26, 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 209/035  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 1855:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-373-124A-1855

Query Match 1.3%; Score 14; DB 1; Length 17;  
Best Local Similarity 57.1%; Pred. No. 1e+02;  
Matches 8; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1763 CAGATTTTAAAAA 1776  
DB 4 CAGAUUUUUAAAA 17

RESULT 113  
US-08-373-124A-1857  
; Sequence 1857, Application US/08373124A  
; Patent No. 5646042  
; GENERAL INFORMATION:  
; APPLICANT: Stinchcomb, Dan T.  
; APPLICANT: Draper, Kenneth  
; APPLICANT: McSwiggen, James  
; APPLICANT: Jarvis, Thale  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR  
; TREATMENT OF RESTENOSIS AND  
; CANCER USING RIBOZYMES  
; NUMBER OF SEQUENCES: 2627  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/373,124A  
; FILING DATE: January 13, 1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/245,466  
; FILING DATE: May 18, 1994  
; APPLICATION NUMBER: 08/192,943  
; FILING DATE: February 7, 1994  
; APPLICATION NUMBER: 07/987,132  
; FILING DATE: December 7, 1992  
; APPLICATION NUMBER: 07/936,422  
; FILING DATE: August 26, 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 209/035  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 1857:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-373-124A-1857

Query Match 1.3%; Score 14; DB 1; Length 17;  
Best Local Similarity 57.1%; Pred. No. 1e+02;  
Matches 8; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1763 CAGATTTTAAAAA 1776  
DB 3 CAGAUUUUUAAAA 16

RESULT 114  
US-08-373-124A-1859  
; Sequence 1859, Application US/08373124A  
; Patent No. 5646042  
; GENERAL INFORMATION:  
; APPLICANT: Stinchcomb, Dan T.  
; APPLICANT: Draper, Kenneth  
; APPLICANT: McSwiggen, James  
; APPLICANT: Jarvis, Thale

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR  
TREATMENT OF RESTENOSIS AND  
CANCER USING RIBOZYMES  
NUMBER OF SEQUENCES: 2627  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage

COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/373,124A  
FILING DATE: January 13, 1995

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/245,466

FILING DATE: May 18, 1994

APPLICATION NUMBER: 08/192,943

FILING DATE: February 7, 1994

APPLICATION NUMBER: 07/987,132

FILING DATE: December 7, 1992

APPLICATION NUMBER: 07/936,422

FILING DATE: August 26, 1992

ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 209/035

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 1859:

SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-373-124A-1859

Query Match 1.3%; Score 14; DB 1; Length 17;  
Best Local Similarity 57.1%; Pred. No. 1e-02;  
Matches 8; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1763 CAGATTTTAAAA 1776  
|||||:|||||  
Db 2 CAGAUUUUUAAAA 15

RESULT 115  
US-08-373-124A-1861

Sequence 1861, Application US/08373124A  
Patent No. 5646042

GENERAL INFORMATION:  
APPLICANT: Stinchcomb, Dan T.

APPLICANT: Draper, Kenneth

APPLICANT: McSwiggen, James

APPLICANT: Jarvis, Thale

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR  
TREATMENT OF RESTENOSIS AND

CANCER USING RIBOZYMES  
NUMBER OF SEQUENCES: 2627

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Los Angeles

STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage

COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/373,124A  
FILING DATE: January 13, 1995

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/245,466

FILING DATE: May 18, 1994

APPLICATION NUMBER: 08/192,943

FILING DATE: February 7, 1994

APPLICATION NUMBER: 07/987,132

FILING DATE: December 7, 1992

APPLICATION NUMBER: 07/936,422

FILING DATE: August 26, 1992

ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 209/035

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 1861:

SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-373-124A-1861

Query Match 1.3%; Score 14; DB 1; Length 17;  
Best Local Similarity 57.1%; Pred. No. 1e-02;  
Matches 8; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1763 CAGATTTTAAAA 1776  
|||||:|||||  
Db 1 CAGAUUUUUAAAA 14

RESULT 116  
US-08-435-628-1060/c

Sequence 1060, Application US/08435628  
Patent No. 5817796

GENERAL INFORMATION:  
APPLICANT: Stinchcomb, Dan T.

APPLICANT: Draper, Kenneth

APPLICANT: McSwiggen, James

APPLICANT: Jarvis, Thale

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR  
TREATMENT OF RESTENOSIS AND

CANCER USING RIBOZYMES  
NUMBER OF SEQUENCES: 2627

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1

;; CURRENT APPLICATION DATA: US/08/435,628  
;; FILING DATE: 05-MAY-1995  
;; CLASSIFICATION: 514  
;; PRIOR APPLICATION NUMBER: 08/373,124  
;; FILING DATE: January 13, 1995  
;; APPLICATION NUMBER: 08/245,466  
;; FILING DATE: February 7, 1994  
;; APPLICATION NUMBER: 08/192,943  
;; FILING DATE: May 18, 1994  
;; APPLICATION NUMBER: 07/987,132  
;; FILING DATE: December 7, 1992  
;; APPLICATION NUMBER: 07/936,422  
;; FILING DATE: August 26, 1992  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Warburg, Richard  
;; REGISTRATION NUMBER: 32,327  
;; REFERENCE/DOCKET NUMBER: 209/035  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (213) 489-1600  
;; TELEFAX: (213) 955-0440  
;; TELEX: 67-3510  
;; INFORMATION FOR SEQ ID NO: 1060:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 17 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
US-08-435-628-1060

Query Match 1.3%; Score 14; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1811 TGTATATATATATA 1824  
DB 15 TGTATATATATATA 2

RESULT 117  
US-08-435-628-1855  
; Sequence 1855, Application US/08/435,628  
; Patent No. 5817796  
; GENERAL INFORMATION:  
; APPLICANT: Stinchcomb, Dan T.  
; APPLICANT: Draper, Kenneth  
; APPLICANT: McSwiggen, James  
; APPLICANT: Jarvis, Thale  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR  
; TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND  
; TITLE OF INVENTION: CANCER USING RIBOZYMES  
; NUMBER OF SEQUENCES: 2627  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/435,628  
; FILING DATE: 05-MAY-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/373,124

;; FILING DATE: January 13, 1995  
;; APPLICATION NUMBER: 08/245,466  
;; FILING DATE: May 18, 1994  
;; APPLICATION NUMBER: 08/192,943  
;; FILING DATE: February 7, 1994  
;; APPLICATION NUMBER: 07/987,132  
;; FILING DATE: December 7, 1992  
;; APPLICATION NUMBER: 07/936,422  
;; FILING DATE: August 26, 1992  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Warburg, Richard  
;; REGISTRATION NUMBER: 32,327  
;; REFERENCE/DOCKET NUMBER: 209/035  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (213) 489-1600  
;; TELEFAX: (213) 955-0440  
;; TELEX: 67-3510  
;; INFORMATION FOR SEQ ID NO: 1855:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 17 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
US-08-435-628-1855

Query Match 1.3%; Score 14; DB 1; Length 17;  
Best Local Similarity 57.1%; Pred. No. 1e+02;  
Matches 8; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1763 CAGATTTTAAAAA 1776  
DB 4 CAGAUUUUUAAAA 17

RESULT 118  
US-08-435-628-1857  
; Sequence 1857, Application US/08/435,628  
; Patent No. 5817796  
; GENERAL INFORMATION:  
; APPLICANT: Stinchcomb, Dan T.  
; APPLICANT: Draper, Kenneth  
; APPLICANT: McSwiggen, James  
; APPLICANT: Jarvis, Thale  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR  
; TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND  
; TITLE OF INVENTION: CANCER USING RIBOZYMES  
; NUMBER OF SEQUENCES: 2627  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/435,628  
; FILING DATE: 05-MAY-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/373,124  
; FILING DATE: January 13, 1995  
; APPLICATION NUMBER: 08/245,466  
; FILING DATE: May 18, 1994  
; APPLICATION NUMBER: 08/192,943  
; FILING DATE: February 7, 1994  
; APPLICATION NUMBER: 07/987,132



FILING DATE: December 7, 1992  
APPLICATION NUMBER: 07/936,422  
FILING DATE: August 26, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 209/035  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 1857:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-435-628-1857

Query Match 1.3%; Score 14; DB 1; Length 17;  
Best Local Similarity 57.1%; Pred. No. 1e-02;  
Matches 8; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1763 CAGATTTTAAAA 1776  
DB 2 CAGAUUUUUAAAA 15

RESULT 120  
US-08-435-628-1861  
Sequence 1861, Application US/08435628  
Patent No. 5817796  
GENERAL INFORMATION:  
APPLICANT: Stinchcomb, Dan T.  
APPLICANT: Draper, Kenneth  
APPLICANT: McSwiggen, James  
APPLICANT: Jarvis, Thale  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR  
TREATMENT OF RESTENOSIS AND  
CANCER USING RIBOZYMES  
NUMBER OF SEQUENCES: 2627  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Suite 4700  
STATE: Los Angeles  
COUNTRY: California  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/435,628  
FILING DATE: 05-MAY-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/373,124  
FILING DATE: January 13, 1995  
APPLICATION NUMBER: 08/245,466  
FILING DATE: May 18, 1994  
APPLICATION NUMBER: 08/192,943  
FILING DATE: February 7, 1994  
APPLICATION NUMBER: 07/987,132  
FILING DATE: December 7, 1992  
APPLICATION NUMBER: 07/936,422  
FILING DATE: August 26, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 209/035  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 1861:

FILING DATE: December 7, 1992  
APPLICATION NUMBER: 07/936,422  
FILING DATE: August 26, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 209/035  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 1857:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-435-628-1857

Query Match 1.3%; Score 14; DB 1; Length 17;  
Best Local Similarity 57.1%; Pred. No. 1e-02;  
Matches 8; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1763 CAGATTTTAAAA 1776  
DB 3 CAGAUUUUUAAAA 16

RESULT 119  
US-08-435-628-1859  
Sequence 1859, Application US/08435628  
Patent No. 5817796  
GENERAL INFORMATION:  
APPLICANT: Stinchcomb, Dan T.  
APPLICANT: Draper, Kenneth  
APPLICANT: McSwiggen, James  
APPLICANT: Jarvis, Thale  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR  
TREATMENT OF RESTENOSIS AND  
CANCER USING RIBOZYMES  
NUMBER OF SEQUENCES: 2627  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Suite 4700  
STATE: Los Angeles  
COUNTRY: California  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/435,628  
FILING DATE: 05-MAY-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/373,124  
FILING DATE: January 13, 1995  
APPLICATION NUMBER: 08/245,466  
FILING DATE: May 18, 1994  
APPLICATION NUMBER: 08/192,943  
FILING DATE: February 7, 1994  
APPLICATION NUMBER: 07/987,132  
FILING DATE: December 7, 1992  
APPLICATION NUMBER: 07/936,422  
FILING DATE: August 26, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard  
REGISTRATION NUMBER: 32,327

; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-435-628-1861

Query Match 1.3%; Score 14; DB 1; Length 17;  
Best Local Similarity 57.1%; Pred. No. 1e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1763 CAGATTTTAAAA 1776  
|||||:|||||  
Db 1 CAGUUUUUUAAA 14

RESULT 121

US-08-849-021-16/c  
; Sequence 16, Application US/08849021  
; Patent No. 5955276  
; GENERAL INFORMATION:

; APPLICANT: MORGANTE, MICHELE  
; APPLICANT: VOGEL, JULIE M.  
; TITLE OF INVENTION: COMPOUND MICROSATELLITE  
; TITLE OF INVENTION: PRIMERS FOR THE  
; TITLE OF INVENTION: DETECTION OF GENETIC  
; TITLE OF INVENTION: POLYMORPHISMS  
; NUMBER OF SEQUENCES: 89  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND  
; ADDRESS: COMPANY  
; STREET: 1007 MARKET STREET  
; CITY: WILMINGTON  
; STATE: DELAWARE  
; COUNTRY: U.S.A.  
; ZIP: 19898

; COMPUTER READABLE FORM:

; MEDIUM TYPE: FLOPPY DISK  
; COMPUTER: IBM PC COMPATIBLE  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PATENT IN RELEASE #1.0, VERSION 1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/849,021  
; FILING DATE:

; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/346,456  
; FILING DATE: 28 NOVEMBER 1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: FLOYD, LINDA AXAMETHY  
; REGISTRATION NUMBER: 33,692  
; REFERENCE/DOCKET NUMBER: BB-1064-A  
; TELEPHONE: 302-892-8112  
; TELEFAX: 302-992-7949  
; INFORMATION FOR SEQ ID NO: 16:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-849-021-16

Query Match 1.3%; Score 14; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTG 1806  
|||||:|||||  
Db 17 TGTGTGTGTGTG 4

RESULT 122

US-08-373-124A-874/c  
; Sequence 874, Application US/08373124A  
; Patent No. 5646042  
; GENERAL INFORMATION:

; APPLICANT: Stinchcomb, Dan T.  
; APPLICANT: Draper, Kenneth  
; APPLICANT: McSwiggen, James  
; APPLICANT: Jarvis, Thale  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR  
; TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND  
; TITLE OF INVENTION: CANCER USING RIBOZYMES  
; NUMBER OF SEQUENCES: 2627  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071

; COMEUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/373,124A  
; FILING DATE: January 13, 1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/245,466  
; FILING DATE: May 18, 1994  
; APPLICATION NUMBER: 08/192,943  
; FILING DATE: February 7, 1994  
; APPLICATION NUMBER: 07/987,132  
; FILING DATE: December 7, 1992  
; APPLICATION NUMBER: 07/936,422  
; FILING DATE: August 26, 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 209/035  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440

; INFORMATION FOR SEQ ID NO: 874:

; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-373-124A-874

Query Match 1.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.1e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1785 GATTTTAAAAATTTAT 1781  
|||||:|||||  
Db 17 GATTTTAAAAATAT 1

RESULT 123

US-08-435-628-874/c  
; Sequence 874, Application US/08435628  
; Patent No. 5817796  
; GENERAL INFORMATION:

; APPLICANT: Stinchcomb, Dan T.  
; APPLICANT: Draper, Kenneth  
; APPLICANT: McSwiggen, James  
; APPLICANT: Jarvis, Thale

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR  
TREATMENT OF RESTENOSIS AND  
CANCER USING RIBOZYMES  
NUMBER OF SEQUENCES: 2627  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage

COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/435,628

FILING DATE: 05-MAY-1995

CLASSIFICATION: 514

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/373,124

FILING DATE: January 13, 1995

APPLICATION NUMBER: 08/245,466

FILING DATE: May 18, 1994

APPLICATION NUMBER: 08/192,943

FILING DATE: February 7, 1994

APPLICATION NUMBER: 07/987,132

FILING DATE: December 7, 1992

APPLICATION NUMBER: 07/936,422

FILING DATE: August 26, 1992

ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 209/035

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 874:

SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-435-628-874

Query Match 1.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.1e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1765 GATTGTTTAAATTTAT 1781  
|||||  
Db 17 GATTGTTTAAATTTAT 1

RESULT 124

US-08-292-620A-1988/C

Sequence 1988, Application US/08292620A

Patent No. 5837542

GENERAL INFORMATION:

APPLICANT: Susan Grimm

APPLICANT: Dan T. Stinchcomb

APPLICANT: James McSwiggen

APPLICANT: Sean Sullivan

APPLICANT: Kenneth G. Draper

TITLE OF INVENTION: RIBOZYME TREATMENT OF

DISEASES OR CONDITIONS

TITLE OF INVENTION: RELATED TO LEVELS OF

TITLE OF INVENTION: INTRACELLULAR ADHESION

TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)

NUMBER OF SEQUENCES: 2390  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/292,620A  
FILING DATE: August 17, 1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/008,895  
FILING DATE: January 19, 1993  
APPLICATION NUMBER: 07/989,849  
FILING DATE: December 7, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 208/149  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 1988:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-292-620A-1988

Query Match 1.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.1e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1537 GTGTAATTGAGAGGAA 1553  
|||||  
Db 17 GGTAAATAGAGAGGAA 1

RESULT 125

US-08-851-843A-132

Sequence 132, Application US/08851843A

Patent No. 6093809

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.

APPLICANT: Lingner, Joachim

APPLICANT: Nakamura, Toru

APPLICANT: Chapman, Karen B.

APPLICANT: Morin, Gregg B.

APPLICANT: Harley, Calvin

APPLICANT: Andrews, William H.

TITLE OF INVENTION: No. 6093809el Telomerase

NUMBER OF SEQUENCES: 225

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, 8th Floor

CITY: San Francisco

STATE: California

COUNTRY: United States of America

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/851,843A  
FILING DATE: 06-MAY-1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA: US 08/846,017  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA: US 08/724,643  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph T.  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002930US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 132:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-851-843A-132

Query Match 1.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.1e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTTT 1881  
DB 1 TTTTATTTTGTGTTTT 17

RESULT 126  
US-09-071-845-1988/c  
; Sequence 1988, Application US/09071845  
; Patent No. 6132967  
; GENERAL INFORMATION:  
; APPLICANT: Susan Grimm  
; APPLICANT: Dan T. Stinchcomb  
; APPLICANT: James McSwiggen  
; APPLICANT: Sean Sullivan  
; APPLICANT: Kenneth G. Draper  
; TITLE OF INVENTION: RIBOZYME TREATMENT OF  
; TITLE OF INVENTION: DISEASES OR CONDITIONS  
; TITLE OF INVENTION: RELATED TO LEVELS OF  
; TITLE OF INVENTION: INTRACELLULAR ADHESION  
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)  
; NUMBER OF SEQUENCES: 2390  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/071,845  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA: US/08/292,620  
APPLICATION NUMBER: US/08/292,620  
FILING DATE: August 17, 1994  
APPLICATION NUMBER: 08/008,895  
FILING DATE: January 19, 1993  
APPLICATION NUMBER: 07/989,849  
FILING DATE: December 7, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 208/149  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 1988:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-071-845-1988

Query Match 1.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.1e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1537 GTGTAATTGAGAGGAA 1553  
DB 17 GGGTAATAGAGAGGAA 1

RESULT 127  
US-09-250-075-5  
; Sequence 5, Application US/09250075  
; Patent No. 6207819  
; GENERAL INFORMATION:  
; APPLICANT: Manoharan, Muthiah  
; APPLICANT: Maier, Martin A  
; TITLE OF INVENTION: Compounds Processes And Intermediates For Synthesis Of  
; TITLE OF INVENTION: Mixed Backbone Oligomeric Compounds  
; FILE REFERENCE: ISIS3299  
; CURRENT APPLICATION NUMBER: US/09/250,075  
; CURRENT FILING DATE: 1999-02-12  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: Patent in ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)..(17)  
; OTHER INFORMATION: 2'-methoxyethoxy (MOE); modified linkage  
; OTHER INFORMATION: Description of Artificial Sequence: No. 6207819el  
; OTHER INFORMATION: Sequence  
US-09-250-075-5

Query Match 1.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.1e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTTT 1881  
DB 1 TTTTATTTTGTGTTTT 17

RESULT 128

```
US-08-854-050-132
; Sequence 132, Application US/08894050
; Patent No. 6261836
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6309867el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,050
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 132:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 132:
US-09-430-323-132
; Query Match 1.3%; Score 13.8; DB 1; Length 17;
; Best Local Similarity 88.2%; Pred. No. 1.1e+02;
; Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1865 TTTTATTATTTTGTGTTT 1881
DB 1 TTTTATTTTATTTT 17
RESULT 130
US-08-584-040-2550
; Sequence 2550, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TREATMENT OF DISEASES OR
```

;; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS  
;; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL  
;; TITLE OF INVENTION: GROWTH FACTOR  
;; NUMBER OF SEQUENCES: 8502  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Lyon & Lyon  
;; STREET: 633 West Fifth Street  
;; CITY: Suite 4700  
;; STATE: Los Angeles  
;; CITY: California  
;; COUNTRY: U.S.A.  
;; ZIP: 90071-2066  
;;  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
;; MEDIUM TYPE: storage  
;; COMPUTER: IBM Compatible  
;; OPERATING SYSTEM: IBM P.C. DOS 5.0  
;; SOFTWARE: Word Perfect 5.1  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/584,040  
;; FILING DATE: January 11, 1996  
;; CLASSIFICATION: 514  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 60/005,974  
;; FILING DATE: October 26, 1995  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Warburg, Richard J.  
;; REGISTRATION NUMBER: 32,327  
;; REFERENCE/DOCKET NUMBER: 218/064  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (213) 489-1600  
;; TELEFAX: (213) 955-0440  
;; TELEX: 67-3510  
;; INFORMATION FOR SEQ ID NO: 2550:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 17 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;;  
;; US-08-584-040-2550  
;;  
Query Match 1.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 5.9%; Pred. No. 1.1e+02;  
Matches 1; Conservative 14; Mismatches 2; Indels 0; Gaps 0;  
;;  
QY 1864 CTTTATTATTTGTTT 1880  
Db 1 CUUUUUUUUUUUUUUU 17  
;;  
RESULT 131  
US-08-584-040-6047  
; Sequence 6047, Application US/08584040  
; Patent No. 6346398  
; GENERAL INFORMATION:  
; APPLICANT: Pavco, Pamela  
; APPLICANT: McSwiggen, James  
; APPLICANT: Stinchcomb, Dan T.  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE  
; TITLE OF INVENTION: TREATMENT OF DISEASES OR  
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS  
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL  
; TITLE OF INVENTION: GROWTH FACTOR  
; NUMBER OF SEQUENCES: 8502  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; CITY: Suite 4700  
; STATE: Los Angeles  
; CITY: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066  
;;

;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
;; MEDIUM TYPE: storage  
;; COMPUTER: IBM Compatible  
;; OPERATING SYSTEM: IBM P.C. DOS 5.0  
;; SOFTWARE: Word Perfect 5.1  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/584,040  
;; FILING DATE: January 11, 1996  
;; CLASSIFICATION: 514  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 60/005,974  
;; FILING DATE: October 26, 1995  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Warburg, Richard J.  
;; REGISTRATION NUMBER: 32,327  
;; REFERENCE/DOCKET NUMBER: 218/064  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (213) 489-1600  
;; TELEFAX: (213) 955-0440  
;; TELEX: 67-3510  
;; INFORMATION FOR SEQ ID NO: 6047:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 17 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;;  
;; US-08-584-040-6047  
;;  
Query Match 1.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 58.8%; Pred. No. 1.1e+02;  
Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;  
;;  
QY 1639 TGTTCCTTAAGTCAGAA 1655  
Db 1 UGUCCCUAAUUCAGAA 17  
;;  
RESULT 132  
US-08-584-040-6049  
; Sequence 6049, Application US/08584040  
; Patent No. 6346398  
; GENERAL INFORMATION:  
; APPLICANT: Pavco, Pamela  
; APPLICANT: McSwiggen, James  
; APPLICANT: Stinchcomb, Dan T.  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE  
; TITLE OF INVENTION: TREATMENT OF DISEASES OR  
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS  
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL  
; TITLE OF INVENTION: GROWTH FACTOR  
; NUMBER OF SEQUENCES: 8502  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; CITY: Suite 4700  
; STATE: Los Angeles  
; CITY: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066  
;;  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
;; MEDIUM TYPE: storage  
;; COMPUTER: IBM Compatible  
;; OPERATING SYSTEM: IBM P.C. DOS 5.0  
;; SOFTWARE: Word Perfect 5.1  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/584,040  
;; FILING DATE: January 11, 1996  
;; CLASSIFICATION: 514  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 60/005,974  
;; FILING DATE: October 26, 1995  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Warburg, Richard J.  
;; REGISTRATION NUMBER: 32,327  
;; REFERENCE/DOCKET NUMBER: 218/064  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (213) 489-1600  
;; TELEFAX: (213) 955-0440  
;; TELEX: 67-3510  
;; INFORMATION FOR SEQ ID NO: 6047:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 17 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;;  
;; US-08-584-040-6047  
;;

; FILING DATE: October 26, 1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard J.  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 218/064  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 6049:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-584-040-6049

Query Match 1.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 70.6%; Pred. No. 1.1e+02;  
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1643 CCTAAGTCAGAACAGC 1659  
Db 1 CCUUAUUCAGAACCC 17

RESULT 133  
US-09-619-103-23/c  
; Sequence 23, Application US/09619103  
; Patent No. 6429300  
; GENERAL INFORMATION:  
; APPLICANT: Kurz, Markus  
; APPLICANT: Lohse, Peter  
; APPLICANT: Wagner, Richard  
; TITLE OF INVENTION: Peptide Acceptor Ligation Methods  
; FILE REFERENCE: 50036/031002  
; CURRENT APPLICATION NUMBER: US/09/619,103  
; PRIOR FILING DATE: 2000-07-19  
; PRIOR APPLICATION NUMBER: 60/145,834  
; PRIOR FILING DATE: 1999-07-27  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 23  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: designed sequence for nucleic acid purification  
US-09-619-103-23

Query Match 1.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.1e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1865 TTTTATTTTGTGTTT 1881  
Db 17 TTTTATTTTGTGTTT 1

RESULT 134  
US-09-726-096A-5  
; Sequence 5, Application US/09726096A  
; Patent No. 6462184  
; GENERAL INFORMATION:  
; APPLICANT: Manoharan, Muthiah  
; APPLICANT: Maier, Martin A.  
; TITLE OF INVENTION: Compounds Processes And Intermediates For Synthesis Of Mixed Back  
; FILE REFERENCE: IS184528  
; CURRENT APPLICATION NUMBER: US/09/726,096A  
; CURRENT FILING DATE: 2000-11-29  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 5  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Oligonucleotide  
; NAME/KEY: misc feature  
; LOCATION: (1)..(19)  
; OTHER INFORMATION: 2'-methoxyethoxy (MOE); phosphorothioate  
; OTHER INFORMATION: internucleoside linkage  
US-09-726-096A-5

Query Match 1.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.1e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1865 TTTTATTTTGTGTTT 1881  
Db 1 TTTTATTTTGTGTTT 17

RESULT 135  
US-09-371-772B-1074  
; Sequence 1074, Application US/09371772B  
; Patent No. 6566127  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel  
; FILE REFERENCE: MEHB00,876-J (237/198)  
; CURRENT APPLICATION NUMBER: US/09/371,772B  
; CURRENT FILING DATE: 1999-08-10  
; PRIOR FILING DATE: 1995-10-26  
; PRIOR APPLICATION NUMBER: US 60/005,374  
; PRIOR FILING DATE: 1996-01-08  
; NUMBER OF SEQ ID NOS: 14225  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1074  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-09-371-772B-1074

Query Match 1.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 5.9%; Pred. No. 1.1e+02;  
Matches 1; Conservative 14; Mismatches 2; Indels 0; Gaps 0;

Qy 1864 CTTTATTTTGTGTTT 1880  
Db 1 CUUUUUUUUUUUUUUU 17

RESULT 136  
US-09-371-772B-2884  
; Sequence 2884, Application US/09371772B  
; Patent No. 6566127  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel  
; FILE REFERENCE: MEHB00,876-J (237/198)  
; CURRENT APPLICATION NUMBER: US/09/371,772B  
; CURRENT FILING DATE: 1999-08-10





Query Match 1.3%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 1.1e+02;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1794 GTGTGTGTGTGTGTGTG 1810  
 DB 1 GTGTGTGTGTGTGTGTG 17

RESULT 141  
 US-09-827-998-387  
 ; Sequence 387, Application US/09827998  
 ; Patent No. 6656700  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gu, Yizhong  
 ; APPLICANT: Shannon, Mark  
 ; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E  
 ; FILE REFERENCE: MDMORF-8  
 ; CURRENT APPLICATION NUMBER: US/09/827,998  
 ; CURRENT FILING DATE: 2001-04-06  
 ; PRIOR APPLICATION NUMBER: US 60/207,456  
 ; PRIOR FILING DATE: 2000-05-26  
 ; PRIOR APPLICATION NUMBER: US 60/236,359  
 ; PRIOR FILING DATE: 2000-09-27  
 ; NUMBER OF SEQ ID NOS: 1881  
 ; SOFTWARE: Aeonica Sequence Listing Engine  
 ; Patent No. 6656700  
 ; SEQ ID NO 387  
 ; LENGTH: 17  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-09-827-998-387

Query Match 1.3%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 1.1e+02;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1793 TGTGTGTGTGTGTGTGT 1809  
 DB 1 TGTGTGTGTGTGTGTGT 17

RESULT 142  
 US-09-827-998-388  
 ; Sequence 388, Application US/09827998  
 ; Patent No. 6656700  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gu, Yizhong  
 ; APPLICANT: Shannon, Mark  
 ; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E  
 ; FILE REFERENCE: MDMORF-8  
 ; CURRENT APPLICATION NUMBER: US/09/827,998  
 ; CURRENT FILING DATE: 2001-04-06  
 ; PRIOR APPLICATION NUMBER: US 60/207,456  
 ; PRIOR FILING DATE: 2000-05-26  
 ; PRIOR APPLICATION NUMBER: US 60/236,359  
 ; PRIOR FILING DATE: 2000-09-27  
 ; NUMBER OF SEQ ID NOS: 1881  
 ; SOFTWARE: Aeonica Sequence Listing Engine  
 ; Patent No. 6656700  
 ; SEQ ID NO 388  
 ; LENGTH: 17  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-09-827-998-388

Query Match 1.3%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 1.1e+02;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1798 GTGTGTGTGTGTGTGTA 1814  
 DB 1 GTGTGTGTGTGTGTGTA 17

Db 1 GTGTGTGTGTGTGTGTA 17  
 RESULT 143  
 US-09-827-998-389  
 ; Sequence 389, Application US/09827998  
 ; Patent No. 6656700  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gu, Yizhong  
 ; APPLICANT: Shannon, Mark  
 ; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E  
 ; FILE REFERENCE: MDMORF-8  
 ; CURRENT APPLICATION NUMBER: US/09/827,998  
 ; CURRENT FILING DATE: 2001-04-06  
 ; PRIOR APPLICATION NUMBER: US 60/207,456  
 ; PRIOR FILING DATE: 2000-05-26  
 ; PRIOR APPLICATION NUMBER: US 60/236,359  
 ; PRIOR FILING DATE: 2000-09-27  
 ; NUMBER OF SEQ ID NOS: 1881  
 ; SOFTWARE: Aeonica Sequence Listing Engine  
 ; Patent No. 6656700  
 ; SEQ ID NO 389  
 ; LENGTH: 17  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-09-827-998-389  
 Query Match 1.3%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 1.1e+02;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1799 TGTGTGTGTGTGTGTAT 1815  
 DB 1 TGTGTGTGTGTGTGTAT 17

RESULT 144  
 US-08-153-051B-52  
 ; Sequence 52, Application US/08153051B  
 ; Patent No. 5645986  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Michael D. West  
 ; APPLICANT: Jerry W. Shay  
 ; APPLICANT: Woodring E. Wright  
 ; APPLICANT: Elizabeth Blackburn  
 ; APPLICANT: Nam Woo Kim  
 ; APPLICANT: Calvin B. Harley  
 ; APPLICANT: Scott L. Weinrich  
 ; APPLICANT: Catherine Strahl  
 ; APPLICANT: Michael J. McEachern  
 ; APPLICANT: Homayoun Vaziri  
 ; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF  
 ; TITLE OF INVENTION: CONDITIONS RELATED TO TELOMERE  
 ; TITLE OF INVENTION: LENGTH AND/OR TELOMERASE ACTIVITY  
 ; NUMBER OF SEQUENCES: 58  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Lyon & Lyon  
 ; STREET: 633 West Fifth Street  
 ; STREET: Suite 4700  
 ; CITY: Los Angeles  
 ; STATE: California  
 ; COUNTRY: U.S.A.  
 ; ZIP: 90071  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 ; MEDIUM TYPE: storage  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: IBM P.C. DOS 5.0  
 ; SOFTWARE: FastSEQ Version 1.5  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/153,051B  
 ; FILING DATE: No. 5645986ember 12, 1993  
 ; PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/038,766  
FILING DATE: March 24, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 204/195  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 52:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-153-051B-52  
Query Match 1.3%; Score 13.4; DB 1; Length 15;  
Best Local Similarity 93.3%; Pred. No. 1e+02; 1; Indels 0; Gaps 0;  
Matches 14; Conservative 0; Mismatches 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1792 TTGTGTGTGTGTGTG 1806  
DB 1 TGGTGTGTGTGTGTG 15  
RESULT 145  
US-08-060-952C-51  
Sequence 51, Application US/08060952C  
Patent No. 5695932  
GENERAL INFORMATION:  
APPLICANT: Michael D. West  
APPLICANT: Jerry W. Shay  
APPLICANT: Woodring E. Wright  
APPLICANT: Elizabeth Blackburn  
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF CONDITIONS  
TITLE OF INVENTION: RELATED TO TELOMERE LENGTH AND/OR  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
SUITE: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/060,952C  
FILING DATE: May 13, 1993  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/882,438  
FILING DATE: May 13, 1992  
APPLICATION NUMBER: 08/038,766  
FILING DATE: March 24, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 202/045  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 51:  
SEQUENCE CHARACTERISTICS:

LENGTH: 15 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-060-952C-51  
Query Match 1.3%; Score 13.4; DB 1; Length 15;  
Best Local Similarity 93.3%; Pred. No. 1e+02; 1; Indels 0; Gaps 0;  
Matches 14; Conservative 0; Mismatches 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1792 TTGTGTGTGTGTGTG 1806  
DB 1 TGGTGTGTGTGTGTG 15  
RESULT 146  
US-08-151-477A-52  
Sequence 52, Application US/08151477A  
Patent No. 5830644  
GENERAL INFORMATION:  
APPLICANT: Michael D. West  
APPLICANT: Jerry W. Shay  
APPLICANT: Woodring E. Wright  
APPLICANT: Elizabeth Blackburn  
APPLICANT: Nam Woo Kim  
APPLICANT: Calvin B. Harley  
APPLICANT: Scott L. Weinrich  
APPLICANT: Catherine Strahl  
APPLICANT: Michael J. McEachern  
APPLICANT: Homayoun Vaziri  
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF  
TITLE OF INVENTION: CONDITIONS RELATED TO TELOMERE  
TITLE OF INVENTION: LENGTH AND/OR TELOMERASE ACTIVITY  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
SUITE: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/151,477A  
FILING DATE: No. 5830644ember 12, 1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/038,766  
FILING DATE: March 24, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 202/189  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 52:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-151-477A-52  
Query Match 1.3%; Score 13.4; DB 1; Length 15;  
Best Local Similarity 93.3%; Pred. No. 1e+02; 1; Indels 0; Gaps 0;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1792 TTGTGTGTGTGTGTG 1806  
Db 1 TGGTGTGTGTGTGTG 15

RESULT 147  
US-08-819-867-79  
Sequence 79, Application US/08819867  
Patent No. 6007989  
GENERAL INFORMATION:  
APPLICANT: Michael D. West  
APPLICANT: Calvin B. Harley  
APPLICANT: Scott L. Weinrich  
APPLICANT: Catherine M. Strahl  
APPLICANT: Michael J. McEachern  
APPLICANT: Jerry Shay  
APPLICANT: Woodring E. Wright  
APPLICANT: Elizabeth H. Blackburn  
APPLICANT: Nam Woo Kim  
APPLICANT: Homayoun Vaziri  
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF  
TITLE OF INVENTION: CONDITIONS RELATED TO  
TITLE OF INVENTION: TELOMERE LENGTH AND/OR  
TITLE OF INVENTION: TELOMERASE ACTIVITY  
NUMBER OF SEQUENCES: 80  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
SUITE: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq for Windows 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/819,867  
FILING DATE: March 14, 1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/153,051  
FILING DATE: No. 6007989ember 12, 1993  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Chambers, Daniel M.  
REGISTRATION NUMBER: 34,561  
REFERENCE/DOCKET NUMBER: 224/232  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 79:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-819-867-79

Query Match 1.3%; Score 13.4; DB 1; Length 15;  
Best Local Similarity 93.3%; Pred. No. 1e+02; 1; Indels 0; Gaps 0;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1792 TTGTGTGTGTGTGTG 1806  
Db 1 TGGTGTGTGTGTGTG 15

RESULT 148  
US-08-464-011B-51  
Sequence 51, Application US/08464011B  
Patent No. 6368789  
GENERAL INFORMATION:  
APPLICANT: Michael D. West  
APPLICANT: Jerry W. Shay  
APPLICANT: Woodring E. Wright  
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF CONDITIONS  
RELATED TO TELOMERE LENGTH AND/OR  
TELOMERASE ACTIVITY  
NUMBER OF SEQUENCES: 61  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
SUITE: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/464,011B  
FILING DATE: 05-Jun-1995  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/882,438  
FILING DATE: May 13, 1992  
APPLICATION NUMBER: 08/038,766  
FILING DATE: March 24, 1993  
APPLICATION NUMBER: 08/060,952  
FILING DATE: May 13, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 202/045  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 51:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 51:  
US-08-464-011B-51  
Query Match 1.3%; Score 13.4; DB 1; Length 15;  
Best Local Similarity 93.3%; Pred. No. 1e+02; 1; Indels 0; Gaps 0;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1792 TTGTGTGTGTGTGTG 1806  
Db 1 TGGTGTGTGTGTGTG 15

RESULT 149  
US-09-475-947A-83/c  
Sequence 83, Application US/09475947A  
Patent No. 6472154  
GENERAL INFORMATION:  
APPLICANT: Garner, Harold R.  
APPLICANT: Wren, Jonathan D.  
APPLICANT: Minna, John D.  
TITLE OF INVENTION: Polymorphic Repeats in Human Genes

FILE REFERENCE: UTSD0667  
CURRENT APPLICATION NUMBER: US/09/475,947A  
CURRENT FILING DATE: 1999-12-31  
NUMBER OF SEQ ID NOS: 346  
SOFTWARE: Patent in Ver. 2.1  
SEQ ID NO 83  
LENGTH: 15  
TYPE: DNA  
ORGANISM: human  
US-09-475-947A-83

Query Match 1.3%; Score 13.4; DB 1; Length 15;  
Best Local Similarity 93.3%; Pred. No. 1e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1811 TGTATATATATAT 1825  
DB 15 TTTATATATATAT 1

RESULT 150  
US-09-378-535-79  
Sequence 79, Application US/09378535  
Patent No. 6551774  
GENERAL INFORMATION:  
APPLICANT: Michael D. West  
Calvin B. Harley  
Scott L. Weinrich  
Catherine M. Strahl  
Michael J. Meeachern  
Jerry Shay  
Woodring E. Wright  
Elizabeth H. Blackburn  
Nam Woo Kim  
Homayoun Vaziri  
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF  
CONDITIONS RELATED TO  
TELOMERE LENGTH AND/OR  
TELOMERASE ACTIVITY  
NUMBER OF SEQUENCES: 80  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq for Windows 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/378,535  
FILING DATE: 20-AUG-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/819,867  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Chambers, Daniel M.  
REGISTRATION NUMBER: 34,561  
REFERENCE/DOCKET NUMBER: 224/232  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 79:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 base pairs  
TYPE: nucleic acid

STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 79:  
US-09-378-535-79

Query Match 1.3%; Score 13.4; DB 1; Length 15;  
Best Local Similarity 93.3%; Pred. No. 1e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1792 TTGTGTGTGTGTG 1806  
DB 1 TGGTGTGTGTGTG 15

RESULT 151  
US-09-371-772B-6067  
Sequence 6067, Application US/09371772B  
Patent No. 6566127  
GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals, Inc.  
APPLICANT: Pavco, Pam  
APPLICANT: McSwiggen, Jim  
APPLICANT: Stinchcomb, Dan  
APPLICANT: Escobedo, Jaime  
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel  
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor  
FILE REFERENCE: MBHB00.876-J (237/198)  
CURRENT APPLICATION NUMBER: US/09/371,772B  
CURRENT FILING DATE: 1999-08-10  
PRIOR APPLICATION NUMBER: US 60/005,974  
PRIOR FILING DATE: 1995-10-26  
PRIOR APPLICATION NUMBER: US 08/584,040  
PRIOR FILING DATE: 1996-01-08  
NUMBER OF SEQ ID NOS: 14225  
SOFTWARE: Patent in version 3.0  
SEQ ID NO 6067  
LENGTH: 16  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-09-371-772B-6067

Query Match 1.3%; Score 13.4; DB 1; Length 16;  
Best Local Similarity 46.7%; Pred. No. 1.1e+02;  
Matches 7; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

QY 1791 ATTGTGTGTGTGTG 1805  
DB 2 ACUGUGUGUGUGUGU 16

RESULT 152  
US-09-479-005A-185/c  
Sequence 185, Application US/09479005A  
Patent No. 656731  
GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals, Inc.  
TITLE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity  
FILE REFERENCE: MBHB00-984-C  
CURRENT APPLICATION NUMBER: US/09/479,005A  
CURRENT FILING DATE: 2000-01-07  
PRIOR APPLICATION NUMBER: US 09/444,209  
PRIOR FILING DATE: 1999-11-19  
PRIOR APPLICATION NUMBER: US 09/159,274  
PRIOR FILING DATE: 1998-09-22  
PRIOR APPLICATION NUMBER: US 60/059,473  
PRIOR FILING DATE: 1997-09-22  
NUMBER OF SEQ ID NOS: 1208  
SOFTWARE: Patent in version 3.0  
SEQ ID NO 185  
LENGTH: 16  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-09-479-005A-185

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Query Match      1.3%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred.No.1.le02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1865 TTTTATTATTTGTTT 1879
          |||||
DB      15 TTTTATTATTTATT 1
          |||||

RESULTS
=====
RESULT 153
US-08-373-124A-1060
; Sequence 1060, Application US/08373124A
; Patent No. 5646042
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Draper, Kenneth
APPLICANT: McSwiggen, James
APPLICANT: Jarvis, Thale
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
TITLE OF INVENTION: CANCER USING RIBOZYMES
NUMBER OF SEQUENCES: 2627
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/373,124A
FILING DATE: January 13, 1995
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER: 08/245,466
FILING DATE: May 18, 1994
APPLICATION NUMBER: 08/192,943
FILING DATE: February 7, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
APPLICATION NUMBER: 07/936,422
FILING DATE: August 26, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/035
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1060:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-373-124A-1060

Query Match      1.3%; Score 13.4; DB 1; Length 17;
Best Local Similarity 46.7%; Pred.No.1.2e+02;
Matches 7; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

QY      1813 TATATATATATATAT 1827
          :|::|::|::|:
DB      2 UAUAUUAUAUACAU 16

```

APPLICANT: MORGANTE, MICHELE  
APPLICANT: VOGEL, JULIE M.  
TITLE OF INVENTION: COMPOUND MICROSATELLITE  
TITLE OF INVENTION: PRIMERS FOR THE  
TITLE OF INVENTION: DETECTION OF GENETIC  
TITLE OF INVENTION: POLYMORPHISMS  
NUMBER OF SEQUENCES: 89  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: E. I. DU PONT DE NEMOURS AND  
ADDRESSEE: COMPANY  
STREET: 1007 MARKET STREET  
CITY: WILMINGTON  
STATE: DELAWARE  
COUNTRY: U.S.A.  
ZIP: 19898  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PATENT IN RELEASE #1.0, VERSION 1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/849,021  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/346,456  
FILING DATE: 28 NOVEMBER 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: FLOYD, LINDA AXAMETHY  
REGISTRATION NUMBER: 33,692  
REFERENCE/DOCKET NUMBER: BB-1064-A  
TELEPHONE: 302-992-8112  
TELEFAX: 302-992-7949  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-849-021-13

Query Match 1.2%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 96;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGT 1805  
Db 13 TGTGTGTGTGTGT 1  
RESULT 156  
US-08-849-021-15  
Sequence 15, Application US/08849021  
Patent No. 5955276  
GENERAL INFORMATION:  
APPLICANT: MORGANTE, MICHELE  
APPLICANT: VOGEL, JULIE M.  
TITLE OF INVENTION: COMPOUND MICROSATELLITE  
TITLE OF INVENTION: PRIMERS FOR THE  
TITLE OF INVENTION: DETECTION OF GENETIC  
TITLE OF INVENTION: POLYMORPHISMS  
NUMBER OF SEQUENCES: 89  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: E. I. DU PONT DE NEMOURS AND  
ADDRESSEE: COMPANY  
STREET: 1007 MARKET STREET  
CITY: WILMINGTON  
STATE: DELAWARE  
COUNTRY: U.S.A.  
ZIP: 19898  
COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PATENT IN RELEASE #1.0, VERSION 1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/849,021  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/346,456  
FILING DATE: 28 NOVEMBER 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: FLOYD, LINDA AXAMETHY  
REGISTRATION NUMBER: 33,692  
REFERENCE/DOCKET NUMBER: BB-1064-A  
TELEPHONE: 302-992-8112  
TELEFAX: 302-992-7949  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-849-021-15

Query Match 1.2%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 96;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGT 1805  
Db 1 TGTGTGTGTGTGT 13  
RESULT 157  
US-09-393-783A-41  
Sequence 41, Application US/09393783A  
Patent No. 6355428  
GENERAL INFORMATION:  
APPLICANT: Bruice, Thomas Wayne  
APPLICANT: Suh, Young J.  
TITLE OF INVENTION: Nucleic Acid Ligand Interaction Assays  
FILE REFERENCE: 4600-0128.30  
CURRENT APPLICATION NUMBER: US/09/393,783A  
CURRENT FILING DATE: 1999-10-09  
PRIOR APPLICATION NUMBER: US 09/151,890  
PRIOR FILING DATE: 1998-09-11  
NUMBER OF SEQ ID NOS: 80  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 41  
LENGTH: 13  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
NAME/KEY: misc binding  
LOCATION: (1)-(13)  
OTHER INFORMATION: synthesized test oligonucleotide for binding  
OTHER INFORMATION: studies  
US-09-393-783A-41

Query Match 1.2%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 96;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGT 1806  
Db 1 GTGTGTGTGTGTGT 13  
RESULT 158

```
US-09-151-890B-41
; Sequence 41, Application US/09151890B
; Patent No. 6420109
; GENERAL INFORMATION:
; APPLICANT: Gary P. Schroth
; APPLICANT: Thomas Wayne Bruice
; APPLICANT: Young J. Suh
; TITLE OF INVENTION: Nucleic Acid Ligand Interaction Assays
; FILE REFERENCE: 4600-0128
; CURRENT APPLICATION NUMBER: US/09/151,890B
; CURRENT FILING DATE: 1998-09-11
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 41
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc.binding
; LOCATION: (1)...(13)
; OTHER INFORMATION: synthesized test oligonucleotide for binding
; OTHER INFORMATION: studies
US-09-151-890B-41

Query Match 1.2%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTG 1806
DB 1 GTGTGTGTGTGTG 13

RESULT 159
US-09-475-947A-83
; Sequence 83, Application US/09475947A
; Patent No. 6472154
; GENERAL INFORMATION:
; APPLICANT: Garner, Harold R.
; APPLICANT: Wren, Jonathan D.
; APPLICANT: Minna, John D.
; TITLE OF INVENTION: Polymorphic Repeats in Human Genes
; FILE REFERENCE: UTSD0667
; CURRENT APPLICATION NUMBER: US/09/475,947A
; CURRENT FILING DATE: 1999-12-31
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 83
; LENGTH: 15
; TYPE: DNA
; ORGANISM: human
US-09-475-947A-83

Query Match 1.2%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1814 ATATATATATATA 1826
DB 1 ATATATATATATA 13

RESULT 160
US-08-291-932A-121/c
; Sequence 121, Application US/08291932A
; Patent No. 5658780
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth G.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
```

```
; TITLE OF INVENTION: NF-KB
; NUMBER OF SEQUENCES: 830
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/291,932A
; FILING DATE: August 15, 1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; PRIOR APPLICATION NUMBER: 08/245,466
; FILING DATE: May 18, 1994
; APPLICATION NUMBER: 07/987,132
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 121:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-291-932A-121

Query Match 1.2%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2152 TCACCTGGAAGCA 2164
DB 15 TCACCTGGAAGCA 3

RESULT 161
US-08-291-932A-194/c
; Sequence 194, Application US/08291932A
; Patent No. 5658780
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth G.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: NF-KB
; NUMBER OF SEQUENCES: 830
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
```

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/291,932A  
FILING DATE: August 15, 1994  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA: including application  
PRIOR APPLICATION DATA: described below:  
APPLICATION NUMBER: 08/245,466  
FILING DATE: May 18, 1994  
FILING DATE: December 7, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 208/157  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 194:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-291-932A-194

Query Match 1.2%; Score 13; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2152 TCACCTGGAAGCA 2164  
Db 15 TCACCTGGAAGCA 3

RESULT 162  
US-08-291-932A-310/c  
Sequence 310, Application US/08291932A  
Patent No. 5658780  
GENERAL INFORMATION:  
APPLICANT: Stinchcomb, Dan T.  
APPLICANT: Draper, Kenneth G.  
APPLICANT: McSwiggen, James  
TITLE OF INVENTION: RIBOZYME TREATMENT OF  
TITLE OF INVENTION: DISEASES OR CONDITIONS  
TITLE OF INVENTION: RELATED TO LEVELS OF  
TITLE OF INVENTION: NF-KB  
NUMBER OF SEQUENCES: 830  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/291,932A  
FILING DATE: August 15, 1994  
CLASSIFICATION: 514

PRIOR APPLICATION DATA: including application  
PRIOR APPLICATION DATA: described below:  
APPLICATION NUMBER: 08/245,466  
FILING DATE: May 18, 1994  
FILING DATE: December 7, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 208/157  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 310:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-291-932A-310

Query Match 1.2%; Score 13; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2152 TCACCTGGAAGCA 2164  
Db 15 TCACCTGGAAGCA 3

RESULT 163  
US-08-812-951B-1  
Sequence 1, Application US/08812951B  
Patent No. 6297006  
GENERAL INFORMATION:  
APPLICANT: Drmanac, Radoje T.  
APPLICANT: Drmanac, Snezana  
APPLICANT: Hou, Aaron  
APPLICANT: Houser, Brian  
TITLE OF INVENTION: Methods and Compositions for  
TITLE OF INVENTION: Detection or Quantification of Nucleic Acid Species  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McCutchen, Doyle, Brown & Enersen LLP  
STREET: Three Embarcadero Center  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/812,951B  
FILING DATE: 04-MAR-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US08/784747  
FILING DATE: 16-JAN-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Kumamoto, Andrew A.  
REGISTRATION NUMBER: 40,690  
REFERENCE/DOCKET NUMBER: 20411-701  
TELEPHONE: 415-393-2000  
TELEFAX: 415-393-2286  
TELEX:  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:



```

; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-812-951B-1

Query Match      1.2%; Score 13; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1863  CCTTTTATTATTG 1876
DBB      1  CCTTTTNTTTTG 14

RESULT 164
US-08-812-951B-2/c
; Sequence 2, Application US/08812951B
; Patent No. 6297006
; GENERAL INFORMATION:
; APPLICANT: Drmanac, Radoje T.
; APPLICANT: Drmanac, Snezana
; APPLICANT: Hou, Aaron
; APPLICANT: Houser, Brian
; TITLE OF INVENTION: Methods and Compositions for
; TITLE OF INVENTION: Detection or Quantification of Nucleic Acid Species
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McCutchen, Doyle, Brown & Enersen LLP
; STREET: Three Embarcadero Center
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/812,951B
; FILING DATE: 04-MAR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US08/784747
; FILING DATE: 16-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Kumamoto, Andrew A
; REGISTRATION NUMBER: 40,690
; REFERENCE/DOCKET NUMBER: 20411-701
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-393-2000
; TELEFAX: 415-393-2286
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-812-951B-2

Query Match      1.2%; Score 13; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1863  CCTTTTATTATTG 1876
DB      15  CCTTTTNTTTTG 2

RESULT 165
US-08-784-747-2

```

APPLICATION NUMBER: US/08/784,747  
FILING DATE: 16-JAN-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Kumamoto, Andrew A  
REGISTRATION NUMBER: 40,690  
REFERENCE/DOCKET NUMBER: 20411-708  
TELEPHONE: 415-393-2000  
TELEFAX: 415-393-2286  
TELEX:  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-784-747-3

Query Match 1.2%; Score 13; DB 1; Length 15;  
Best Local Similarity 92.9%; Pred. No. 1.1e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1863 CCTTTTATTTTG 1876

DB 15 CCTTTTNTTTTG 2

RESULT 167

US-09-409-778-9  
Sequence 9, Application US/09409778

Patent No. 6472173  
GENERAL INFORMATION:  
APPLICANT: Ford, John  
TITLE OF INVENTION: A NOVEL CHEMOKINE RECEPTOR OBTAINED FROM  
TITLE OF INVENTION: A CDNA LIBRARY OF FETAL LIVER-SPLEEN  
FILE REFERENCE: 20411-742CON2 (now 28110/36057B)  
CURRENT APPLICATION NUMBER: US/09/409,778  
PRIOR FILING DATE: 1999-09-22  
PRIOR APPLICATION NUMBER: PCT/US99/12829  
PRIOR FILING DATE: 1999-06-29  
PRIOR APPLICATION NUMBER: US 09/236,166  
PRIOR FILING DATE: 1999-01-22  
PRIOR APPLICATION NUMBER: US 09/106,800  
PRIOR FILING DATE: 1998-06-26  
NUMBER OF SEQ ID NOS: 25  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 9  
LENGTH: 15  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Exemplary oligonucleotide primer used in sequence assembly process  
NAME/KEY: misc\_feature  
LOCATION: (8)...(8)  
OTHER INFORMATION: n = A, T, C, G or 1-(2-deoxy-D-ribofuranosyl)-3-nitropyrrrole  
US-09-409-778-9

Query Match 1.2%; Score 13; DB 1; Length 15;  
Best Local Similarity 92.9%; Pred. No. 1.1e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1863 CCTTTTATTTTG 1876

DB 1 CCTTTTNTTTTG 14

RESULT 168

US-09-409-778-10/c

Sequence 10, Application US/09409778  
Patent No. 6472173  
GENERAL INFORMATION:  
APPLICANT: Ford, John  
TITLE OF INVENTION: A NOVEL CHEMOKINE RECEPTOR OBTAINED FROM  
TITLE OF INVENTION: A CDNA LIBRARY OF FETAL LIVER-SPLEEN  
FILE REFERENCE: 20411-742CON2 (now 28110/36057B)  
CURRENT APPLICATION NUMBER: US/09/409,778  
PRIOR FILING DATE: 1999-09-22  
PRIOR APPLICATION NUMBER: PCT/US99/12829  
PRIOR FILING DATE: 1999-06-29  
PRIOR APPLICATION NUMBER: US 09/236,166  
PRIOR FILING DATE: 1999-01-22  
PRIOR APPLICATION NUMBER: US 09/106,800  
PRIOR FILING DATE: 1998-06-26  
NUMBER OF SEQ ID NOS: 25  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 10  
LENGTH: 15  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Exemplary oligonucleotide primer used in sequence assembly process  
NAME/KEY: misc\_feature  
LOCATION: (8)...(8)  
OTHER INFORMATION: n = A, T, C, G or 1-(2-deoxy-D-ribofuranosyl)-3-nitropyrrrole  
US-09-409-778-10

Query Match 1.2%; Score 13; DB 1; Length 15;  
Best Local Similarity 92.9%; Pred. No. 1.1e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1863 CCTTTTATTTTG 1876

DB 15 CCTTTTNTTTTG 2

RESULT 169

US-09-479-005A-117  
Sequence 117, Application US/09479005A  
Patent No. 6656731  
GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals, Inc.  
TITLE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity  
FILE REFERENCE: MSH00-884-C  
CURRENT APPLICATION NUMBER: US/09/479,005A  
CURRENT FILING DATE: 2000-01-07  
PRIOR APPLICATION NUMBER: US 09/444,209  
PRIOR FILING DATE: 1999-11-19  
PRIOR APPLICATION NUMBER: US 09/159,274  
PRIOR FILING DATE: 1998-09-22  
PRIOR APPLICATION NUMBER: US 60/059,473  
NUMBER OF SEQ ID NOS: 1208  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 117  
LENGTH: 16  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-09-479-005A-117

Query Match 1.2%; Score 13; DB 1; Length 16;  
Best Local Similarity 38.5%; Pred. No. 1.2e+02;  
Matches 5; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

QY 2268 TTTTTCCTATATA 2280

DB 1 UUUUUUUAUAAA 13

RESULT 170

US-07-971-978-36

Sequence 36, Application US/07971978  
Patent No. 5614617  
GENERAL INFORMATION:  
APPLICANT: Cook and Sanghvi  
TITLE OF INVENTION: Nuclease Resistant, Pyrimidine  
TITLE OF INVENTION: Modified Oligonucleotides that Detect and Modulate  
TITLE OF INVENTION: Gene Expression  
NUMBER OF SEQUENCES: 65  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and  
ADDRESSEE: No. 5614617ris  
STREET: One Liberty Place - 46th Floor  
CITY: Philadelphia  
STATE: PA  
COUNTRY: U.S.A.  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/971,978  
FILING DATE: February 18, 1993  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/558,806  
FILING DATE: July 27, 1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Joseph Lucci  
REGISTRATION NUMBER: 33,307  
REFERENCE/DOCKET NUMBER: ISIS-0333  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-568-3100  
TELEFAX: 215-568-3439  
INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 1  
OTHER INFORMATION: 5-fluoro-2'-deoxyuridine  
OTHER INFORMATION: substitution  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 2  
OTHER INFORMATION: 5-fluoro-2'-deoxyuridine  
OTHER INFORMATION: substitution  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 3  
OTHER INFORMATION: 5-fluoro-2'-deoxyuridine  
OTHER INFORMATION: substitution  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 4  
OTHER INFORMATION: 5-fluoro-2'-deoxyuridine  
OTHER INFORMATION: substitution  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 5  
OTHER INFORMATION: 5-fluoro-2'-deoxyuridine  
OTHER INFORMATION: substitution  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 6  
OTHER INFORMATION: 5-fluoro-2'-deoxyuridine  
OTHER INFORMATION: substitution  
FEATURE:

NAME/KEY: Modified-site  
LOCATION: 7  
OTHER INFORMATION: 5-fluoro-2'-deoxyuridine  
OTHER INFORMATION: substitution  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 8  
OTHER INFORMATION: 5-fluoro-2'-deoxyuridine  
OTHER INFORMATION: substitution  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 9  
OTHER INFORMATION: 5-fluoro-2'-deoxyuridine  
OTHER INFORMATION: substitution  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 10  
OTHER INFORMATION: 5-fluoro-2'-deoxyuridine  
OTHER INFORMATION: substitution  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 11  
OTHER INFORMATION: 5-fluoro-2'-deoxyuridine  
OTHER INFORMATION: substitution  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 12  
OTHER INFORMATION: 5-fluoro-2'-deoxyuridine  
OTHER INFORMATION: substitution  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 13  
OTHER INFORMATION: 5-fluoro-2'-deoxyuridine  
OTHER INFORMATION: substitution  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 14  
OTHER INFORMATION: 5-fluoro-2'-deoxyuridine  
OTHER INFORMATION: substitution  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 15  
OTHER INFORMATION: 5-fluoro-2'-deoxyuridine  
OTHER INFORMATION: substitution  
US-07-971-978-36  
Query Match 1.2%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 1.3e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1865 TTTTATTATTGTTT 1880  
Db 1 TTTTATTATTGTTT 16  
RESULT 171  
US-07-971-978-42  
Sequence 42, Application US/07971978  
Patent No. 5614617  
GENERAL INFORMATION:  
APPLICANT: Cook and Sanghvi  
TITLE OF INVENTION: Nuclease Resistant, Pyrimidine  
TITLE OF INVENTION: Modified Oligonucleotides that Detect and Modulate  
TITLE OF INVENTION: Gene Expression  
NUMBER OF SEQUENCES: 65  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and  
ADDRESSEE: No. 5614617ris  
STREET: One Liberty Place - 46th Floor  
CITY: Philadelphia  
STATE: PA  
COUNTRY: U.S.A.  
ZIP: 19103

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/971,978  
FILING DATE: February 18, 1993  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/558,806  
FILING DATE: July 27, 1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Joseph Lucci  
REGISTRATION NUMBER: 33,307  
REFERENCE/DOCKET NUMBER: ISIS-0333  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-568-3100  
TELEFAX: 215-568-3439  
INFORMATION FOR SEQ ID NO: 42:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 1  
OTHER INFORMATION: 5-bromo-2'-deoxyuridine  
OTHER INFORMATION: substitution  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 2  
OTHER INFORMATION: 5-bromo-2'-deoxyuridine  
OTHER INFORMATION: substitution  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 3  
OTHER INFORMATION: 5-bromo-2'-deoxyuridine  
OTHER INFORMATION: substitution  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 4  
OTHER INFORMATION: 5-bromo-2'-deoxyuridine  
OTHER INFORMATION: substitution  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 5  
OTHER INFORMATION: 5-bromo-2'-deoxyuridine  
OTHER INFORMATION: substitution  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 6  
OTHER INFORMATION: 5-bromo-2'-deoxyuridine  
OTHER INFORMATION: substitution  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 7  
OTHER INFORMATION: 5-bromo-2'-deoxyuridine  
OTHER INFORMATION: substitution  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 8  
OTHER INFORMATION: 5-bromo-2'-deoxyuridine  
OTHER INFORMATION: substitution  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 9  
OTHER INFORMATION: 5-bromo-2'-deoxyuridine  
OTHER INFORMATION: substitution  
FEATURE:  
NAME/KEY: Modified-site

LOCATION: 10  
OTHER INFORMATION: 5-bromo-2'-deoxyuridine  
OTHER INFORMATION: substitution  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 11  
OTHER INFORMATION: 5-bromo-2'-deoxyuridine  
OTHER INFORMATION: substitution  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 12  
OTHER INFORMATION: 5-bromo-2'-deoxyuridine  
OTHER INFORMATION: substitution  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 13  
OTHER INFORMATION: 5-bromo-2'-deoxyuridine  
OTHER INFORMATION: substitution  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 14  
OTHER INFORMATION: 5-bromo-2'-deoxyuridine  
OTHER INFORMATION: substitution  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 15  
OTHER INFORMATION: 5-bromo-2'-deoxyuridine  
OTHER INFORMATION: substitution  
US-07-971-978-42  
Query Match 1.2%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 1.3e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTT 1880

DB 1 TTTTATTTTGTGTTT 16

## RESULT 172

US-07-971-978-60  
Sequence 60, Application US/07971978  
Patent No. 5614617  
GENERAL INFORMATION:  
APPLICANT: Cook and Sanghvi  
TITLE OF INVENTION: Nuclease Resistant, Pyrimidine  
TITLE OF INVENTION: Modified Oligonucleotides that Detect and Modulate  
TITLE OF INVENTION: Gene Expression  
NUMBER OF SEQUENCES: 65  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and  
ADDRESSEE: No. 5614617ris  
STREET: One Liberty Place - 46th Floor  
CITY: Philadelphia  
STATE: PA  
COUNTRY: U.S.A.  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/971,978  
FILING DATE: February 18, 1993  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/558,806  
FILING DATE: July 27, 1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Joseph Lucci  
REGISTRATION NUMBER: 33,307  
REFERENCE/DOCKET NUMBER: ISIS-0333

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-568-3100  
TELEFAX: 215-568-3439  
INFORMATION FOR SEQ ID NO: 60:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 1  
OTHER INFORMATION: 5-iodo-2'-deoxyuridine  
OTHER INFORMATION: substitution  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 2  
OTHER INFORMATION: 5-iodo-2'-deoxyuridine  
OTHER INFORMATION: substitution  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 3  
OTHER INFORMATION: 5-iodo-2'-deoxyuridine  
OTHER INFORMATION: substitution  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 4  
OTHER INFORMATION: 5-iodo-2'-deoxyuridine  
OTHER INFORMATION: substitution  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 5  
OTHER INFORMATION: 5-iodo-2'-deoxyuridine  
OTHER INFORMATION: substitution  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 6  
OTHER INFORMATION: 5-iodo-2'-deoxyuridine  
OTHER INFORMATION: substitution  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 7  
OTHER INFORMATION: 5-iodo-2'-deoxyuridine  
OTHER INFORMATION: substitution  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 8  
OTHER INFORMATION: 5-iodo-2'-deoxyuridine  
OTHER INFORMATION: substitution  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 9  
OTHER INFORMATION: 5-iodo-2'-deoxyuridine  
OTHER INFORMATION: substitution  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 10  
OTHER INFORMATION: 5-iodo-2'-deoxyuridine  
OTHER INFORMATION: substitution  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 11  
OTHER INFORMATION: 5-iodo-2'-deoxyuridine  
OTHER INFORMATION: substitution  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 12  
OTHER INFORMATION: 5-iodo-2'-deoxyuridine  
OTHER INFORMATION: substitution  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 13

OTHER INFORMATION: 5-iodo-2'-deoxyuridine  
OTHER INFORMATION: substitution  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 14  
OTHER INFORMATION: 5-iodo-2'-deoxyuridine  
OTHER INFORMATION: substitution  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 15  
OTHER INFORMATION: 5-iodo-2'-deoxyuridine  
OTHER INFORMATION: substitution  
US-07-971-978-60  
Query Match 1.2%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 1.3e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1865 TTTTATTTTGTGTTT 1880  
DB 1 TTTTATTTTGTGTTT 16  
RESULT 173  
US-08-415-370-2  
Sequence 2, Application US/08415370  
Patent No. 580155  
GENERAL INFORMATION:  
APPLICANT: Kutyavin, Igor V.  
APPLICANT: Lukhtanov, Eugeny A.  
APPLICANT: Gamper, Howard B.  
APPLICANT: Meyer, Jr., Rich B.  
TITLE OF INVENTION: COVALENTLY LINKED OLIGONUCLEOTIDE MINOR  
TITLE OF INVENTION: GROOVE BINDER CONJUGATES  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESS: KLEIN & SZEKERES  
STREET: 4199 Campus Drive, Suite 700  
CITY: Irvine  
STATE: CA  
COUNTRY: USA  
ZIP: 92715  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA: US/08/415,370  
APPLICATION NUMBER: US/08/415,370  
FILING DATE: 03-APR-1995  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Szekeres, Gabor L.  
REGISTRATION NUMBER: 28,675  
REFERENCE/DOCKET NUMBER: 491-09-PA  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 714-854-5502  
TELEFAX: 714-854-4897  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-415-370-2  
Query Match 1.2%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 1.3e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1865 TTTTATTTTGTGTTT 1880  
DB 1 TTTTATTTTGTGTTT 16

RESULT 174  
US-08-687-551-15  
; Sequence 15, Application US/08687551  
; Patent No. 5856435  
; GENERAL INFORMATION:  
; APPLICANT: BAZILE, Didier  
; APPLICANT: EMILE, Carole  
; APPLICANT: HELENE, Claude  
; APPLICANT: SPENLEHAUER, Gilles  
; TITLE OF INVENTION: NUCLEIC ACID-CONTAINING COMPOSITION, ITS  
; PREPARATION AND USE  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Rhone-Poulenc Rorer Inc.  
; STREET: 500 Arcola Rd. 3C43  
; CITY: Collegeville  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19426  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION NUMBER: US/08/687,551  
; FILING DATE: 27-JAN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 94/01381  
; FILING DATE: 08-FEB-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/FR95/00098  
; FILING DATE: 27-JAN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith Ph. D. Julie K.  
; REGISTRATION NUMBER: 38,619  
; REFERENCE/DOCKET NUMBER: ST94007-US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (610)454-3808  
; TELEFAX: (610)454-3808  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; DESCRIPTION: /desc = "oligonucleotide"  
US-08-687-551-15

Query Match 1.2%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 1.3e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTT 1880  
|||||  
DB 1 TTTTATTTTGTGTTT 16

RESULT 175  
US-08-893-614-1  
; Sequence 1, Application US/08893614  
; Patent No. 5936077  
; GENERAL INFORMATION:  
; APPLICANT: PELEIDERER, Wolfgang  
; APPLICANT: BEIER, Markus  
; TITLE OF INVENTION: SOLID PHASE SYNTHESIS OF  
; OLIGONUCLEOTIDES  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/893,614  
; FILING DATE: 11-JUL-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: DE 19627898.8  
; FILING DATE: 11-JUL-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SANDERCOCK, Colin G.  
; REGISTRATION NUMBER: 31,298  
; REFERENCE/DOCKET NUMBER: 18748/343/HOCE  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)672-5300  
; TELEFAX: (202)672-5399  
; TELEX: 904136  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-893-614-1

Query Match 1.2%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 1.3e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1836 ATCTAAGTTAATTAA 1851  
|||||  
DB 1 ATTTAATTAAATTAA 16

RESULT 176  
US-09-141-764-2  
; Sequence 2, Application US/09141764  
; Patent No. 6084102  
; GENERAL INFORMATION:  
; APPLICANT: Kutyavin, Igor V.  
; APPLICANT: Lukhtanov, Eugeny A.  
; APPLICANT: Gamber, Howard B.  
; APPLICANT: Meyer, Jr., Rich B.  
; TITLE OF INVENTION: COVALENTLY LINKED OLIGONUCLEOTIDE  
; TITLE OF INVENTION: MINOR  
; TITLE OF INVENTION: GROOVE BINDER CONJUGATES  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: KLEIN & SZEKERES  
; STREET: 4199 Campus Drive, Suite 700  
; CITY: Irvine  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92715  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/141,764  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/415,370  
FILING DATE: 03-APR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Szekeres, Gabor L.  
REGISTRATION NUMBER: 28,675  
REFERENCE/DOCKET NUMBER: 491-09-PA  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 714-854-5502  
TELEFAX: 714-854-4897  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-141-764-2

Query Match 1.2%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 1.3e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTT 1880  
||||| ||||| |||||  
Db 1 TTTTATTTTGTGTTT 16

RESULT 177  
US-08-851-843A-131/c  
Sequence 131, Application US/08851843A  
Patent No. 6093809  
GENERAL INFORMATION:  
APPLICANT: Cech, Thomas R.  
APPLICANT: Lingner, Joachim  
APPLICANT: Nakamura, Toru  
APPLICANT: Chapman, Karen B.  
APPLICANT: Morin, Gregg B.  
APPLICANT: Harley, Calvin  
APPLICANT: Andrews, William H.  
TITLE OF INVENTION: No. 6093809el Telomerase  
NUMBER OF SEQUENCES: 225  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: United States of America  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/851,843A  
FILING DATE: 06-MAY-1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph T.  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002930US  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 131:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-851-843A-131

Query Match 1.2%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 1.3e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTT 1880  
||||| ||||| |||||  
Db 16 TTTTATTTTGTGTTT 1

RESULT 178  
US-08-854-050-131/c  
Sequence 131, Application US/08854050  
Patent No. 6261836  
GENERAL INFORMATION:  
APPLICANT: Cech, Thomas R.  
APPLICANT: Lingner, Joachim  
APPLICANT: Nakamura, Toru  
APPLICANT: Chapman, Karen B.  
APPLICANT: Morin, Gregg B.  
APPLICANT: Harley, Calvin  
APPLICANT: Andrews, William H.  
TITLE OF INVENTION: No. 6261836el Telomerase  
NUMBER OF SEQUENCES: 225  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: United States of America  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/854,050  
FILING DATE: 09-MAY-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph T.  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002930US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 131:

SEQUENCE CHARACTERISTICS:  
LENGTH: 16 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-854-050-131

Query Match 1.2%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 1.3e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTT 1880  
Db 16 TTTTATTTTGTGTTT 1

RESULT 179

US-09-430-323-131/c  
Sequence 131, Application US/09430323  
Patent No. 6309867

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.  
Lingner, Joachim  
Nakamura, Toru  
Chapman, Karen B.  
Morin, Gregg B.  
Harley, Calvin  
Andrews, William H.

TITLE OF INVENTION: No. 6309867el Telomerase

NUMBER OF SEQUENCES: 225

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: United States of America  
ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/430,323  
FILING DATE: 29-Oct-1999  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/854,050  
FILING DATE: 09-MAY-1997  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996

ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph T.  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-0029300US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0300  
TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 131:

SEQUENCE CHARACTERISTICS:

LENGTH: 16 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 131:  
US-09-430-323-131

Query Match 1.2%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 1.3e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTT 1880  
Db 16 TTTTATTTTGTGTTT 1

RESULT 180

US-09-507-345A-2  
Sequence 2, Application US/09507345A  
Patent No. 6426408

GENERAL INFORMATION:

APPLICANT: Kutyavin, Igor V.  
Lukhtanov, Eugeny A.  
Gamber, Howard B.  
Meyer Jr., Rich B.

TITLE OF INVENTION: Covalently Linked Oligonucleotide Minor  
Groove Binder Conjugates

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/507,345A  
FILING DATE: 18-Feb-2000  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/415,370  
FILING DATE: 03-APR-1995  
APPLICATION NUMBER: US 09/141,764  
FILING DATE: 27-AUG-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Kezer, William B.  
REGISTRATION NUMBER: 37,369  
REFERENCE/DOCKET NUMBER: 17682A-003500US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:  
LENGTH: 16 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-09-507-345A-2

Query Match 1.2%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 1.3e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTT 1880  
Db 1 TTTTATTTTGTGTTT 16

RESULT 181

US-09-619-103-22/c  
Sequence 22, Application US/09619103  
Patent No. 6429300

GENERAL INFORMATION:



```
; APPLICANT: Kurz, Markus
; APPLICANT: Lohse, Peter
; APPLICANT: Wagner, Richard
; TITLE OF INVENTION: Peptide Acceptor Ligation Methods
; FILE REFERENCE: 50036/031002
; CURRENT APPLICATION NUMBER: US/09/619,103
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 60/145,834
; PRIOR FILING DATE: 1999-07-27
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: designed sequence for nucleic acid purification
US-09-619-103-22

Query Match      1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTGTTT 1880
      ||||| ||||| |||||
Db 16 TTTTATTGTTT 1

RESULT 182
US-09-739-928-2
; Sequence 2, Application US/09739928
; Patent No. 6486308
; GENERAL INFORMATION:
; APPLICANT: Kutyavin, Igor V.
; APPLICANT: Lukhtanov, Eugeny A.
; APPLICANT: Gamber, Howard B.
; APPLICANT: Meyer Jr., Rich B.
; TITLE OF INVENTION: Covalently Linked Oligonucleotide Minor
; Groove Binder Conjugates
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/739,928
; FILING DATE: 11-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/415,370
; FILING DATE: 03-APR-1995
; APPLICATION NUMBER: US 09/141,764
; FILING DATE: 27-AUG-1998
; APPLICATION NUMBER: US 09/507,345
; FILING DATE: 18-FEB-2000
; ATTORNEY/AGENT INFORMATION:
; NAME: Keizer, William B.
; REGISTRATION NUMBER: 37,369
; REFERENCE/DOCKET NUMBER: 17682A-003510US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
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; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-739-928-2

Query Match      1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTGTTT 1880
      ||||| ||||| |||||
Db 1 TTTTATTGTTT 16

RESULT 183
US-09-371-772B-6072
; Sequence 6072, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6072
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Hmo sapiens
US-09-371-772B-6072

Query Match      1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 50.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGT 1809
      ||||| ||||| |||||
Db 1 GUGUGUGUGUGUGGU 16

RESULT 184
US-09-371-772B-6074
; Sequence 6074, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
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; SEQ ID NO 6074
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-6074

Query Match      1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 43.8%; Pred. No. 1.3e+02;
Matches 7; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGT 1809
DB 1 CUGGGUGUAGUGUGU 16

RESULT 185
US-09-479-005A-522
; Sequence 522, Application US/09479005A
; Patent No. 6656731
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity
; FILE REFERENCE: MBH00-884-C
; CURRENT APPLICATION NUMBER: US/09/479,005A
; CURRENT FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/444,209
; PRIOR FILING DATE: 1993-11-19
; PRIOR APPLICATION NUMBER: US 09/159,274
; PRIOR FILING DATE: 1998-09-22
; PRIOR APPLICATION NUMBER: US 60/059,473
; PRIOR FILING DATE: 1997-09-22
; NUMBER OF SEQ ID NOS: 1208
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 522
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-479-005A-522

Query Match      1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 43.8%; Pred. No. 1.3e+02;
Matches 7; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 1832 AGTTATCTAAGTTAAT 1847
DB 1 AGUUAUGUAGUUAU 16

RESULT 186
US-08-373-124A-1058
; Sequence 1058, Application US/08373124A
; Patent No. 5645042
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth
; APPLICANT: McSwiggen, James
; APPLICANT: Jarvis, Thale
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
; TITLE OF INVENTION: CANCER USING RIBOZYMES
; NUMBER OF SEQUENCES: 2627
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,628
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/373,124
; FILING DATE: January 13, 1995
```

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; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/373,124A
; FILING DATE: January 13, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/345,466
; FILING DATE: May 18, 1994
; APPLICATION NUMBER: 08/192,943
; FILING DATE: February 7, 1994
; APPLICATION NUMBER: 07/987,132
; FILING DATE: December 7, 1992
; APPLICATION NUMBER: 07/936,422
; FILING DATE: August 26, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 209/035
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1058:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-373-124A-1058

Query Match      1.2%; Score 12.8; DB 1; Length 17;
Best Local Similarity 43.8%; Pred. No. 1.4e+02;
Matches 7; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 1811 TGTATATATATATATA 1826
DB 2 UUUUAUUAUUAUACA 17

RESULT 187
US-08-435-628-1058
; Sequence 1058, Application US/08435628
; Patent No. 5817796
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth
; APPLICANT: McSwiggen, James
; APPLICANT: Jarvis, Thale
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
; TITLE OF INVENTION: CANCER USING RIBOZYMES
; NUMBER OF SEQUENCES: 2627
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,628
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/373,124
; FILING DATE: January 13, 1995
```

APPLICATION NUMBER: 08/245,466  
FILING DATE: May 18, 1994  
APPLICATION NUMBER: 08/192,943  
FILING DATE: February 7, 1994  
APPLICATION NUMBER: 07/987,132  
FILING DATE: December 7, 1992  
APPLICATION NUMBER: 07/936,422  
FILING DATE: August 26, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 209/035  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 1058:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-435-628-1058

Query Match 1.2%; Score 12.8; DB 1; Length 17;  
Best Local Similarity 43.8%; Pred. No. 1.4e+02;  
Matches 7; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 1811 TGTATATATATATATA 1826  
Db 2 UUAUAUAUAUAUA 17

RESULT 188  
US-08-153-051B-57  
Sequence 57, Application US/08153051B  
Patent No. 5645986  
GENERAL INFORMATION:  
APPLICANT: Michael D. West  
APPLICANT: Jerry W. Shay  
APPLICANT: Woodring E. Wright  
APPLICANT: Elizabeth Blackburn  
APPLICANT: Nam Woo Kim  
APPLICANT: Calvin B. Harley  
APPLICANT: Scott L. Weinrich  
APPLICANT: Catherine Strahl  
APPLICANT: Michael J. McEachern  
APPLICANT: Homayoun Vaziri  
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF  
TITLE OF INVENTION: CONDITIONS RELATED TO TELOMERE  
TITLE OF INVENTION: LENGTH AND/OR TELOMERASE ACTIVITY  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/153,051B  
FILING DATE: No. 5645986ember 12, 1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/038,766  
FILING DATE: March 24, 1993  
ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 204/195  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 57:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-153-051B-57

Query Match 1.2%; Score 12.4; DB 1; Length 14;  
Best Local Similarity 92.9%; Pred. No. 1.2e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTG 1806  
Db 1 TGGGTGTGTGTGTG 14

RESULT 189  
US-08-060-952C-56  
Sequence 56, Application US/08060952C  
Patent No. 5695932  
GENERAL INFORMATION:  
APPLICANT: Michael D. West  
APPLICANT: Jerry W. Shay  
APPLICANT: Woodring E. Wright  
APPLICANT: Elizabeth Blackburn  
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF CONDITIONS  
TITLE OF INVENTION: RELATED TO TELOMERE LENGTH AND/OR  
TITLE OF INVENTION: TELOMERASE ACTIVITY  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/060,952C  
FILING DATE: May 13, 1993  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/882,438  
FILING DATE: May 13, 1992  
APPLICATION NUMBER: 08/038,766  
FILING DATE: March 24, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 202/045  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 56:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single

TOPOLOGY: linear  
US-08-060-952C-56  
Query Match 1.2%; Score 12.4; DB 1; Length 14;  
Best Local Similarity 92.9%; Pred. No. 1.2e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1793 TGTGTGTGTGTGTG 1806  
Db 1 TGGGTGTGTGTGTG 14  
RESULT 190  
US-08-151-477A-57  
Sequence 57, Application US/08151477A  
Patent No. 5830644  
GENERAL INFORMATION:  
APPLICANT: Michael D. West  
APPLICANT: Jerry W. Shay  
APPLICANT: Woodring E. Wright  
APPLICANT: Elizabeth Blackburn  
APPLICANT: Nam Woo Kim  
APPLICANT: Calvin B. Harley  
APPLICANT: Scott L. Weinrich  
APPLICANT: Catherine Strahl  
APPLICANT: Michael J. McEachern  
APPLICANT: Homayoun Vaziri  
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF  
CONDITIONS RELATED TO  
TELOMERE  
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF  
CONDITIONS RELATED TO  
TELOMERE  
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF  
CONDITIONS RELATED TO  
TELOMERE  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FASTSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/151,477A  
FILING DATE: NO. 5830644ember 12, 1993  
PRIOR APPLICATION NUMBER:  
FILING DATE: March 24, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 202/189  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 57:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-151-477A-57  
Query Match 1.2%; Score 12.4; DB 1; Length 14;  
Best Local Similarity 92.9%; Pred. No. 1.2e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1793 TGTGTGTGTGTGTG 1806  
Db 1 TGGGTGTGTGTGTG 14

Db 1 TGGGTGTGTGTGTG 14  
RESULT 191  
US-08-819-867-78  
Sequence 78, Application US/08819867  
Patent No. 6007989  
GENERAL INFORMATION:  
APPLICANT: Michael D. West  
APPLICANT: Calvin B. Harley  
APPLICANT: Scott L. Weinrich  
APPLICANT: Catherine M. Strahl  
APPLICANT: Michael J. McEachern  
APPLICANT: Jerry Shay  
APPLICANT: Woodring E. Wright  
APPLICANT: Elizabeth H. Blackburn  
APPLICANT: Nam Woo Kim  
APPLICANT: Homayoun Vaziri  
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF  
CONDITIONS RELATED TO  
TELOMERE  
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF  
CONDITIONS RELATED TO  
TELOMERE  
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF  
CONDITIONS RELATED TO  
TELOMERE  
NUMBER OF SEQUENCES: 80  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FASTSEQ for Windows 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/819,867  
FILING DATE: March 14, 1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/153,051  
FILING DATE: NO. 6007989ember 12, 1993  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Chambers, Daniel M.  
REGISTRATION NUMBER: 34,561  
REFERENCE/DOCKET NUMBER: 224/232  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 78:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-819-867-78  
Query Match 1.2%; Score 12.4; DB 1; Length 14;  
Best Local Similarity 92.9%; Pred. No. 1.2e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1793 TGTGTGTGTGTGTG 1806  
Db 1 TGGGTGTGTGTGTG 14  
RESULT 192  
US-08-998-099-351

Sequence 351, Application US/08998099A  
Patent No. 6103890  
GENERAL INFORMATION:  
APPLICANT: JARVIS, THALE  
APPLICANT: MCSWIGGEN, JAMES A.  
APPLICANT: STINCHCOMB, DAN T.  
TITLE OF INVENTION: ENZYMAIC NUCLEIC ACID TREATMENT OF DISEASES  
TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS OF C-FOS  
FILE REFERENCE: 231/175  
CURRENT APPLICATION NUMBER: US/08/998,099A  
CURRENT FILING DATE: 1997-12-24  
EARLIER APPLICATION NUMBER: 60/037,658  
EARLIER FILING DATE: 1997-01-23  
EARLIER APPLICATION NUMBER: 08/373,124  
EARLIER FILING DATE: 1995-01-13  
EARLIER APPLICATION NUMBER: 08/245,466  
EARLIER FILING DATE: 1994-05-18  
NUMBER OF SEQ ID NOS: 375  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 351  
LENGTH: 14  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-08-998-099-351

Query Match 1.2%; Score 12.4; DB 1; Length 14;  
Best Local Similarity 71.4%; Pred. No. 1.2e+02;  
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1567 TCACGACCTGCT 1580  
Db 1 UCACCGACCGCCU 14

RESULT 193  
US-08-464-011B-56  
Sequence 56, Application US/08464011B  
Patent No. 6368789  
GENERAL INFORMATION:  
APPLICANT: Michael D. West  
Jerry W. Shay  
Woodring E. Wright  
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF CONDITIONS  
RELATED TO TELOMERE LENGTH AND/OR  
TELOMERASE ACTIVITY  
NUMBER OF SEQUENCES: 61  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/464,011B  
FILING DATE: 05-Jun-1995  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/882,438  
FILING DATE: May 13, 1992  
APPLICATION NUMBER: 08/038,766  
FILING DATE: March 24, 1993  
APPLICATION NUMBER: 08/060,952  
FILING DATE: May 13, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.

REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 202/045  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 56:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 56:  
US-08-464-011B-56

Query Match 1.2%; Score 12.4; DB 1; Length 14;  
Best Local Similarity 92.9%; Pred. No. 1.2e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTG 1806  
Db 1 TGGGTGTGTGTGTG 14

RESULT 194  
US-09-378-535-78  
Sequence 78, Application US/09378535  
Patent No. 6551774  
GENERAL INFORMATION:  
APPLICANT: Michael D. West  
Calvin B. Harley  
Scott L. Weinrich  
Catherine M. Strahl  
Michael J. Mceachern  
Jerry Shay  
Woodring E. Wright  
Elizabeth H. Blackburn  
Nam Woo Kim  
Homayoun Vaziri  
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF  
CONDITIONS RELATED TO  
TELOMERE LENGTH AND/OR  
TELOMERASE ACTIVITY  
NUMBER OF SEQUENCES: 80  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq for Windows 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/378,535  
FILING DATE: 20-Aug-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/819,867  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Chambers, Daniel M.  
REGISTRATION NUMBER: 34,561  
REFERENCE/DOCKET NUMBER: 224/232  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 78:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 78:

US-09-378-535-78

Query Match 1.2%; Score 12.4; DB 1; Length 14;  
Best Local Similarity 92.9%; Pred. No. 1.2e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTG 1806  
DB 1 TGGGTGTGTGTGTG 14

## RESULT 195

US-08-319-492B-474  
; Sequence 474, Application US/08319492B  
; Patent No. 5616488  
; GENERAL INFORMATION:  
; APPLICANT: Sullivan, Sean M.  
; APPLICANT: Draper, Kenneth G.  
; APPLICANT: McSwiggen, James  
; APPLICANT: Stinchcomb, Dan T.  
; TITLE OF INVENTION: RIBOZYME TREATMENT OF DISEASES  
; TITLE OF INVENTION: OF IL-5  
; NUMBER OF SEQUENCES: 751  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; CITY: Suite 4700  
; STATE: Los Angeles  
; COUNTRY: California  
; ZIP: 90071

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: Storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/319,492B  
FILING DATE: October 7, 1994

PRIOR APPLICATION DATA: including application  
PRIOR APPLICATION DATA: described below:

APPLICATION NUMBER: 08/008,895  
FILING DATE: January 19, 1993  
APPLICATION NUMBER: 07/989,849  
FILING DATE: December 7, 1992

ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 209/276  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 474:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

US-08-319-492B-474

Query Match 1.2%; Score 12.4; DB 1; Length 15;  
Best Local Similarity 78.6%; Pred. No. 1.3e+02;

Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 1956 AAAGCATGAATGG 1969  
DB 1 AAAGCAUAAAUUGG 14

## RESULT 196

US-08-319-492B-491  
; Sequence 491, Application US/08319492B  
; Patent No. 5616488  
; GENERAL INFORMATION:  
; APPLICANT: Sullivan, Sean M.  
; APPLICANT: Draper, Kenneth G.  
; APPLICANT: McSwiggen, James  
; APPLICANT: Stinchcomb, Dan T.  
; TITLE OF INVENTION: RIBOZYME TREATMENT OF DISEASES  
; TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS  
; TITLE OF INVENTION: OF IL-5  
; NUMBER OF SEQUENCES: 751  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; CITY: Suite 4700  
; STATE: Los Angeles  
; COUNTRY: California  
; ZIP: 90071

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: Storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/319,492B  
FILING DATE: October 7, 1994

PRIOR APPLICATION DATA: including application  
PRIOR APPLICATION DATA: described below:

APPLICATION NUMBER: 08/008,895  
FILING DATE: January 19, 1993  
APPLICATION NUMBER: 07/989,849  
FILING DATE: December 7, 1992

ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 209/276  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 491:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

US-08-319-492B-491

Query Match 1.2%; Score 12.4; DB 1; Length 15;  
Best Local Similarity 35.7%; Pred. No. 1.3e+02;  
Matches 5; Conservative 8; Mismatches 1; Indels 0; Gaps 0;

QY 1284 TTATTTAAATCTGT 1297  
DB 2 UUAUUAUUCUGU 15

## RESULT 197

US-08-334-847-335/c  
; Sequence 335, Application US/08334847  
; Patent No. 5693532

```

GENERAL INFORMATION:
APPLICANT: McSwiggen, James
APPLICANT: Draper, Kenneth
APPLICANT: Pavco, Pam
APPLICANT: Woolf, Tod
TITLE OF INVENTION: METHOD AND REAGENT FOR
TITLE OF INVENTION: INHIBITING RESPIRATORY
TITLE OF INVENTION: SYNCTIAL VIRUS
NUMBER OF SEQUENCES: 909
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/334,847
FILING DATE: No. 5693532ember 4, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/032
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 335:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-334-847-335

Query Match 1.2%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 1.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1784 TGTAAATATTGTGT 1797
Db 14 TGTCAATATTGTGT 1

RESULT 198
US-08-292-620A-331
; Sequence 331, Application US/08292620A
; Patent No. 5837542
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street

```

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STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/292,620A
FILING DATE: August 17, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/149
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 331:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-292-620A-331

Query Match 1.2%; Score 12.4; DB 1; Length 15;
Best Local Similarity 42.9%; Pred. No. 1.3e+02;
Matches 6; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

QY 1801 TGTGTGTGTGTGT 1814
Db 1 UGUGUGAUGUGUA 14

RESULT 199
US-08-832-021-20
; Sequence 20, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
; APPLICANT: Combates, N.
; APPLICANT: Pardini, J.
; APPLICANT: Pardini, S.
; APPLICANT: Prouty, S.
; APPLICANT: Stenn, K.
; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
; FILE REFERENCE: JBP-382
; CURRENT APPLICATION NUMBER: US/08/832,021
; CURRENT FILING DATE: 1997-04-02
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 20
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-20

Query Match 1.2%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 1.3e+02;

```

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1871 TTTTGTGTTTAAAT 1884  
Db 2 TTTTGTGTTTAAAT 15

RESULT 200  
US-08-832-021-64  
; Sequence 64, Application US/08932021  
; Patent No. 6045998  
; GENERAL INFORMATION:  
; APPLICANT: Combates, N.  
; APPLICANT: Bardin, J.  
; APPLICANT: Parimoo, S.  
; APPLICANT: Prouty, S.  
; APPLICANT: Steen, K.  
; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY  
; FILE REFERENCE: JBP-382  
; CURRENT APPLICATION NUMBER: US/08/832,021  
; CURRENT FILING DATE: 1997-04-02  
; NUMBER OF SEQ ID NOS: 64  
; SOFTWARE: Patent in Ver. 2.0  
; SEQ ID NO 64  
; LENGTH: 15  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: primer  
US-08-832-021-64

Query Match 1.2%; Score 12.4; DB 1; Length 15;  
Best Local Similarity 92.9%; Pred. No. 1.3e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1865 TTTTGTGTTTGT 1878  
Db 2 TTTTGTGTTTGT 15

RESULT 201  
US-09-071-845-331  
; Sequence 331, Application US/09071845  
; Patent No. 6132967  
; GENERAL INFORMATION:  
; APPLICANT: Susan Grimm  
; APPLICANT: Dan T. Stinchcomb  
; APPLICANT: James McSwiggen  
; APPLICANT: Sean Sullivan  
; APPLICANT: Kenneth G. Draper  
; TITLE OF INVENTION: RIBOZYME TREATMENT OF  
; TITLE OF INVENTION: DISEASES OR CONDITIONS  
; TITLE OF INVENTION: RELATED TO LEVELS OF  
; TITLE OF INVENTION: INTRACELLULAR ADHESION  
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)  
; NUMBER OF SEQUENCES: 2390  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/071,845  
; FILING DATE:

CLASSIFICATION:  
PRIOR APPLICATION NUMBER: US/08/292,620  
FILING DATE: August 17, 1994  
APPLICATION NUMBER: 08/008,895  
FILING DATE: January 19, 1993  
APPLICATION NUMBER: 07/989,849  
FILING DATE: December 7, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 208/149  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 331:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-071-845-331

Query Match 1.2%; Score 12.4; DB 1; Length 15;  
Best Local Similarity 42.9%; Pred. No. 1.3e+02;  
Matches 6; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

QY 1801 TGTGTGTGTGTA 1814  
Db 1 UGUGUGUAGUGUA 14

RESULT 202  
US-08-444-818-203  
; Sequence 203, Application US/08444818  
; Patent No. 6150087  
; GENERAL INFORMATION:  
; APPLICANT: Chien, David Y.  
; APPLICANT: Rutter, William J.  
; TITLE OF INVENTION: NANOV Diagnostics and Vaccines  
; NUMBER OF SEQUENCES: 777  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Chiron Corporation  
; STREET: 4560 Horton Street  
; CITY: Emeryville  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94608-2916  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/444,818  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/403,590  
; FILING DATE: 14-MAR-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Harbin, Alisa A.  
; REGISTRATION NUMBER: 33,895  
; REFERENCE/DOCKET NUMBER: 0110.002  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (508) 359-3876  
; TELEFAX: (508) 359-3885  
; INFORMATION FOR SEQ ID NO: 203:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single



TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "primer based on clone 11b."  
US-08-444-818-203

Query Match 1.2%; Score 12.4; DB 1; Length 15;  
Best Local Similarity 92.9%; Pred. No. 1.3e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1378 CTGGTTTGAAGAAT 1391  
DB 1 CTGGCTTGAGAAT 14

RESULT 203  
US-08-875-710-1  
Sequence 1, Application US/08875710  
Patent No. 6326139  
GENERAL INFORMATION:  
APPLICANT: Soreq, Hermona  
APPLICANT: Zakuc, Haim  
TITLE OF INVENTION: METHOD OF SCREENING FOR GENETIC PREDISPOSITION TO  
TITLE OF INVENTION: ANTICHOLINESTERASE THERAPY  
FILE REFERENCE: 2391.00076  
CURRENT APPLICATION NUMBER: US/08/875,710  
CURRENT FILING DATE: 1997-10-06  
EARLIER APPLICATION NUMBER: PCT/US96/00322  
EARLIER FILING DATE: 1996-01-11  
NUMBER OF SEQ ID NOS: 5  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 1  
LENGTH: 15  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-08-875-710-1

Query Match 1.2%; Score 12.4; DB 1; Length 15;  
Best Local Similarity 92.9%; Pred. No. 1.3e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2174 ACTTGATGATGACT 2187  
DB 2 ACTTGCTATGACT 15

RESULT 204  
US-09-475-947A-158  
Sequence 158, Application US/09475947A  
Patent No. 6472154  
GENERAL INFORMATION:  
APPLICANT: Garner, Harold R.  
APPLICANT: Wren, Jonathan D.  
APPLICANT: Mirna, John D.  
TITLE OF INVENTION: Polymorphic Repeats in Human Genes  
FILE REFERENCE: UTSD0667  
CURRENT APPLICATION NUMBER: US/09/475,947A  
CURRENT FILING DATE: 1999-12-31  
NUMBER OF SEQ ID NOS: 346  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 158  
LENGTH: 15  
TYPE: DNA  
ORGANISM: human  
FEATURE:  
OTHER INFORMATION: n signifies a, t, c or g.  
US-09-475-947A-158

Query Match 1.2%; Score 12.4; DB 1; Length 15;  
Best Local Similarity 86.7%; Pred. No. 1.3e+02;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTGTTT 1879  
TTTTT

Db 1 TTTTTTTTTTTT 15

RESULT 205  
US-08-222-177A-433/c  
Sequence 433, Application US/08222177A  
Patent No. 5582979  
GENERAL INFORMATION:  
APPLICANT: Weber, James L.  
TITLE OF INVENTION: LENGTH POLYMORPHISMS IN  
TITLE OF INVENTION: (GC-CA)n.(GG-CT)n SEQUENCES AND METHODS OF USING SAME  
NUMBER OF SEQUENCES: 460  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dewitt Ross & Stevens, S.C.  
STREET: 8000 Excelsior Drive, Suite 401  
CITY: Madison  
STATE: Wisconsin  
COUNTRY: USA  
ZIP: 53717-1914

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/222,177A  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/341,562  
FILING DATE: 21-APR-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Sara, Charles S.  
REGISTRATION NUMBER: 30,492  
REFERENCE/DOCKET NUMBER: 09865.601  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (608) 831-2100  
TELEFAX: (608) 831-2106  
TELEX:  
INFORMATION FOR SEQ ID NO: 433:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-222-177A-433

Query Match 1.1%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGT 1805  
DB 12 GTGTGTGTGTGT 1

RESULT 206  
US-09-164-249B-2/c  
Sequence 2, Application US/09164249B  
Patent No. 6322971  
GENERAL INFORMATION:  
APPLICANT: Chetverin, Alexander B.  
APPLICANT: Kramer, Fred Russel  
TITLE OF INVENTION: NOVEL OLIGONUCLEOTIDE ARRAYS AND THEIR USE FOR SORTING,  
TITLE OF INVENTION: ISOLATING, SEQUENCING, AND MANIPULATING NUCLEIC ACIDS  
FILE REFERENCE: 07763-004003  
CURRENT APPLICATION NUMBER: US/09/164,249B  
CURRENT FILING DATE: 1998-09-30  
PRIOR APPLICATION NUMBER: US 08/473,010  
PRIOR FILING DATE: 1995-06-07  
PRIOR APPLICATION NUMBER: US 08/247,530  
PRIOR FILING DATE: 1994-05-23

QY 1793 TGTGTGTGTGTG 1804  
Db 1 TGTGTGTGTGTG 12  
RESULT 208  
US-09-958-221A-1/c  
; Sequence 1, Application US/09958221A  
; Patent No. 6686160  
; GENERAL INFORMATION:  
; APPLICANT: Haeringen van, Willem A.  
; TITLE OF INVENTION: UNIVERSAL VARIABLE FRAGMENTS  
; FILE REFERENCE: 92750/64  
; CURRENT FILING DATE: 2001-10-03  
; PRIOR APPLICATION NUMBER: EP 00200757.3  
; PRIOR FILING DATE: 2000-03-03  
; PRIOR APPLICATION NUMBER: PCT/NL01/00177  
; PRIOR FILING DATE: 2001-03-05  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: primer  
US-09-958-221A-1  
Query Match 1.1%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1793 TGTGTGTGTGTG 1804  
Db 12 TGTGTGTGTGTG 1  
RESULT 209  
US-08-291-932A-120/c  
; Sequence 120, Application US/08291932A  
; Patent No. 5658780  
; GENERAL INFORMATION:  
; APPLICANT: Stinchcomb, Dan T.  
; APPLICANT: Draper, Kenneth G.  
; APPLICANT: McSwiggen, James  
; TITLE OF INVENTION: RIBOZYME TREATMENT OF  
; TITLE OF INVENTION: DISEASES OR CONDITIONS  
; TITLE OF INVENTION: RELATED TO LEVELS OF  
; TITLE OF INVENTION: NF-KB  
; NUMBER OF SEQUENCES: 830  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2056  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/291,932A  
; FILING DATE: August 15, 1994  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; PRIOR APPLICATION DATA: including application  
; PRIOR APPLICATION DATA: described below;

Two

; PRIOR APPLICATION NUMBER: US 07/838,607  
; PRIOR FILING DATE: 1992-02-19  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetically derived DNA  
US-09-164-249B-2  
Query Match 1.1%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1794 GTGTGTGTGTGTG 1805  
Db 12 GTGTGTGTGTGTG 1  
RESULT 207  
US-09-281-481A-21  
; Sequence 21, Application US/09281481A  
; Patent No. 6383747  
; GENERAL INFORMATION:  
; APPLICANT: DAWKINS, Roger L. and ABRAHAM, Lawrence J.  
; TITLE OF INVENTION: GENETIC ANALYSIS  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SCULLY SCOTT MURPHY & PRESSER  
; STREET: 400 GARDEN CITY PLAZA  
; CITY: GARDEN CITY  
; STATE: NEW YORK  
; COUNTRY: UNITED STATES OF AMERICA  
; ZIP: 11530-0299  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/281,481A  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/893,971  
; FILING DATE: 16-JUL-1997  
; APPLICATION NUMBER: US 232,229  
; FILING DATE: 29-APR-1994  
; APPLICATION NUMBER: PK9279 (AU)  
; FILING DATE: 01-NOV-1991  
; APPLICATION NUMBER: PCT/AU92/00583  
; FILING DATE: 30-OCT-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: DIGILIO, FRANK S  
; REFERENCE/DOCKET NUMBER: 9279  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: +516 742 4343  
; TELEFAX: +516 742 4366  
; INFORMATION FOR SEQ ID NO: 21:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
US-09-281-481A-21  
Query Match 1.1%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

APPLICATION NUMBER: 08/245,466  
 FILING DATE: May 18, 1994  
 APPLICATION NUMBER: 07/987,132  
 FILING DATE: December 7, 1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Warburg, Richard J.  
 REGISTRATION NUMBER: 32,327  
 REFERENCE/DOCKET NUMBER: 208/157  
 TELEPHONE: (213) 489-1600  
 TELEFAX: (213) 955-0440  
 TELEX: 67-3510  
 INFORMATION FOR SEQ ID NO: 120:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 15 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US-08-291-932A-120

Query Match 1.1%; Score 12; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2153 CACCTGGAAGCA 2164  
 |||||  
 Db 15 CACCTGGAAGCA 4

RESULT 210  
 US-08-291-932A-193/c  
 ; Sequence 193, Application US/08291932A  
 ; Patent No. 5658780  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Stinchcomb, Dan T.  
 ; APPLICANT: Draper, Kenneth G.  
 ; APPLICANT: McSwiggen, James  
 ; TITLE OF INVENTION: RIBOZYME TREATMENT OF  
 ; TITLE OF INVENTION: DISEASES OR CONDITIONS  
 ; TITLE OF INVENTION: RELATED TO LEVELS OF  
 ; TITLE OF INVENTION: NF-KB  
 ; NUMBER OF SEQUENCES: 830  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Lyon & Lyon  
 ; STREET: 633 West Fifth Street  
 ; STREET: Suite 4700  
 ; CITY: Los Angeles  
 ; STATE: California  
 ; COUNTRY: U.S.A.  
 ; ZIP: 90071-2066  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 ; MEDIUM TYPE: storage  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: IBM P.C. DOS 5.0  
 ; SOFTWARE: Word Perfect 5.1  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/291,932A  
 ; FILING DATE: August 15, 1994  
 ; CLASSIFICATION: 514  
 ; PRIOR APPLICATION DATA:  
 ; PRIOR APPLICATION DATA: including application  
 ; PRIOR APPLICATION DATA: described below:  
 ; APPLICATION NUMBER: 08/245,466  
 ; FILING DATE: May 18, 1994  
 ; APPLICATION NUMBER: 07/987,132  
 ; FILING DATE: December 7, 1992  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Warburg, Richard J.  
 ; REGISTRATION NUMBER: 32,327  
 ; REFERENCE/DOCKET NUMBER: 208/157  
 ; TELEPHONE: (213) 489-1600  
 ; TELEFAX: (213) 955-0440  
 ; TELEX: 67-3510  
 ; INFORMATION FOR SEQ ID NO: 120:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 15 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; US-08-291-932A-120

TELEFAX: (213) 955-0440  
 TELEX: 67-3510  
 INFORMATION FOR SEQ ID NO: 193:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 15 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US-08-291-932A-193  
 Query Match 1.1%; Score 12; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2153 CACCTGGAAGCA 2164  
 |||||  
 Db 15 CACCTGGAAGCA 4  
 RESULT 211  
 US-08-291-932A-309/c  
 ; Sequence 309, Application US/08291932A  
 ; Patent No. 5658780  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Stinchcomb, Dan T.  
 ; APPLICANT: Draper, Kenneth G.  
 ; APPLICANT: McSwiggen, James  
 ; TITLE OF INVENTION: RIBOZYME TREATMENT OF  
 ; TITLE OF INVENTION: DISEASES OR CONDITIONS  
 ; TITLE OF INVENTION: RELATED TO LEVELS OF  
 ; TITLE OF INVENTION: NF-KB  
 ; NUMBER OF SEQUENCES: 830  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Lyon & Lyon  
 ; STREET: 633 West Fifth Street  
 ; STREET: Suite 4700  
 ; CITY: Los Angeles  
 ; STATE: California  
 ; COUNTRY: U.S.A.  
 ; ZIP: 90071-2066  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 ; MEDIUM TYPE: storage  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: IBM P.C. DOS 5.0  
 ; SOFTWARE: Word Perfect 5.1  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/291,932A  
 ; FILING DATE: August 15, 1994  
 ; CLASSIFICATION: 514  
 ; PRIOR APPLICATION DATA:  
 ; PRIOR APPLICATION DATA: including application  
 ; PRIOR APPLICATION DATA: described below:  
 ; APPLICATION NUMBER: 08/245,466  
 ; FILING DATE: May 18, 1994  
 ; APPLICATION NUMBER: 07/987,132  
 ; FILING DATE: December 7, 1992  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Warburg, Richard J.  
 ; REGISTRATION NUMBER: 32,327  
 ; REFERENCE/DOCKET NUMBER: 208/157  
 ; TELEPHONE: (213) 489-1600  
 ; TELEFAX: (213) 955-0440  
 ; TELEX: 67-3510  
 ; INFORMATION FOR SEQ ID NO: 309:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 15 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; US-08-291-932A-309

Query Match 1.1%; Score 12; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2153 CACCTGGAACGA 2164  
15 CACCTGGAACGA 4

Db

RESULT 212  
US-08-143-219-16  
; Sequence 16, Application US/08143219  
; Patent No. 5670330  
; GENERAL INFORMATION:

APPLICANT: Sonenberg, Nahum  
APPLICANT: Katze, Michael G.  
APPLICANT: Roy, Sophie  
APPLICANT: Koromilas, Antonis E.  
APPLICANT: Barber, Glen N.  
TITLE OF INVENTION: TUMOR-CELL ASSAY METHOD AND KIT  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 611 West Sixth Street  
CITY: Los Angeles  
STATE: CA  
COUNTRY: USA  
ZIP: 90017

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM compatible  
OPERATING SYSTEM: PC-DOS (Version 5.0)  
SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/143,219  
FILING DATE: October 25, 1993  
CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
PRIOR APPLICATION DATA: including application  
PRIOR APPLICATION DATA: described below:  
APPLICATION NUMBER: 08/141,244  
FILING DATE: October 22, 1993  
APPLICATION NUMBER: 07/953,681  
FILING DATE: September 29, 1992

ATTORNEY/AGENT INFORMATION:  
NAME: Douglas E. Olson  
REGISTRATION NUMBER: 22,798  
REFERENCE/DOCKET NUMBER: 204/139  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: COMPLEMENTARY TO THE RNA PROBE FOR  
INDIVIDUAL ISOLATE: PR-IV, FIGURE 5  
US-08-143-219-16

Query Match 1.1%; Score 12; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1784 TGTAATATTGT 1795  
3 TGTAATATTGT 14

Db

RESULT 213  
US-08-334-847-32/c  
; Sequence 32, Application US/08334847  
; Patent No. 5693532  
; GENERAL INFORMATION:

APPLICANT: McSwiggen, James  
APPLICANT: Draper, Kenneth  
APPLICANT: Pavco, Pam  
APPLICANT: Woolf, Tod  
TITLE OF INVENTION: METHOD AND REAGENT FOR  
TITLE OF INVENTION: INHIBITING RESPIRATORY  
TITLE OF INVENTION: SYNCYTIAL VIRUS  
NUMBER OF SEQUENCES: 909  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/334,847  
FILING DATE: No. 5693532ember 4, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:

FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 209/032  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-334-847-32

Query Match 1.1%; Score 12; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1347 TGCAACAAT 1358  
13 TGCAACAAT 2

Db

RESULT 214  
US-08-334-847-33/c  
; Sequence 33, Application US/08334847  
; Patent No. 5693532  
; GENERAL INFORMATION:

APPLICANT: McSwiggen, James  
APPLICANT: Draper, Kenneth  
APPLICANT: Pavco, Pam  
APPLICANT: Woolf, Tod  
TITLE OF INVENTION: METHOD AND REAGENT FOR  
TITLE OF INVENTION: INHIBITING RESPIRATORY  
TITLE OF INVENTION: SYNCYTIAL VIRUS  
NUMBER OF SEQUENCES: 909  
CORRESPONDENCE ADDRESS:

```

; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/334,847
; FILING DATE: No. 5693532ember 4, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 209/032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-334-847-33

Query Match 1.1%; Score 12; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1347 TGTCACAAAT 1358
DB 12 TGTCACAAAT 1

RESULT 215
US-09-340-798A-51/c
; Sequence 51, Application US/09340798A
; Patent No. 6534312
; GENERAL INFORMATION:
; APPLICANT: SHIVER, JOHN W.
; LIU, MARGARET A.
; PERRY, HELEN C.
; DAVIES, MARY-ELLEN M.
; FREED, DANIEL C.
; TITLE OF INVENTION: VACCINES COMPRISING SYNTHETIC GENES
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: J. MARK HAND - MERCK & CO., INC.
; STREET: 126 E. LINCOLN AVE., P.O. BOX 2000
; CITY: RAHWAY
; STATE: NEW JERSEY
; COUNTRY: US
; ZIP: 07065-0907
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/340,798A
; FILING DATE: 28-Jun-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:

```

```

; APPLICATION NUMBER: US/08/877,418
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: HAND, J. MARK
; REGISTRATION NUMBER: 36,545
; REFERENCE/DOCKET NUMBER: 19729Y
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908-594-3905
; TELEFAX: 908-594-4720
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "oligonucleotide"
; SEQUENCE DESCRIPTION: SEQ ID NO: 51:
US-09-340-798A-51

Query Match 1.1%; Score 12; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1521 ATGCGTGTATT 1532
DB 13 ATGCGTGTATT 2

RESULT 216
US-08-849-021-88
; Sequence 88, Application US/08849021
; Patent No. 5955276
; GENERAL INFORMATION:
; APPLICANT: MORGANTE, MICHELE
; APPLICANT: VOGEL, JULIE M.
; TITLE OF INVENTION: COMPOUND MICROSATELLITE
; TITLE OF INVENTION: PRIMERS FOR THE
; TITLE OF INVENTION: DETECTION OF GENETIC
; TITLE OF INVENTION: POLYMORPHISMS
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND
; COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: U.S.A.
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PATENT IN RELEASE #1.0, VERSION 1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/849,021
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/346,456
; FILING DATE: 28 NOVEMBER 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: FLOYD, LINDA AXAMETHY
; REGISTRATION NUMBER: 33,692
; REFERENCE/DOCKET NUMBER: BB-1064-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-892-8112
; TELEFAX: 302-992-7949
; INFORMATION FOR SEQ ID NO: 88:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

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TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-849-021-88

Query Match 1.1%; Score 12; DB 1; Length 22;  
Best Local Similarity 75.0%; Pred. No. 2.1e+02;  
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1813 TATATATATATATGTCACA 1832  
DB 1 TATATATATACACACACA 20

## RESULT 217

US-08-476-614-5  
Sequence 5, Application US/08476614  
Patent No. 5618673  
GENERAL INFORMATION:  
APPLICANT: NARANG, HARASH K  
TITLE OF INVENTION: OLIGONUCLEOTIDES AND THEIR USE IN AN  
TITLE OF INVENTION: ASSAY  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON & VANDERHVE P.C.  
STREET: 8TH FLOOR, 1100 NORTH GLEBE ROAD  
CITY: ARLINGTON  
STATE: VIRGINIA  
COUNTRY: USA  
ZIP: 22201-4714  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/476,614  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MITCHARD, LEONARD C  
REGISTRATION NUMBER: 29,009  
REFERENCE/DOCKET NUMBER: 604-349  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 816 4000  
TELEFAX: (703) 816 4100  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-476-614-5

Query Match 1.1%; Score 11.4; DB 1; Length 13;  
Best Local Similarity 92.3%; Pred. No. 1.4e+02;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1818 ATATATATATGTA 1830  
DB 1 ATATATATACGTA 13

## RESULT 218

US-08-153-051B-51  
Sequence 51, Application US/08153051B  
Patent No. 5645966  
GENERAL INFORMATION:  
APPLICANT: Michael D. West  
APPLICANT: Jerry W. Shay  
APPLICANT: Woodring E. Wright

APPLICANT: Elizabeth Blackburn  
APPLICANT: Nam Woo Kim  
APPLICANT: Calvin B. Harley  
APPLICANT: Scott L. Weinrich  
APPLICANT: Catherine Strahl  
APPLICANT: Michael J. McEachern  
APPLICANT: Homayoun Vaziri  
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF  
TITLE OF INVENTION: CONDITIONS RELATED TO TELOMERE  
TITLE OF INVENTION: LENGTH AND/OR TELOMERASE ACTIVITY  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 MB  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/153,051B  
FILING DATE: No. 5645966ember 12, 1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/038,766  
FILING DATE: March 24, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 204/195  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 51:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-153-051B-51

Query Match 1.1%; Score 11.4; DB 1; Length 13;  
Best Local Similarity 92.3%; Pred. No. 1.4e+02;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1792 TTGTGTGTGTGTG 1804  
DB 1 TGGTGTGTGTGTG 13

## RESULT 219

US-08-060-952C-50  
Sequence 50, Application US/08060952C  
Patent No. 5695932  
GENERAL INFORMATION:  
APPLICANT: Michael D. West  
APPLICANT: Jerry W. Shay  
APPLICANT: Woodring E. Wright  
APPLICANT: Elizabeth Blackburn  
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF CONDITIONS  
TITLE OF INVENTION: RELATED TO TELOMERE LENGTH AND/OR  
TITLE OF INVENTION: TELOMERASE ACTIVITY  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700

CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/060,952C  
FILING DATE: May 13, 1993  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/882,438  
FILING DATE: May 13, 1992  
APPLICATION NUMBER: 08/038,766  
FILING DATE: March 24, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 202/045  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 50:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-060-952C-50

Query Match 1.1%; Score 11.4; DB 1; Length 13;  
Best Local Similarity 92.3%; Pred. No. 1.4e+02;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1792 TTGTGTGTGTGTG 1804  
Db 1 TGGTGTGTGTGTG 13

RESULT 220  
US-08-431-080-2  
Sequence 2, Application US/08431080  
Patent No. 589886  
GENERAL INFORMATION:  
APPLICANT: Gottschling, Daniel B.  
APPLICANT: Singer, Miriam S.  
TITLE OF INVENTION: Telomerase Compositions and Methods  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: TEXAS  
COUNTRY: UNITED STATES OF AMERICA  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/431,080  
FILING DATE: Concurrently Herewith  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: SN 08/326,781  
FILING DATE: October 20, 1994  
CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:  
NAME: Parker, David L.  
REGISTRATION NUMBER: 32,165  
REFERENCE/DOCKET NUMBER: ARCD:155/PAR  
TELEPHONE: (512) 418-3000  
TELEFAX: (713) 789-2679  
TELEX: 79-0924  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-431-080-2

Query Match 1.1%; Score 11.4; DB 1; Length 13;  
Best Local Similarity 92.3%; Pred. No. 1.4e+02;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTG 1806  
Db 1 GTGTGTGTGTGTG 13

RESULT 221  
US-08-151-477A-51  
Sequence 51, Application US/08151477A  
Patent No. 5830644  
GENERAL INFORMATION:  
APPLICANT: Michael D. West  
APPLICANT: Jerry W. Shay  
APPLICANT: Woodring E. Wright  
APPLICANT: Elizabeth Blackburn  
APPLICANT: Nam Woo Kim  
APPLICANT: Calvin B. Harley  
APPLICANT: Scott L. Weinrich  
APPLICANT: Catherine Strahl  
APPLICANT: Michael J. McEachern  
APPLICANT: Homayoun Vaziri  
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF  
CONDITIONS RELATED TO TELOMERE  
TITLE OF INVENTION: LENGTH AND/OR TELOMERASE ACTIVITY  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/151,477A  
FILING DATE: No. 5830644ember 12, 1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/038,766  
FILING DATE: March 24, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 202/189  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 51:

SEQUENCE CHARACTERISTICS:  
LENGTH: 13 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-151-477A-51

Query Match 1.1%; Score 11.4; DB 1; Length 13;  
Best Local Similarity 92.3%; Pred. No. 1.4e+02;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1792 TTGTGTGTGTGTG 1804  
DB 1 TGTGTGTGTGTG 13

RESULT 222

US-08-938-534-2  
Sequence 2, Application US/08938534  
Patent No. 5916752  
GENERAL INFORMATION:  
APPLICANT: Gottschling, Daniel E.  
APPLICANT: Singer, Miriam S.  
TITLE OF INVENTION: Telomerase Compositions and Methods  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: TEXAS  
COUNTRY: UNITED STATES OF AMERICA  
ZIP: 77210

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/938,534  
FILING DATE: 26-SEP-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/431,080  
FILING DATE:  
APPLICATION NUMBER: SN 08/326,781  
FILING DATE: October 20, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Parker, David L.  
REGISTRATION NUMBER: 32,165  
REFERENCE/DOCKET NUMBER: ARCD:155/PAR  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (512) 418-3000  
TELEFAX: (713) 789-2679  
TELEX: 79-0924

INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-938-534-2

Query Match 1.1%; Score 11.4; DB 1; Length 13;  
Best Local Similarity 92.3%; Pred. No. 1.4e+02;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTG 1806  
DB 1 GTGTGTGTGTGTG 13

RESULT 223

US-08-819-867-77

Sequence 77, Application US/08819867  
Patent No. 6007989  
GENERAL INFORMATION:  
APPLICANT: Michael D. West  
APPLICANT: Calvin B. Harley  
APPLICANT: Scott L. Weinrich  
APPLICANT: Catherine M. Strahl  
APPLICANT: Michael J. Moeachein  
APPLICANT: Jerry Shay  
APPLICANT: Woodring E. Wright  
APPLICANT: Elizabeth H. Blackburn  
APPLICANT: Nam Woo Kim  
APPLICANT: Homayoun Vaziri  
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF  
TITLE OF INVENTION: CONDITIONS RELATED TO  
TITLE OF INVENTION: TELOMERE LENGTH AND/OR  
TITLE OF INVENTION: TELOMERASE ACTIVITY  
NUMBER OF SEQUENCES: 80  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq for Windows 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/819,867  
FILING DATE: March 14, 1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/153,051  
FILING DATE: No. 6007989ember 12, 1993  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Chambers, Daniel M.  
REGISTRATION NUMBER: 34,561  
REFERENCE/DOCKET NUMBER: 224/232  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 77:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-819-867-77

Query Match 1.1%; Score 11.4; DB 1; Length 13;  
Best Local Similarity 92.3%; Pred. No. 1.4e+02;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1792 TTGTGTGTGTGTG 1804  
DB 1 TGTGTGTGTGTG 13

RESULT 224

US-08-464-011B-50  
Sequence 50, Application US/08464011B  
Patent No. 6388789  
GENERAL INFORMATION:  
APPLICANT: Michael D. West  
APPLICANT: Jerry W. Shay



```

;
; Woodring E. Wright
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF CONDITIONS
; RELATED TO TELOMERASE LENGTH AND/OR
; TELOMERASE ACTIVITY
;
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; SUITE: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 MB
; storage
;
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,011B
; FILING DATE: 05-Jun-1995
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/892,438
; FILING DATE: May 13, 1992
; APPLICATION NUMBER: 08/038,766
; FILING DATE: March 24, 1993
; APPLICATION NUMBER: 08/060,952
; FILING DATE: May 13, 1993
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 202/045
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1800
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
;
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 50:
US-08-464-011B-50
;
; Query Match 1.1%; Score 11.4; DB 1; Length 13;
; Best Local Similarity 92.3%; Pred. No. 1.4e+02;
; Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
; Qy 1792 TTGTGTGTGTGTG 1804
; | |||||
; Db 1 TGGTGTGTGTGTG 13
;
; RESULT 225
; US-09-345-294-2
; Sequence 2, Application US/09345294
; Patent No. 6387619
; GENERAL INFORMATION:
; APPLICANT: Gottschling, Daniel E.
; SINGER, Miriam S.
; TITLE OF INVENTION: Telomerase Compositions and Methods
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TEXAS
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 77210
;
; COMPUTER READABLE FORM:

```

```

;
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
; SOFTWARE: Patentin Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/345,294
; FILING DATE: 30-Jun-1999
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/431,080
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, David L.
; REGISTRATION NUMBER: 32,165
; REFERENCE/DOCKET NUMBER: ARCD:155/PAR
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (713) 789-2679
; TELEX: 79-0924
;
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-345-294-2
;
; Query Match 1.1%; Score 11.4; DB 1; Length 13;
; Best Local Similarity 92.3%; Pred. No. 1.4e+02;
; Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
; Qy 1794 GTGTGTGTGTGTG 1806
; | |||||
; Db 1 GTGTGTGTGTGTG 13
;
; RESULT 226
; US-09-922-445-10
; Sequence 10, Application US/09922445
; Patent No. 6528268
; GENERAL INFORMATION:
; APPLICANT: Andersson, Maria K.
; APPLICANT: Berglund, Lars G. T.
; APPLICANT: Reneland, Rikard H.
; APPLICANT: Adam, Gail I. R.
; TITLE OF INVENTION: REAGENTS AND METHODS FOR DETECTION OF HEART FAILURE
; FILE REFERENCE: G3126US
; CURRENT APPLICATION NUMBER: US/09/922,445
; CURRENT FILING DATE: 2001-08-03
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 10
; LENGTH: 13
; TYPE: DNA
; ORGANISM: synthetic
;
; US-09-922-445-10
;
; Query Match 1.1%; Score 11.4; DB 1; Length 13;
; Best Local Similarity 92.3%; Pred. No. 1.4e+02;
; Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
; Qy 1319 TTCCACCCCAATT 1331
; | |||||
; Db 1 TTCCACCCCAATT 13
;
; RESULT 227
; US-09-922-445-35/c
; Sequence 35, Application US/09922445
; Patent No. 6528268
; GENERAL INFORMATION:
; APPLICANT: Andersson, Maria K.

```

APPLICANT: Berglund, Lars G. T.  
APPLICANT: Rensland, Rikard H.  
APPLICANT: Adam, Gail I. R.  
TITLE OF INVENTION: REAGENTS AND METHODS FOR DETECTION OF HEART FAILURE  
FILE REFERENCE: GGI2605  
CURRENT APPLICATION NUMBER: US/09/922.445  
CURRENT FILING DATE: 2001-08-03  
NUMBER OF SEQ ID NOS: 51  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 35  
LENGTH: 13  
TYPE: DNA  
ORGANISM: synthetic  
US-09-922-445-35

Query Match 1.1%; Score 11.4; DB 1; Length 13;  
Best Local Similarity 92.3%; Pred. No. 1.4e+02;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1319 TTCCACCCCAATT 1331  
DB 13 TTCCACCCCAATT 1

RESULT 228  
US-09-378-535-77  
Sequence 77, Application US/09378535  
Patent No. 6551774

GENERAL INFORMATION:  
APPLICANT: Michael D. West  
Calvin B. Harley  
Scott L. Weinrich  
Catherine M. Strahl  
Michael J. Mceachern  
Jerry Shay  
Woodring E. Wright  
Elizabeth H. Blackburn  
Nam Woo Kim  
Homayoun Vaziri

TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF  
CONDITIONS RELATED TO  
TELOMERE LENGTH AND/OR  
TELOMERASE ACTIVITY

NUMBER OF SEQUENCES: 80  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
Suite 4700

CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
storage

COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSEQ for Windows 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/378,535  
FILING DATE: 20-Aug-1999  
CLASSIFICATION: <unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/819,867  
FILING DATE: <unknown>

ATTORNEY/AGENT INFORMATION:  
NAME: Chambers, Daniel M.

REGISTRATION NUMBER: 34,561  
REFERENCE/DOCKET NUMBER: 224/232

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440  
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 77:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 77:  
US-09-378-535-77

Query Match 1.1%; Score 11.4; DB 1; Length 13;  
Best Local Similarity 92.3%; Pred. No. 1.4e+02;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1792 TTGTGTGTGTGTG 1804  
DB 1 TGGTGTGTGTGTG 13

RESULT 229

US-09-377-497-56  
Sequence 56, Application US/09377497  
Patent No. 8670119

GENERAL INFORMATION:  
APPLICANT: YOSHIKAWA, YOSHIE  
APPLICANT: MURAI, HIROYUKI  
APPLICANT: ASADA, KIYOZO  
APPLICANT: HINO, FUMITSUGU  
APPLICANT: KATO, IKUNOSHIN  
TITLE OF INVENTION: CANCER-ASSOCIATED GENES  
FILE REFERENCE: 1422-388P  
CURRENT APPLICATION NUMBER: US/09/377,497  
CURRENT FILING DATE: 1999-08-20  
NUMBER OF SEQ ID NOS: 70  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 56

LENGTH: 13  
TYPE: DNA  
ORGANISM: Artificial Sequence

FEATURE:  
OTHER INFORMATION: any n or Xaa = unknown

FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA  
US-09-377-497-56

Query Match 1.1%; Score 11.4; DB 1; Length 13;  
Best Local Similarity 92.3%; Pred. No. 1.4e+02;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1871 TTTTGTGTGTAA 1883  
DB 1 TTTTGTGTGTAA 13

RESULT 230

US-08-284-534-28  
Sequence 28, Application US/08264534  
Patent No. 5648464

GENERAL INFORMATION:

APPLICANT: Artavanis-Tsakonas, Spyridon et al.

TITLE OF INVENTION: Human No. 5648464ch And Delta, Binding Domains  
TITLE OF INVENTION: In Topolythmic Proteins, And Methods Based Thereon  
NUMBER OF SEQUENCES: 34

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA: US/08/264,534  
;; APPLICATION NUMBER: US/08/264,534  
;; FILING DATE:  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/695,189  
;; FILING DATE: 03-MAY-1991  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Mirock, S. Leslie  
;; REGISTRATION NUMBER: 19,872  
;; REFERENCE/DOCKET NUMBER: 7326-004  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 212 790-9090  
;; TELEFAX: 212 8698864/9741  
;; TELEX: 66141 PENNIE  
;; INFORMATION FOR SEQ ID NO: 28:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 14 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: unknown  
;; MOLECULE TYPE: CDNA  
US-08-264-534-28

Query Match 1.1%; Score 11.4; DB 1; Length 14;  
Best Local Similarity 92.3%; Pred. No. 1.6e+02;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1839 TAAGTTAACTTAA 1851  
Db 2 TAAGTTAACTTAA 14

RESULT 231  
US-08-264-534-28/c  
;; Sequence 28, Application US/08264534  
;; Patent No. 5648464  
;; GENERAL INFORMATION:  
;; APPLICANT: Artavanis-Tsakonas, Spyridon et al.  
;; TITLE OF INVENTION: Human No. 5648464ch And Delta, Binding Domains  
;; TITLE OF INVENTION: In Toporythmic Proteins, And Methods Based Thereon  
;; NUMBER OF SEQUENCES: 34  
;; CORRESPONDENCE ADDRESSES:  
;; ADDRESSEE: Pennie & Edmonds  
;; STREET: 1155 Avenue of the Americas  
;; CITY: New York  
;; STATE: New York  
;; COUNTRY: U.S.A.  
;; ZIP: 10036  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/264,534  
;; FILING DATE:  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/695,189  
;; FILING DATE: 03-MAY-1991  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Mirock, S. Leslie  
;; REGISTRATION NUMBER: 19,872  
;; REFERENCE/DOCKET NUMBER: 7326-004  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 212 790-9090  
;; TELEFAX: 212 8698864/9741  
;; TELEX: 66141 PENNIE  
;; INFORMATION FOR SEQ ID NO: 28:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 14 base pairs

;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: unknown  
;; MOLECULE TYPE: CDNA  
US-08-264-534-28

Query Match 1.1%; Score 11.4; DB 1; Length 14;  
Best Local Similarity 92.3%; Pred. No. 1.6e+02;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1839 TAAGTTAACTTAA 1851  
Db 13 TAAGTTAACTTAA 1

RESULT 232  
US-08-268-799-6  
;; Sequence 6, Application US/08268799  
;; Patent No. 5654195  
;; GENERAL INFORMATION:  
;; APPLICANT: Sodroski, Joseph  
;; APPLICANT: Haseltine, William A.  
;; APPLICANT: Letvin, No. 5654195man  
;; APPLICANT: Li, John  
;; TITLE OF INVENTION: Vectors Expressing Hybrid Viruses,  
;; TITLE OF INVENTION: Methods Of Use And No. 5654195el Assays  
;; NUMBER OF SEQUENCES: 8  
;; CORRESPONDENCE ADDRESSES:  
;; ADDRESSEE: Dike, Bronstein, Roberts and Cushman  
;; STREET: 130 Water Street  
;; CITY: Boston  
;; STATE: Massachusetts  
;; COUNTRY: USA  
;; ZIP: 02109  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/268,799  
;; FILING DATE:  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/887,505  
;; FILING DATE: 22-MAY-1992  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Eisenstein, Ronald I.  
;; REGISTRATION NUMBER: 30628  
;; REFERENCE/DOCKET NUMBER: 41858  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (617) 523-3400  
;; TELEFAX: (617) 523-6440  
;; TELEX: 200291 stre ur  
;; INFORMATION FOR SEQ ID NO: 6:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 14 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: unknown  
;; TOPOLOGY: unknown  
US-08-268-799-6

Query Match 1.1%; Score 11.4; DB 1; Length 14;  
Best Local Similarity 92.3%; Pred. No. 1.6e+02;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1958 AGCATGAATGGA 1970  
Db 1 AGCAGAGATGGA 13

RESULT 233  
US-08-465-500-28

; Sequence 28, Application US/08465500  
; Patent No. 5789195  
; GENERAL INFORMATION:  
; APPLICANT: Artavanis-Tsakonas, Spyridon  
; APPLICANT: Muskavitch, Marc A.T.  
; APPLICANT: Fehon, Richard G.  
; APPLICANT: Rebay, Ilaria  
; APPLICANT: Blumweller, Cristine M.  
; APPLICANT: Shepard, Scott B.  
; TITLE OF INVENTION: HUMAN NOTCH AND DELTA, BINDING DOMAINS  
; TITLE OF INVENTION: IN TOPORHYTHMIC PROTEINS, AND METHODS BASED THEREON  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PENNIE & EDMONDS  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/465,500  
; FILING DATE: 05-JUN-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mistock, S. Lealie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 7326-034  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; INFORMATION FOR SEQ ID NO: 28:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 14 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: unknown  
; MOLECULE TYPE: cDNA  
; US-08-465-500-28  
; Query Match 1.1%; Score 11.4; DB 1; Length 14;  
; Best Local Similarity 92.3%; Pred. No. 1.6e+02;  
; Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1839 TAAGTTAACTTAA 1851  
DB 2 TAAGTTAACTTAA 14  
RESULT 234  
US-08-465-500-28/c  
; Sequence 28, Application US/08465500  
; Patent No. 5789195  
; GENERAL INFORMATION:  
; APPLICANT: Artavanis-Tsakonas, Spyridon  
; APPLICANT: Muskavitch, Marc A.T.  
; APPLICANT: Fehon, Richard G.  
; APPLICANT: Rebay, Ilaria  
; APPLICANT: Blumweller, Cristine M.  
; APPLICANT: Shepard, Scott B.  
; TITLE OF INVENTION: HUMAN NOTCH AND DELTA, BINDING DOMAINS  
; TITLE OF INVENTION: IN TOPORHYTHMIC PROTEINS, AND METHODS BASED THEREON  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PENNIE & EDMONDS  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA

; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/465,500  
; FILING DATE: 05-JUN-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mistock, S. Lealie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 7326-034  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; INFORMATION FOR SEQ ID NO: 28:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 14 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: unknown  
; MOLECULE TYPE: cDNA  
; US-08-465-500-28  
; Query Match 1.1%; Score 11.4; DB 1; Length 14;  
; Best Local Similarity 92.3%; Pred. No. 1.6e+02;  
; Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1839 TAAGTTAACTTAA 1851  
DB 13 TAAGTTAACTTAA 1  
RESULT 235  
US-08-672-564-11  
; Sequence 11, Application US/08672564  
; Patent No. 5824503  
; GENERAL INFORMATION:  
; APPLICANT: KUROME, Yoko  
; APPLICANT: IZU, Hiroyuki  
; APPLICANT: IZUMI, Yoshiya  
; APPLICANT: SANO, Mutsumi  
; APPLICANT: KATO, Ikunoshin  
; APPLICANT: ITO, Makoto  
; TITLE OF INVENTION: GENE ENCODING ENDOGLYCOCERAMIDASE ACTIVATOR  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP  
; STREET: P.O. Box 747  
; CITY: Falls Church  
; STATE: Virginia  
; COUNTRY: USA  
; ZIP: 22040-0747  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/672,564  
; FILING DATE: 28 JUNE 1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: WEINER, Marc S.  
; REGISTRATION NUMBER: 32,181  
; REFERENCE/DOCKET NUMBER: 1422-0263P  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 205-8000  
; TELEFAX: (703) 205-8050  
; TELEX: 248345  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:

```

; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid (synthetic DNA)
US-08-672-564-11

Query Match
  1.1%; Score 11.4; DB 1; Length 14;
Best Local Similarity 92.3%; Pred. No. 1.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1839 TAAGTTAACTTAA 1851
Db 2 TAAGTTAACTTAA 14

RESULT 236
US-08-672-564-11/c
; Sequence 11, Application US/08672564
; Patent No. 5824503
; GENERAL INFORMATION:
; APPLICANT: KURUME, Yoko
; APPLICANT: IZU, Hiroyuki
; APPLICANT: IZUMI, Yoshiya
; APPLICANT: SANO, Mutsumi
; APPLICANT: KATO, Ikunoshin
; APPLICANT: ITO, Makoto
; TITLE OF INVENTION: GENE ENCODING ENDOGLYCCERAMIDASE ACTIVATOR
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
; STREET: P.O. Box 747
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,564
; Filing DATE: 28 JUNE 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: WEINER, Marc S.
; REGISTRATION NUMBER: 32,181
; REFERENCE/DOCKET NUMBER: 1422-0263P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid (synthetic DNA)
US-08-672-564-11

Query Match
  1.1%; Score 11.4; DB 1; Length 14;
Best Local Similarity 92.3%; Pred. No. 1.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1839 TAAGTTAACTTAA 1851
Db 13 TAAGTTAACTTAA 1

RESULT 237
US-08-346-126-28
; Sequence 28, Application US/08346126
```

```

; Patent No. 5849869
; GENERAL INFORMATION:
; APPLICANT: Artavanis-Tsakonas, Spyridon et al.
; TITLE OF INVENTION: Human No. 5849869ch And Delta, Binding Domains
; TITLE OF INVENTION: In Topolythmic Proteins, And Methods Based Thereon
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/346,126
; Filing DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/791,923
; Filing DATE: 14-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 19,872
; REFERENCE/DOCKET NUMBER: 7326-007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 8698864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
US-08-346-126-28

Query Match
  1.1%; Score 11.4; DB 1; Length 14;
Best Local Similarity 92.3%; Pred. No. 1.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1839 TAAGTTAACTTAA 1851
Db 2 TAAGTTAACTTAA 14

RESULT 238
US-08-346-126-28/c
; Sequence 28, Application US/08346126
; Patent No. 5849869
; GENERAL INFORMATION:
; APPLICANT: Artavanis-Tsakonas, Spyridon et al.
; TITLE OF INVENTION: Human No. 5849869ch And Delta, Binding Domains
; TITLE OF INVENTION: In Topolythmic Proteins, And Methods Based Thereon
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
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```

; APPLICATION NUMBER: US/08/346,126
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION NUMBER: 07/791,923
; APPLICATION NUMBER: 07/791,923
; FILING DATE: 14-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7326-007
; TELEPHONE: 212 790-9090
; TELEFAX: 212 8698864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: CDNA
; US-08-346-126-28

Query Match 1.1%; Score 11.4; DB 1; Length 14;
Best Local Similarity 92.3%; Pred. No. 1.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1839 TAAGTTAACTTAA 1851
DB 13 TAAGTTAACTTAA 1

RESULT 239
US-08-346-128-28
; Sequence 28, Application US/08346128
; Patent No. 5856441
; GENERAL INFORMATION:
; APPLICANT: Artavanis-Tsakonas, Spyridon et al.
; TITLE OF INVENTION: Human No. 5856441ch And Delta, Binding Domains
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/346,128
; APPLICATION NUMBER: US/08/346,128
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION NUMBER: 07/879,038
; APPLICATION NUMBER: 07/879,038
; FILING DATE: 30-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7326-009
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 8698864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: CDNA
; US-08-346-128-28

Query Match 1.1%; Score 11.4; DB 1; Length 14;
Best Local Similarity 92.3%; Pred. No. 1.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1839 TAAGTTAACTTAA 1851
DB 13 TAAGTTAACTTAA 1

RESULT 241
US-08-682-847-8
; Sequence 8, Application US/08682847
; Patent No. 5858989
; GENERAL INFORMATION:
; APPLICANT: BABIUK, LORNE
```

```

; TOPOLOGY: unknown
; MOLECULE TYPE: CDNA
; US-08-346-128-28

Query Match 1.1%; Score 11.4; DB 1; Length 14;
Best Local Similarity 92.3%; Pred. No. 1.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1839 TAAGTTAACTTAA 1851
DB 2 TAAGTTAACTTAA 14

RESULT 240
US-08-346-128-28/c
; Sequence 28, Application US/08346128
; Patent No. 5856441
; GENERAL INFORMATION:
; APPLICANT: Artavanis-Tsakonas, Spyridon et al.
; TITLE OF INVENTION: Human No. 5856441ch And Delta, Binding Domains
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/346,128
; APPLICATION NUMBER: US/08/346,128
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION NUMBER: 07/879,038
; APPLICATION NUMBER: 07/879,038
; FILING DATE: 30-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7326-009
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 8698864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: CDNA
; US-08-346-128-28

Query Match 1.1%; Score 11.4; DB 1; Length 14;
Best Local Similarity 92.3%; Pred. No. 1.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1839 TAAGTTAACTTAA 1851
DB 13 TAAGTTAACTTAA 1

RESULT 241
US-08-682-847-8
; Sequence 8, Application US/08682847
; Patent No. 5858989
; GENERAL INFORMATION:
; APPLICANT: BABIUK, LORNE
```

```

; APPLICANT: VAN DEN HURK, SYLVIA
; APPLICANT: ZAMB, TIM
; APPLICANT: FITZPATRICK, DAVID
; TITLE OF INVENTION: RECOMBINANT BOVINE HERPESVIRUS TYPE 1
; TITLE OF INVENTION: POLYPEPTIDES AND VACCINES
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/682,847
; FILING DATE: 12-JUL-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: PARK, FREDDIE K.
; REGISTRATION NUMBER: 35,636
; REFERENCE/DOCKET NUMBER: 29310-20005.10
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-682-847-8

Query Match 1.1%; Score 11.4; DB 1; Length 14;
Best Local Similarity 92.3%; Pred. No. 1.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1839 TAAGTTAACTTAA 1851
DB 2 TAAGTTAACTTAA 14
|||||

```

RESULT 242

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US-08-682-847-8/c
; Sequence 8, Application US/08682847
; Patent No. 585899
; GENERAL INFORMATION:
; APPLICANT: BABIUK, LORNE
; APPLICANT: VAN DEN HURK, SYLVIA
; APPLICANT: ZAMB, TIM
; APPLICANT: FITZPATRICK, DAVID
; TITLE OF INVENTION: RECOMBINANT BOVINE HERPESVIRUS TYPE 1
; TITLE OF INVENTION: POLYPEPTIDES AND VACCINES
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

```

```

; APPLICATION NUMBER: US/08/682,847
; FILING DATE: 12-JUL-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: PARK, FREDDIE K.
; REGISTRATION NUMBER: 35,636
; REFERENCE/DOCKET NUMBER: 29310-20005.10
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-682-847-8

Query Match 1.1%; Score 11.4; DB 1; Length 14;
Best Local Similarity 92.3%; Pred. No. 1.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1839 TAAGTTAACTTAA 1851
DB 13 TAAGTTAACTTAA 1
|||||

```

RESULT 243

```

US-08-544-381B-216/C
; Sequence 216, Application US/08544381B
; Patent No. 6027880
; GENERAL INFORMATION:
; APPLICANT: Cronin, Maureen T.
; APPLICANT: Miyada, Charles Garrett
; APPLICANT: Hubbell, Earl A.
; APPLICANT: Chee, Mark
; APPLICANT: Fodor, Stephen P.A.
; APPLICANT: Huang, Xiaohua C.
; APPLICANT: Lipshutz, Robert J.
; APPLICANT: Lobban, Peter E.
; APPLICANT: Morris, Macdonald S.
; APPLICANT: Sheldon, Edward L.
; TITLE OF INVENTION: Arrays of Nucleic Acid Probes for
; TITLE OF INVENTION: Detecting Cystic Fibrosis
; NUMBER OF SEQUENCES: 250
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/544,381B
; FILING DATE: 10-OCT-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/510,521
; FILING DATE: 02-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/12305
; FILING DATE: 26-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/284,064
; FILING DATE: 02-AUG-1994
; PRIOR APPLICATION DATA:

```

```

; APPLICATION NUMBER: US 08/143,312
; FILING DATE: 26-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebeschuetz, Joe
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 018547-0041300S
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 216:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (oligonucleotide)
US-08-544-381B-216

Query Match 1.1%; Score 11.4; DB 1; Length 14;
Best Local Similarity 92.3%; Pred. NO. 1.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1564 TGCTCACTGACCT 1576
Db 13 TGCTCACTGACCT 1

RESULT 244
US-08-832-021-5
; Sequence 5, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
; APPLICANT: Combates, N.
; APPLICANT: Pardinas, J.
; APPLICANT: Parimoo, S.
; APPLICANT: Prouty, S.
; APPLICANT: Stenn, K.
; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
; FILE REFERENCE: JBP-382
; CURRENT APPLICATION NUMBER: US/08/832,021
; CURRENT FILING DATE: 1997-04-02
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 5
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-5

Query Match 1.1%; Score 11.4; DB 1; Length 14;
Best Local Similarity 92.3%; Pred. NO. 1.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1871 TTTTGTGTTTAA 1883
Db 2 TTTTGTGTTTAA 14

RESULT 245
US-08-832-021-16
; Sequence 16, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
; APPLICANT: Combates, N.
; APPLICANT: Pardinas, J.
; APPLICANT: Parimoo, S.
; APPLICANT: Prouty, S.
; APPLICANT: Stenn, K.
; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
; FILE REFERENCE: JBP-382
; CURRENT APPLICATION NUMBER: US/08/832,021
; FILING DATE: 1997-04-02
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 16
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-16

Query Match 1.1%; Score 11.4; DB 1; Length 14;
Best Local Similarity 92.3%; Pred. NO. 1.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGT 1877
Db 2 TTTTATTTTGT 14

RESULT 246
US-08-724-466B-14
; Sequence 14, Application US/08724466B
; Patent No. 6063606
; GENERAL INFORMATION:
; APPLICANT: Petrovich, P. Martin, White, Jay A.,
; APPLICANT: Beckett, Barbara R., Jones, Glenville
; TITLE OF INVENTION: Retinoid Metabolizing Protein
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Blake, Cassels & Graydon
; STREET: Box 25, Commerce Court West
; CITY: Toronto
; ZIP: M5L 1A9
; COUNTRY: Canada
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
; COMPUTER: COMPAQ, IBM PC compatible
; OPERATING SYSTEM: MS-DOS 5.1
; SOFTWARE: WORD PERFECT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/724,466B
; FILING DATE: October 1, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/667,546
; FILING DATE: June 21, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunt, John C.
; REGISTRATION NUMBER: 36,424
; REFERENCE/DOCKET NUMBER: 50767/00004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 863-4344
; TELEFAX: (416) 863-2653
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-724-466B-14

Query Match 1.1%; Score 11.4; DB 1; Length 14;
Best Local Similarity 92.3%; Pred. NO. 1.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGT 1877
Db 2 TTTTATTTTGT 14

RESULT 247
US-08-724-466B-17
; Sequence 17, Application US/08724466B
; FILING DATE: 1997-04-02
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 17
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-16

Query Match 1.1%; Score 11.4; DB 1; Length 14;
Best Local Similarity 92.3%; Pred. NO. 1.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGT 1877
Db 2 TTTTATTTTGT 14

RESULT 247
US-08-724-466B-17
; Sequence 17, Application US/08724466B
; FILING DATE: 1997-04-02
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 17
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-16
```



Patent No. 6063606  
GENERAL INFORMATION:  
APPLICANT: Petkovich, P. Martin, White, Jay A.  
APPLICANT: Beckett, Barbara R., Jones, Glenville  
TITLE OF INVENTION: Retinoid Metabolizing Protein  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Blake, Cassels & Graydon  
STREET: Box 25, Commerce Court West  
CITY: Toronto  
ZIP: M5L 1A9  
COUNTRY: Canada  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage  
COMPUTER: COMPAQ, IBM PC compatible  
OPERATING SYSTEM: MS-DOS 5.1  
SOFTWARE: WORD PERFECT  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/724,466B  
FILING DATE: October 1, 1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/667,546  
FILING DATE: June 21, 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Hunt, John C.  
REGISTRATION NUMBER: 36,424  
REFERENCE/DOCKET NUMBER: 50767/00004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (416) 863-4344  
TELEFAX: (416) 863-2653  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-724-466B-17

Query Match 1.1%; Score 11.4; DB 1; Length 14;  
Best Local Similarity 92.3%; Pred. No. 1.6e+02;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1871 TTTTGTGTTTAA 1883  
|||||  
Db 2 TTTTGTGTTTAA 14

RESULT 248  
US-08-893-828-28  
Sequence 28, Application US/08893828  
Patent No. 6090922  
GENERAL INFORMATION:  
APPLICANT: Artavanis-Tsakonas, Spyridon  
APPLICANT: Muskavitch, Marc A.T.  
APPLICANT: Fehon, Richard G.  
APPLICANT: Rebay, Ilaria  
APPLICANT: Blaumueller, Cristine M.  
APPLICANT: Shepard, Scott B.  
TITLE OF INVENTION: HUMAN NOTCH AND DELTA, BINDING DOMAINS  
NUMBER OF SEQUENCES: 34  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PENNIE & EDMONDS  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/893,828  
FILING DATE: 11-JUL-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Misrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 7326-050  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864/9741  
INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: CDNA

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/893,828  
FILING DATE: 11-JUL-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Misrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 7326-050  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864/9741  
INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: CDNA  
US-08-893-828-28

Query Match 1.1%; Score 11.4; DB 1; Length 14;  
Best Local Similarity 92.3%; Pred. No. 1.6e+02;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1839 TAAGTTAAATTAA 1851  
|||||  
Db 2 TAAGTTAACTTAA 14

RESULT 249  
US-08-893-828-28/c  
Sequence 28, Application US/08893828  
Patent No. 6090922  
GENERAL INFORMATION:  
APPLICANT: Artavanis-Tsakonas, Spyridon  
APPLICANT: Muskavitch, Marc A.T.  
APPLICANT: Fehon, Richard G.  
APPLICANT: Rebay, Ilaria  
APPLICANT: Blaumueller, Cristine M.  
APPLICANT: Shepard, Scott B.  
TITLE OF INVENTION: HUMAN NOTCH AND DELTA, BINDING DOMAINS  
NUMBER OF SEQUENCES: 34  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PENNIE & EDMONDS  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/893,828  
FILING DATE: 11-JUL-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Misrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 7326-050  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864/9741  
INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: CDNA

US-08-893-828-28

Query Match 1.1%; Score 11.4; DB 1; Length 14;  
Best Local Similarity 92.3%; Pred. No. 1.6e+02;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1839 TAAGTTAATTAA 1851  
Db 13 TAAGTTAATTAA 1

RESULT 250

US-09-019-095A-26  
Sequence 26, Application US/09019095A

Patent No. 6287858  
GENERAL INFORMATION:  
APPLICANT: D'Andrea, Alan D.  
APPLICANT: Zhu, Yuan  
TITLE OF INVENTION: Deubiquitinating Enzymes That Regulate  
TITLE OF INVENTION: Cell Growth  
FILE REFERENCE: DFCI-435P2A2  
CURRENT APPLICATION NUMBER: US/09/019,095A  
CURRENT FILING DATE: 1998-02-05  
PRIOR APPLICATION NUMBER: PCT/US96/12884  
PRIOR FILING DATE: 1996-08-07  
PRIOR APPLICATION NUMBER: US 60/002,066  
PRIOR FILING DATE: 1995-08-09  
PRIOR APPLICATION NUMBER: US 60/019,787  
PRIOR FILING DATE: 1996-06-14  
NUMBER OF SEQ ID NOS: 51  
SEQ ID NO 26  
SOFTWARE: FastSeq for Windows Version 3.0  
LENGTH: 14  
TYPE: DNA  
ORGANISM: murine  
US-09-019-095A-26

Query Match 1.1%; Score 11.4; DB 1; Length 14;  
Best Local Similarity 92.3%; Pred. No. 1.6e+02;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1865 TTTTATTTTGT 1877  
Db 2 TTTTATTTTGT 14

RESULT 251

US-08-882-164D-14  
Sequence 14, Application US/08882164D

Patent No. 6306624  
GENERAL INFORMATION:  
APPLICANT: Petkovich, P. Martin, White, Jay A.,  
APPLICANT: Beckett, Barbara R., Jones, Glenville  
TITLE OF INVENTION: Retinoid Metabolizing Protein  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Blake, Cassels & Graydon  
STREET: Box 25, Commerce Court West  
CITY: Toronto  
STATE: Ontario  
COUNTRY: Canada  
ZIP: M5L 1A9  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage  
COMPUTER: COMPAQ, IBM PC compatible  
OPERATING SYSTEM: MS-DOS 5.1  
SOFTWARE: WORD PERFECT  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/882,164D  
FILING DATE: June 25, 1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/667,546  
FILING DATE: June 21, 1996  
APPLICATION NUMBER: 08/724,466  
FILING DATE: October 1, 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Hunt, John C.  
REGISTRATION NUMBER: 36,424  
REFERENCE/DOCKET NUMBER: 50767/00010  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (416) 863-4344  
TELEFAX: (416) 863-2653  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-882-164D-17

Query Match 1.1%; Score 11.4; DB 1; Length 14;  
Best Local Similarity 92.3%; Pred. No. 1.6e+02;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

APPLICATION NUMBER: 08/724,466  
FILING DATE: October 1, 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Hunt, John C.  
REGISTRATION NUMBER: 36,424  
REFERENCE/DOCKET NUMBER: 50767/00010  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (416) 863-4344  
TELEFAX: (416) 863-2653  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-882-164D-14

Query Match 1.1%; Score 11.4; DB 1; Length 14;  
Best Local Similarity 92.3%; Pred. No. 1.6e+02;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1865 TTTTATTTTGT 1877  
Db 2 TTTTATTTTGT 14

RESULT 252

US-08-882-164D-17  
Sequence 17, Application US/08882164D

Patent No. 6306624  
GENERAL INFORMATION:  
APPLICANT: Petkovich, P. Martin, White, Jay A.,  
APPLICANT: Beckett, Barbara R., Jones, Glenville  
TITLE OF INVENTION: Retinoid Metabolizing Protein  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Blake, Cassels & Graydon  
STREET: Box 25, Commerce Court West  
CITY: Toronto  
STATE: Ontario  
COUNTRY: Canada  
ZIP: M5L 1A9  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage  
COMPUTER: COMPAQ, IBM PC compatible  
OPERATING SYSTEM: MS-DOS 5.1  
SOFTWARE: WORD PERFECT  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/882,164D  
FILING DATE: June 25, 1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/667,546  
FILING DATE: June 21, 1996  
APPLICATION NUMBER: 08/724,466  
FILING DATE: October 1, 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Hunt, John C.  
REGISTRATION NUMBER: 36,424  
REFERENCE/DOCKET NUMBER: 50767/00010  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (416) 863-4344  
TELEFAX: (416) 863-2653  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-882-164D-17

Query Match 1.1%; Score 11.4; DB 1; Length 14;  
Best Local Similarity 92.3%; Pred. No. 1.6e+02;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1871 TTTTGTGTTTTAA 1893  
Db 2 TTTTGTGTTTTAA 14

RESULT 253  
US-09-475-947A-296  
; Sequence 296, Application US/09475947A  
; Patent No. 6472154  
; GENERAL INFORMATION:  
; APPLICANT: Garner, Harold R.  
; APPLICANT: Wren, Jonathan D.  
; APPLICANT: Minna, John D.  
; TITLE OF INVENTION: Polymorphic Repeats in Human Genes  
; FILE REFERENCE: UTSD0667  
; CURRENT APPLICATION NUMBER: US/09/475,947A  
; CURRENT FILING DATE: 1999-12-31  
; NUMBER OF SEQ ID NOS: 346  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 296  
; LENGTH: 14  
; TYPE: DNA  
; ORGANISM: human  
US-09-475-947A-296

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QY 1794 GTGTGTGTGTGTG 1806  
Db 1 GTGTGTGTGTGTG 13

RESULT 254  
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; Sequence 13, Application US/09375673B  
; Patent No. 6605431  
; GENERAL INFORMATION:  
; APPLICANT: GOURSE, RICHARD L.  
; APPLICANT: ESTREM, SHAWN T.  
; APPLICANT: ROSS, WILMA E.  
; APPLICANT: GAAL, TAMAS  
; TITLE OF INVENTION: PROMOTER ELEMENTS AND METHODS OF USE  
; FILE REFERENCE: 11900130101  
; CURRENT APPLICATION NUMBER: US/09/375,673B  
; CURRENT FILING DATE: 1999-08-17  
; NUMBER OF SEQ ID NOS: 89  
; SOFTWARE: Patentin Ver. 2.1  
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; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Distal  
; OTHER INFORMATION: accessory promoter element  
US-09-375-673B-13

Query Match 1.1%; Score 11.4; DB 1; Length 14;  
Best Local Similarity 92.3%; Pred. No. 1.6e+02;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1773 AAAATTTTATTTG 1785  
Db 2 AAAATTTTATTTG 14

Search completed: April 2, 2004, 14:34:11  
Job time : 3 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 2, 2004, 14:38:01 ; Search time 3 seconds  
(without alignments)  
2.527 Million cell updates/sec

Title: us-10-006-191-19

Perfect score: 1049

Sequence: 1 ttgaactgattcacatctca.....gtgtatatattttctataaa 1049

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 0.5

Searched: 210 seqs, 3614 residues

Total number of hits satisfying chosen parameters: 420

Minimum DB seq length: 8

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 239 summaries

Database : rnpb.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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C 4	22.2	2.1	27	1	US-09-735-363A-5
C 5	22.2	2.1	27	1	US-09-263-959-770
C 6	21.8	2.1	27	1	US-09-735-363A-1
C 7	21.8	2.1	27	1	US-09-735-363A-66
C 8	21.4	2.0	24	1	US-10-168-327-2
C 9	21.4	2.0	24	1	US-09-735-363A-21
C 10	21.4	2.0	24	1	US-09-776-479-1068
C 11	21.4	2.0	24	1	US-10-112-653-1012
C 12	21.4	2.0	24	1	US-10-017-895-1068
C 13	21.4	2.0	24	1	US-09-735-363A-19
C 14	21	2.0	21	1	US-09-776-479-907
C 15	21	2.0	21	1	US-10-112-653-876
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C 17	21	2.0	21	1	US-10-017-995-907
C 18	20	1.9	20	1	US-09-845-742B-2
C 19	20	1.9	20	1	US-10-085-906-33
C 20	20	1.9	20	1	US-10-165-854-1
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C 23	20	1.9	20	1	US-10-219-238-2
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C 25	20	1.9	20	1	US-10-006-191-40
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C 59	18	1.7	18	1	US-10-006-191-74
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C 64	17.4	1.7	20	1	US-10-006-191-79
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C 67	17	1.6	17	1	US-10-006-191-82
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C 72	16.8	1.6	20	1	US-10-006-191-87
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C 87	15	1.4	15	1	US-10-006-191-102
C 88	15	1.4	15	1	US-10-006-191-103
C 89	15	1.4	15	1	US-10-006-191-104
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C 92	14.4	1.4	14	1	US-10-006-191-107
C 93	14.4	1.4	14	1	US-10-006-191-108
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C 95	14.4	1.4	14	1	US-10-006-191-110
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C 98	14.2	1.4	14	1	US-10-006-191-113
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C 105	14	1.3	14	1	US-10-006-191-120
C 106	14	1.3	14	1	US-10-006-191-121

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; APPLICANT: SVERDRUP, Fran  
 ; APPLICANT: CARMICHAEL, David  
 ; TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR (CTGF) AND METHODS OF  
 ; TITLE OF INVENTION: USE  
 ; FILE REFERENCE: FIBRO100-1  
 ; CURRENT APPLICATION NUMBER: US/10/101,040  
 ; CURRENT FILING DATE: 2002-03-18  
 ; PRIOR APPLICATION NUMBER: 09/292,036  
 ; PRIOR FILING DATE: 1999-04-14  
 ; PRIOR APPLICATION NUMBER: US 09/292,036  
 ; PRIOR FILING DATE: 1999-04-14  
 ; PRIOR APPLICATION NUMBER: US 09/187,478  
 ; PRIOR FILING DATE: 1998-11-06  
 ; NUMBER OF SEQ ID NOS: 18  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 9  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: Artificial sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Antisense CTGF oligonucleotide  
 US-10-101-040-9

Query Match 2.4%; Score 25; DB 1; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 3;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1718 ATTAGCTGGACAGCTTGTGGCAAG 1742  
 Db 25 ATTAGCTGGACAGCTTGTGGCAAG 1

RESULT 2  
 US-10-101-040-10/c  
 ; Sequence 10, Application US/10101040  
 ; Publication No. US20020142353A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: FIBROGEN, INC  
 ; APPLICANT: SCHMIDT, Brian  
 ; APPLICANT: ALLEN, Margaret  
 ; APPLICANT: SVERDRUP, Fran  
 ; APPLICANT: CARMICHAEL, David  
 ; TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR (CTGF) AND METHODS OF  
 ; TITLE OF INVENTION: USE  
 ; FILE REFERENCE: FIBRO100-1  
 ; CURRENT APPLICATION NUMBER: US/10/101,040  
 ; CURRENT FILING DATE: 2002-03-18  
 ; PRIOR APPLICATION NUMBER: 09/292,036  
 ; PRIOR FILING DATE: 1999-04-14  
 ; PRIOR APPLICATION NUMBER: US 09/292,036  
 ; PRIOR FILING DATE: 1999-04-14  
 ; PRIOR APPLICATION NUMBER: US 09/187,478  
 ; PRIOR FILING DATE: 1998-11-06  
 ; NUMBER OF SEQ ID NOS: 18  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 10  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: Artificial sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Antisense CTGF oligonucleotide  
 US-10-101-040-10

Query Match 2.2%; Score 23.4; DB 1; Length 25;  
 Best Local Similarity 96.0%; Pred. No. 5.1;  
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1742 GTGAATTCCTGTAACAGCCAGA 1766  
 Db 25 GTGAATTCCTGTAACAGCCAGA 1

RESULT 3

US-09-754-853A-601/c  
 ; Sequence 601, Application US/09754853A  
 ; Publication No. US20030005491A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hauge, Brian M.  
 ; APPLICANT: Farnell, Laurence D.  
 ; APPLICANT: Parsons, Jeremy D.  
 ; APPLICANT: Wang, Ming Li  
 ; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With  
 ; TITLE OF INVENTION: Soybean Cyst Nematode Resistance  
 ; FILE REFERENCE: 38-10(15810)B  
 ; CURRENT APPLICATION NUMBER: US/09/754,853A  
 ; CURRENT FILING DATE: 2001-01-05  
 ; PRIOR APPLICATION NUMBER: US 60/174,880  
 ; PRIOR FILING DATE: 2000-01-07  
 ; NUMBER OF SEQ ID NOS: 1119  
 ; SEQ ID NO 601  
 ; LENGTH: 27  
 ; TYPE: DNA  
 ; ORGANISM: Glycine max  
 ; FEATURE:  
 ; OTHER INFORMATION: Clone ID: 240017\_region\_G3\_11301\_29\_Forward\_Primer  
 US-09-754-853A-601

Query Match 2.2%; Score 23.4; DB 1; Length 27;  
 Best Local Similarity 96.0%; Pred. No. 5.2;  
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1795 TGTGTGTGTGTGTGTGTATAT 1819  
 Db 27 TGTGTGTGTGTGTGTATATAAT 3

RESULT 4  
 US-09-735-363A-5  
 ; Sequence 5, Application US/09735363A  
 ; Patent No. US20010041681A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Fillion, Mario  
 ; APPLICANT: Phillip, Nigel  
 ; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides  
 ; FILE REFERENCE: 02811-0181  
 ; CURRENT APPLICATION NUMBER: US/09/735,363A  
 ; CURRENT FILING DATE: 2000-12-12  
 ; PRIOR APPLICATION NUMBER: 60/170,325  
 ; PRIOR FILING DATE: 1999-12-13  
 ; PRIOR APPLICATION NUMBER: 60/228,925  
 ; PRIOR FILING DATE: 2000-08-29  
 ; NUMBER OF SEQ ID NOS: 87  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 5  
 ; LENGTH: 27  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Synthetic Oligonucleotide  
 US-09-735-363A-5

Query Match 2.1%; Score 22.2; DB 1; Length 27;  
 Best Local Similarity 88.9%; Pred. No. 7.7;  
 Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1793 TGTGTGTGTGTGTGTGTATAT 1819  
 Db 1 TGTGTGTGTGTGTGTGTGTGTGTGT 27

RESULT 5  
 US-09-263-959-770  
 ; Sequence 770, Application US/09263959  
 ; Patent No. US20020150891A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hood, Leroy E.

```

; APPLICANT: Rowen, Lee
; APPLICANT: Koop, Ben F.
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
; NUMBER OF SEQUENCES: 1279
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/263,959
; FILING DATE: 05-MAR-1999
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mcmasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 920010.426C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 770:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-09-263-959-770

Query Match 2.1%; Score 22.2; DB 1; Length 27;
Best Local Similarity 88.9%; Pred. No. 7.7;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTATAT 1819
DB 1 TGTGTGTGTGTGTGTGTGTGTGTGT 27

RESULT 6
US-09-735-363A-1
; Sequence 1, Application US/09735363A
; Patent No. US20010041681A1
; GENERAL INFORMATION:
; APPLICANT: Fillion, Mario
; APPLICANT: Phillip, Nigel
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
; FILE REFERENCE: 02811-0181
; CURRENT APPLICATION NUMBER: US/09/735,363A
; CURRENT FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/170,325
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 60/228,925
; PRIOR FILING DATE: 2000-08-29
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
;
US-09-735-363A-1

Query Match 2.1%; Score 21.8; DB 1; Length 27;
Best Local Similarity 92.0%; Pred. No. 8.8;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTATAT 1819
DB 1 TGTGTGTGTGTGTGTGTGTGTGTGT 27

RESULT 6
US-09-735-363A-1
; Sequence 1, Application US/09735363A
; Patent No. US20010041681A1
; GENERAL INFORMATION:
; APPLICANT: Fillion, Mario
; APPLICANT: Phillip, Nigel
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
; FILE REFERENCE: 02811-0181
; CURRENT APPLICATION NUMBER: US/09/735,363A
; CURRENT FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/170,325
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 60/228,925
; PRIOR FILING DATE: 2000-08-29
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
;
US-09-735-363A-1

Query Match 2.1%; Score 21.8; DB 1; Length 27;
Best Local Similarity 92.0%; Pred. No. 8.8;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTATAT 1817
DB 2 TGTGTGTGTGTGTGTGTGTGTGTGT 26

RESULT 7
US-09-735-363A-66
; Sequence 66, Application US/09735363A
; Patent No. US20010041681A1
; GENERAL INFORMATION:
; APPLICANT: Fillion, Mario
; APPLICANT: Phillip, Nigel
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
; FILE REFERENCE: 02811-0181
; CURRENT APPLICATION NUMBER: US/09/735,363A
; CURRENT FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/170,325
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 60/228,925
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 66
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
;
US-09-735-363A-66

Query Match 2.1%; Score 21.8; DB 1; Length 27;
Best Local Similarity 92.0%; Pred. No. 8.8;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTATAT 1817
DB 2 TGTGTGTGTGTGTGTGTGTGTGTGT 26

RESULT 8
US-10-168-327-2
; Sequence 2, Application US/10168327
; Publication No. US20030176381A1
; GENERAL INFORMATION:
; APPLICANT: Phillips, Nigel C.
; APPLICANT: Fillion, Mario C.
; TITLE OF INVENTION: Hyaluronic Acid in the Treatment of Cancer
; FILE REFERENCE: 02811-0211 (42368-274915)
; CURRENT APPLICATION NUMBER: US/10/168,327
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: PCT/CA00/01562
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
;
US-10-168-327-2

Query Match 2.1%; Score 21.8; DB 1; Length 27;
Best Local Similarity 92.0%; Pred. No. 8.8;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTATAT 1817
DB 2 TGTGTGTGTGTGTGTGTGTGTGTGT 26

RESULT 9
US-09-735-363A-21
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```

QY 1793 TGTGTGTGTGTGTGTGTATAT 1817
DB 2 TGTGTGTGTGTGTGTGTGTGTGTGT 26

RESULT 7
US-09-735-363A-66
; Sequence 66, Application US/09735363A
; Patent No. US20010041681A1
; GENERAL INFORMATION:
; APPLICANT: Fillion, Mario
; APPLICANT: Phillip, Nigel
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
; FILE REFERENCE: 02811-0181
; CURRENT APPLICATION NUMBER: US/09/735,363A
; CURRENT FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/170,325
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 60/228,925
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 66
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
;
US-09-735-363A-66

Query Match 2.1%; Score 21.8; DB 1; Length 27;
Best Local Similarity 92.0%; Pred. No. 8.8;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTATAT 1817
DB 2 TGTGTGTGTGTGTGTGTGTGTGTGT 26

RESULT 8
US-10-168-327-2
; Sequence 2, Application US/10168327
; Publication No. US20030176381A1
; GENERAL INFORMATION:
; APPLICANT: Phillips, Nigel C.
; APPLICANT: Fillion, Mario C.
; TITLE OF INVENTION: Hyaluronic Acid in the Treatment of Cancer
; FILE REFERENCE: 02811-0211 (42368-274915)
; CURRENT APPLICATION NUMBER: US/10/168,327
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: PCT/CA00/01562
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
;
US-10-168-327-2

Query Match 2.1%; Score 21.8; DB 1; Length 27;
Best Local Similarity 92.0%; Pred. No. 8.8;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTATAT 1817
DB 2 TGTGTGTGTGTGTGTGTGTGTGTGT 26

RESULT 9
US-09-735-363A-21
```

```
; Sequence 21, Application US/09735363A
; Patent No. US20010041681A1
; GENERAL INFORMATION:
; APPLICANT: Fillion, Mario
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
; FILE REFERENCE: 02811-0181
; CURRENT APPLICATION NUMBER: US/09/735,363A
; CURRENT FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/170,325
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 60/228,925
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 21
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-735-363A-21

Query Match      2.0%; Score 21.4; DB 1; Length 24;
Best Local Similarity 95.7%; Pred. No. 9.6;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTAT 1815
Db 1 TGTGTGTGTGTGTGTGTGTGT 23

RESULT 10
US-09-735-363A-22
; Sequence 22, Application US/09735363A
; Patent No. US20010041681A1
; GENERAL INFORMATION:
; APPLICANT: Fillion, Mario
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
; FILE REFERENCE: 02811-0181
; CURRENT APPLICATION NUMBER: US/09/735,363A
; CURRENT FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/170,325
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 60/228,925
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-735-363A-22

Query Match      2.0%; Score 21.4; DB 1; Length 24;
Best Local Similarity 95.7%; Pred. No. 9.6;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTAT 1815
Db 2 TGTGTGTGTGTGTGTGTGTGT 24

RESULT 11
US-09-776-479-1068
; Sequence 1068, Application US/09776479
; Publication No. US2003008748A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
```

```
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; TITLE OF INVENTION: Treatment of Asthma and Allergy
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1068
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-1068

Query Match      2.0%; Score 21.4; DB 1; Length 24;
Best Local Similarity 95.7%; Pred. No. 9.6;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTAT 1815
Db 1 TGTGTGTGTGTGTGTGTGTGT 23

RESULT 12
US-10-112-653-1012
; Sequence 1012, Application US/10112653
; Publication No. US20030050268A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Berg, Daniel J.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR
; TITLE OF INVENTION: TREATMENT OF NON-ALLERGIC INFLAMMATORY DISEASES
; FILE REFERENCE: C01039/70060(AWS)
; CURRENT APPLICATION NUMBER: US/10/112,653
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/279,642
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 1040
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1012
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-112-653-1012

Query Match      2.0%; Score 21.4; DB 1; Length 24;
Best Local Similarity 95.7%; Pred. No. 9.6;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTAT 1815
Db 1 TGTGTGTGTGTGTGTGTGTGT 23

RESULT 13
US-10-017-995-1068
; Sequence 1068, Application US/10017995
; Publication No. US20030055014A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids
; FILE REFERENCE: C1037/7025 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/017,995
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/255,534
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 1093
```



; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1068  
; LENGTH: 24  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Sequence  
US-10-017-995-1068

Query Match 2.0%; Score 21.4; DB 1; Length 24;  
Best Local Similarity 95.7%; Pred. No. 9.6;  
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTGT 1815  
DB 1 TGTGTGTGTGTGTGTGTGTGT 23

RESULT 14  
US-09-735-363A-19  
; Sequence 19, Application US/09735363A  
; Patent No. US20010041681A1  
; GENERAL INFORMATION:  
; APPLICANT: Fillon, Mario  
; APPLICANT: Phillip, Nigel  
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides  
; FILE REFERENCE: 02811-0181  
; CURRENT APPLICATION NUMBER: US/09/735,363A  
; CURRENT FILING DATE: 2000-12-12  
; PRIOR APPLICATION NUMBER: 60/170,325  
; PRIOR FILING DATE: 1999-12-13  
; PRIOR APPLICATION NUMBER: 60/228,925  
; PRIOR FILING DATE: 2000-08-29  
; NUMBER OF SEQ ID NOS: 87  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 19  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Oligonucleotide  
US-09-735-363A-19

Query Match 2.0%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 10;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTGT 1813  
DB 1 TGTGTGTGTGTGTGTGTGTGT 21

RESULT 15  
US-09-776-479-907  
; Sequence 907, Application US/09776479  
; Publication No. US20030087848A1  
; GENERAL INFORMATION:  
; APPLICANT: Bratzler, Robert L.  
; APPLICANT: Petersen, Deanna M.  
; APPLICANT: Fouron, Yves  
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the  
; FILE REFERENCE: C1037/7013 (HCL/MAT)  
; CURRENT APPLICATION NUMBER: US/09/776,479  
; CURRENT FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: US 60/179,991  
; PRIOR FILING DATE: 2000-02-03  
; NUMBER OF SEQ ID NOS: 1093  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 907  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Artificial Sequence

; FEATURE:  
; OTHER INFORMATION: Synthetic Sequence  
US-09-776-479-907

Query Match 2.0%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 10;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTGT 1813  
DB 1 TGTGTGTGTGTGTGTGTGTGT 21

RESULT 16  
US-10-112-653-876  
; Sequence 876, Application US/10112653  
; Publication No. US20030050268A1  
; GENERAL INFORMATION:  
; APPLICANT: Krieg, Arthur M.  
; APPLICANT: Berg, Daniel J.  
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR  
; FILE REFERENCE: C01039/70060 (AWS)  
; CURRENT APPLICATION NUMBER: US/10/112,653  
; CURRENT FILING DATE: 2002-03-29  
; PRIOR APPLICATION NUMBER: US 60/279,842  
; PRIOR FILING DATE: 2001-03-29  
; NUMBER OF SEQ ID NOS: 1040  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 876  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Oligonucleotide  
US-10-112-653-876

Query Match 2.0%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 10;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTGT 1813  
DB 1 TGTGTGTGTGTGTGTGTGTGT 21

RESULT 17  
US-10-017-995-907  
; Sequence 907, Application US/10017995  
; Publication No. US20030055014A1  
; GENERAL INFORMATION:  
; APPLICANT: Bratzler, Robert L.  
; TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids  
; FILE REFERENCE: C1037/7025 (HCL/MAT)  
; CURRENT APPLICATION NUMBER: US/10/017,995  
; CURRENT FILING DATE: 2001-12-18  
; PRIOR APPLICATION NUMBER: US 60/255,534  
; PRIOR FILING DATE: 2000-12-14  
; NUMBER OF SEQ ID NOS: 1093  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 907  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Sequence  
US-10-017-995-907

Query Match 2.0%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 10;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTGT 1813

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Db      1  TGTGTGTGTGTGTGTGTGT 21
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RESULT 18
US-09-845-742B-1
; Sequence 1, Application US/09845742B
; Publication No. US20030215801A1
; GENERAL INFORMATION:
; APPLICANT: Picken, Wolfgang
; APPLICANT: Wolter, Andreas
; APPLICANT: Sebesta P, David
; APPLICANT: Leuck, Michael
; APPLICANT: Latham-Timmons A, Hallie
; APPLICANT: Pilon, John
; APPLICANT: Husar M, Gregory
; TITLE OF INVENTION: METHOD FOR IMMOBILIZING OLIGONUCLEOTIDES EMPLOYING THE
; TITLE OF INVENTION: CYCLOADDITION BIOCONJUGATION METHOD
; FILE REFERENCE: PRO.03
; CURRENT APPLICATION NUMBER: US/09/845,742B
; CURRENT FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: 60/201,561
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/265,020
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 09/341,337
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: PCT/US98/00649
; PRIOR FILING DATE: 1998-01-08
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO.1
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Nucleic Acid Ligand
US-09-845-742B-1
Query Match      1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1793  TGTGTGTGTGTGTGTGTGT 1812
Db      20  TGTGTGTGTGTGTGTGTGT 1
|||||
RESULT 20
US-10-085-906-33
; Sequence 33, Application US/10085906
; Publication No. US20030054371A1
; GENERAL INFORMATION:
; APPLICANT: Ying, Vincent
; APPLICANT: Wu, Paul
; APPLICANT: Gray, Gary S.
; TITLE OF INVENTION: POLYMORPHIC ELEMENTS IN THE
; TITLE OF INVENTION: COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF
; FILE REFERENCE: GNN-5343CP2
; CURRENT APPLICATION NUMBER: US/10/085,906
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 60/126,215
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: US 09/534,061
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: PCT/US00/07938
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 545
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-085-906-33
Query Match      1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1794  GTGTGTGTGTGTGTGTGTGT 1813
Db      1  GTGTGTGTGTGTGTGTGTGT 20
|||||
RESULT 21
US-10-165-854-1/c
; Sequence 1, Application US/10165854
; Publication No. US20030059807A1
; GENERAL INFORMATION:
; APPLICANT: Roach, Jeffrey Shawn
; APPLICANT: Wolter, Andreas
; TITLE OF INVENTION: MICROCALORIMETRIC DETECTION OF ANALYTES AND BINDING EVENTS
; FILE REFERENCE: PRO06
; CURRENT APPLICATION NUMBER: US/10/165,854
; CURRENT FILING DATE: 2002-06-07
```

;; PRIOR APPLICATION NUMBER: 60/296,685  
;; PRIOR FILING DATE: 2001-06-07  
;; NUMBER OF SEQ ID NOS: 4  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 1:  
;; LENGTH: 20  
;; TYPE: DNA  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Synthetic Nucleic Acid Ligand  
US-10-165-854-1

Query Match 1.9%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTG 1812  
DB 20 TGTGTGTGTGTGTGTGTG 1

RESULT 22  
US-10-165-854-2  
;; Sequence 2, Application US/10165854  
;; Publication No. US20030059807A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Roach, Jeffrey Shawn  
;; TITLE OF INVENTION: MICROCALORIMETRIC DETECTION OF ANALYTES AND BINDING EVENTS  
;; FILE REFERENCE: PRO6  
;; CURRENT FILING DATE: 2002-06-07  
;; PRIOR APPLICATION NUMBER: US/10/165,854  
;; PRIOR FILING DATE: 2001-06-07  
;; NUMBER OF SEQ ID NOS: 4  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 2  
;; LENGTH: 20  
;; TYPE: DNA  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Synthetic Nucleic Acid Ligand  
US-10-165-854-2

Query Match 1.9%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTG 1812  
DB 1 TGTGTGTGTGTGTGTGTG 20

RESULT 23  
US-10-219-238-1  
;; Sequence 1, Application US/10219238  
;; Publication No. US20030114405A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Linnik, Matthew D.  
;; APPLICANT: Hepburn, Bonnie  
;; TITLE OF INVENTION: METHODS OF TREATING SYSTEMIC LUPUS  
;; TITLE OF INVENTION: ERYTHEMATOSUS IN INDIVIDUALS HAVING  
;; TITLE OF INVENTION: SIGNIFICANTLY IMPAIRED RENAL FUNCTION  
;; FILE REFERENCE: 252312007800  
;; CURRENT FILING DATE: 2003-01-10  
;; PRIOR APPLICATION NUMBER: US 60/314,281  
;; PRIOR FILING DATE: 2001-08-22  
;; PRIOR APPLICATION NUMBER: US 60/311,858  
;; PRIOR FILING DATE: 2001-08-13  
;; NUMBER OF SEQ ID NOS: 2  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 1

;; LENGTH: 20  
;; TYPE: DNA  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Synthetic Construct  
US-10-219-238-1

Query Match 1.9%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTGTG 1813  
DB 1 GTGTGTGTGTGTGTGTGTG 20

RESULT 24  
US-10-219-238-2/c  
;; Sequence 2, Application US/10219238  
;; Publication No. US20030114405A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Linnik, Matthew D.  
;; APPLICANT: Hepburn, Bonnie  
;; TITLE OF INVENTION: METHODS OF TREATING SYSTEMIC LUPUS  
;; TITLE OF INVENTION: ERYTHEMATOSUS IN INDIVIDUALS HAVING  
;; TITLE OF INVENTION: SIGNIFICANTLY IMPAIRED RENAL FUNCTION  
;; FILE REFERENCE: 252312007800  
;; CURRENT FILING DATE: 2003-01-10  
;; PRIOR APPLICATION NUMBER: US 60/314,281  
;; PRIOR FILING DATE: 2001-08-22  
;; PRIOR APPLICATION NUMBER: US 60/311,858  
;; PRIOR FILING DATE: 2001-08-13  
;; NUMBER OF SEQ ID NOS: 2  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 2  
;; LENGTH: 20  
;; TYPE: DNA  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Synthetic Construct  
US-10-219-238-2

Query Match 1.9%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTG 1812  
DB 20 TGTGTGTGTGTGTGTGTG 1

RESULT 25  
US-10-006-191-39/c  
;; Sequence 39, Application US/10006191  
;; Publication No. US20030144223A1  
;; GENERAL INFORMATION:  
;; APPLICANT: William Gaarde  
;; APPLICANT: Andrew T. Watt  
;; TITLE OF INVENTION: ANTISENSE MODULATION OF CONNECTIVE TISSUE GROWTH FACTOR EXPRESSION  
;; FILE REFERENCE: RTS-0274  
;; CURRENT FILING DATE: 2001-12-10  
;; CURRENT APPLICATION NUMBER: US/10/006,191  
;; NUMBER OF SEQ ID NOS: 153  
;; SEQ ID NO 39  
;; LENGTH: 20  
;; TYPE: DNA  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-006-191-39

Query Match 1.9%; Score 20; DB 1; Length 20;

```
Best Local Similarity 100.0%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1719 TTAGACTGGACAGCTTGTTGG 1738
Db 20 TTAGACTGGACAGCTTGTTGG 1

RESULT 26
US-10-006-191-40/c
; Sequence 40, Application US/10006191
; Publication No. US20030144223A1
; GENERAL INFORMATION:
; APPLICANT: William Gaarde
; TITLE OF INVENTION: ANTISENSE MODULATION OF CONNECTIVE TISSUE GROWTH FACTOR EXPRESSION
; FILE REFERENCE: RTS-0274
; CURRENT APPLICATION NUMBER: US/10/006,191
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 40
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-006-191-40
Query Match 1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1724 CTGGACAGCTTGTCGCAAGT 1743
Db 20 CTGGACAGCTTGTCGCAAGT 1

RESULT 27
US-10-006-191-41/c
; Sequence 41, Application US/10006191
; Publication No. US20030144223A1
; GENERAL INFORMATION:
; APPLICANT: William Gaarde
; TITLE OF INVENTION: ANTISENSE MODULATION OF CONNECTIVE TISSUE GROWTH FACTOR EXPRESSION
; FILE REFERENCE: RTS-0274
; CURRENT APPLICATION NUMBER: US/10/006,191
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 41
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-006-191-41
Query Match 1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1727 TGTACAGTTATCTAAGTTAA 1846
Db 20 TGTACAGTTATCTAAGTTAA 1

RESULT 28
US-10-006-191-42/c
; Sequence 42, Application US/10006191
; Publication No. US20030144223A1
; GENERAL INFORMATION:
; APPLICANT: William Gaarde
; TITLE OF INVENTION: ANTISENSE MODULATION OF CONNECTIVE TISSUE GROWTH FACTOR EXPRESSION
; FILE REFERENCE: RTS-0274
; CURRENT APPLICATION NUMBER: US/10/006,191
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 42
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-006-191-42
Query Match 1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1719 TTAGACTGGACAGCTTGTTGG 1738
Db 20 TTAGACTGGACAGCTTGTTGG 1

RESULT 29
US-10-006-191-43/c
; Sequence 43, Application US/10006191
; Publication No. US20030144223A1
; GENERAL INFORMATION:
; APPLICANT: William Gaarde
; TITLE OF INVENTION: ANTISENSE MODULATION OF CONNECTIVE TISSUE GROWTH FACTOR EXPRESSION
; FILE REFERENCE: RTS-0274
; CURRENT APPLICATION NUMBER: US/10/006,191
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 43
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-006-191-43
Query Match 1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1832 AGTTATCTAAGTTAATTAA 1851
Db 20 AGTTATCTAAGTTAATTAA 1

RESULT 30
US-10-006-191-44/c
; Sequence 44, Application US/10006191
; Publication No. US20030144223A1
; GENERAL INFORMATION:
; APPLICANT: William Gaarde
; TITLE OF INVENTION: ANTISENSE MODULATION OF CONNECTIVE TISSUE GROWTH FACTOR EXPRESSION
; FILE REFERENCE: RTS-0274
; CURRENT APPLICATION NUMBER: US/10/006,191
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 44
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-006-191-44
Query Match 1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2198 CAGTTTATTGTGAGTG 2217
DB 20 CAGTTTATTGTGAGTG 1
RESULT 31
US-10-006-191-45/c
; Sequence 45, Application US/10006191
; Publication No. US20030144223A1
; GENERAL INFORMATION:
; APPLICANT: William Gaarde
; TITLE OF INVENTION: ANTISENSE MODULATION OF CONNECTIVE TISSUE GROWTH FACTOR EXPRESSION
; FILE REFERENCE: RTS-0274
; CURRENT APPLICATION NUMBER: US/10/006,191
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 45
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-006-191-45
Query Match 1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2203 TATTGTTGAGAGTGACC 2222
DB 20 TATTGTTGAGAGTGACC 1
RESULT 32
US-10-006-191-46/c
; Sequence 46, Application US/10006191
; Publication No. US20030144223A1
; GENERAL INFORMATION:
; APPLICANT: William Gaarde
; TITLE OF INVENTION: ANTISENSE MODULATION OF CONNECTIVE TISSUE GROWTH FACTOR EXPRESSION
; FILE REFERENCE: RTS-0274
; CURRENT APPLICATION NUMBER: US/10/006,191
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 46
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-006-191-46
Query Match 1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2208 GTTGAGAGTGACCAAG 2227
DB 20 GTTGAGAGTGACCAAG 1
RESULT 33
US-10-006-191-47/c
; Sequence 47, Application US/10006191
; Publication No. US20030144223A1
; GENERAL INFORMATION:
; APPLICANT: William Gaarde
; TITLE OF INVENTION: ANTISENSE MODULATION OF CONNECTIVE TISSUE GROWTH FACTOR EXPRESSION

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; FILE REFERENCE: RTS-0274
; CURRENT APPLICATION NUMBER: US/10/006,191
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 47
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-006-191-47
Query Match 1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2213 GAGTGTGACCAAGTTACA 2232
DB 20 GAGTGTGACCAAGTTACA 1
RESULT 34
US-10-006-191-48/c
; Sequence 48, Application US/10006191
; Publication No. US20030144223A1
; GENERAL INFORMATION:
; APPLICANT: William Gaarde
; TITLE OF INVENTION: ANTISENSE MODULATION OF CONNECTIVE TISSUE GROWTH FACTOR EXPRESSION
; FILE REFERENCE: RTS-0274
; CURRENT APPLICATION NUMBER: US/10/006,191
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 48
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-006-191-48
Query Match 1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2218 TGACCAAAAGTTACATGTTT 2237
DB 20 TGACCAAAAGTTACATGTTT 1
RESULT 35
US-10-006-191-49/c
; Sequence 49, Application US/10006191
; Publication No. US20030144223A1
; GENERAL INFORMATION:
; APPLICANT: William Gaarde
; TITLE OF INVENTION: ANTISENSE MODULATION OF CONNECTIVE TISSUE GROWTH FACTOR EXPRESSION
; FILE REFERENCE: RTS-0274
; CURRENT APPLICATION NUMBER: US/10/006,191
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 49
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-006-191-49
Query Match 1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 2242 CTTTCTAGTTGAATAAAG 2261  
 |||||  
 Db 20 CTTTCTAGTTGAATAAAG 1

RESULT 36

US-10-006-191-59/c  
 ; Sequence 59, Application US/10006191  
 ; Publication No. US20030144223A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: William Gaarde  
 ; APPLICANT: Andrew T. Watt  
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF CONNECTIVE TISSUE GROWTH FACTOR EXPRESSION  
 ; FILE REFERENCE: RTS-0274  
 ; CURRENT APPLICATION NUMBER: US/10/006,191  
 ; CURRENT FILING DATE: 2001-12-10  
 ; NUMBER OF SEQ ID NOS: 153  
 ; SEQ ID NO 59  
 ; LENGTH: 20  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Antisense Oligonucleotide  
 US-10-006-191-59

Query Match 1.9%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 14;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1723 ACTGGACAGCTTGTGGCAAG 1742  
 |||||  
 Db 20 ACTGGACAGCTTGTGGCAAG 1

RESULT 37

US-10-006-191-60/c  
 ; Sequence 60, Application US/10006191  
 ; Publication No. US20030144223A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: William Gaarde  
 ; APPLICANT: Andrew T. Watt  
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF CONNECTIVE TISSUE GROWTH FACTOR EXPRESSION  
 ; FILE REFERENCE: RTS-0274  
 ; CURRENT APPLICATION NUMBER: US/10/006,191  
 ; CURRENT FILING DATE: 2001-12-10  
 ; NUMBER OF SEQ ID NOS: 153  
 ; SEQ ID NO 60  
 ; LENGTH: 20  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Antisense Oligonucleotide  
 US-10-006-191-60

Query Match 1.9%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 14;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1752 CTGTACACAGCCAGATTTT 1771  
 |||||  
 Db 20 CTGTACACAGCCAGATTTT 1

RESULT 38

US-10-006-191-61/c  
 ; Sequence 61, Application US/10006191  
 ; Publication No. US20030144223A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: William Gaarde  
 ; APPLICANT: Andrew T. Watt  
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF CONNECTIVE TISSUE GROWTH FACTOR EXPRESSION  
 ; FILE REFERENCE: RTS-0274

Query Match 1.9%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 14;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; CURRENT APPLICATION NUMBER: US/10/006,191  
 ; CURRENT FILING DATE: 2001-12-10  
 ; NUMBER OF SEQ ID NOS: 153  
 ; SEQ ID NO 61  
 ; LENGTH: 20  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Antisense Oligonucleotide  
 US-10-006-191-61

Query Match 1.9%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 14;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1834 TTATCTAAGTTAATTTAAAG 1853  
 |||||  
 Db 20 TTATCTAAGTTAATTTAAAG 1

RESULT 39

US-10-006-191-62/c  
 ; Sequence 62, Application US/10006191  
 ; Publication No. US20030144223A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: William Gaarde  
 ; APPLICANT: Andrew T. Watt  
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF CONNECTIVE TISSUE GROWTH FACTOR EXPRESSION  
 ; FILE REFERENCE: RTS-0274  
 ; CURRENT APPLICATION NUMBER: US/10/006,191  
 ; CURRENT FILING DATE: 2001-12-10  
 ; NUMBER OF SEQ ID NOS: 153  
 ; SEQ ID NO 62  
 ; LENGTH: 20  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Antisense Oligonucleotide  
 US-10-006-191-62

Query Match 1.9%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 14;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2206 TTGTTGAGAGTGTGACCAA 2225  
 |||||  
 Db 20 TTGTTGAGAGTGTGACCAA 1

RESULT 40

US-10-006-191-63/c  
 ; Sequence 63, Application US/10006191  
 ; Publication No. US20030144223A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: William Gaarde  
 ; APPLICANT: Andrew T. Watt  
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF CONNECTIVE TISSUE GROWTH FACTOR EXPRESSION  
 ; FILE REFERENCE: RTS-0274  
 ; CURRENT APPLICATION NUMBER: US/10/006,191  
 ; CURRENT FILING DATE: 2001-12-10  
 ; NUMBER OF SEQ ID NOS: 153  
 ; SEQ ID NO 63  
 ; LENGTH: 20  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Antisense Oligonucleotide  
 US-10-006-191-63

Query Match 1.9%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 14;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2212 AGAGTGTGACCAAAAGTTAC 2231  
|||||  
Db 20 AGAGTGTGACCAAAAGTTAC 1

## RESULT 41

US-10-006-191-64/c  
; Sequence 64, Application US/10006191  
; Publication No. US20030144223A1  
; GENERAL INFORMATION:  
; APPLICANT: William Gaarde  
; APPLICANT: Andrew T. Watt  
; TITLE OF INVENTION: ANTISENSE MODULATION OF CONNECTIVE TISSUE GROWTH FACTOR EXPRESSION  
; FILE REFERENCE: RTS-0274  
; CURRENT APPLICATION NUMBER: US/10/006,191  
; CURRENT FILING DATE: 2001-12-10  
; NUMBER OF SEQ ID NOS: 153  
; SEQ ID NO 64  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-006-191-64

Query Match 1.9%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2219 GACCAAAAGTTACATGTTG 2238  
|||||  
Db 20 GACCAAAAGTTACATGTTG 1

## RESULT 42

US-10-006-191-65/c  
; Sequence 65, Application US/10006191  
; Publication No. US20030144223A1  
; GENERAL INFORMATION:  
; APPLICANT: William Gaarde  
; APPLICANT: Andrew T. Watt  
; TITLE OF INVENTION: ANTISENSE MODULATION OF CONNECTIVE TISSUE GROWTH FACTOR EXPRESSION  
; FILE REFERENCE: RTS-0274  
; CURRENT APPLICATION NUMBER: US/10/006,191  
; CURRENT FILING DATE: 2001-12-10  
; NUMBER OF SEQ ID NOS: 153  
; SEQ ID NO 65  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-006-191-65

Query Match 1.9%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2243 TTTCTAGTTGAAATAAAGT 2262  
|||||  
Db 20 TTTCTAGTTGAAATAAAGT 1

## RESULT 43

US-10-006-191-92/c  
; Sequence 92, Application US/10006191  
; Publication No. US20030144223A1  
; GENERAL INFORMATION:  
; APPLICANT: William Gaarde  
; APPLICANT: Andrew T. Watt  
; TITLE OF INVENTION: ANTISENSE MODULATION OF CONNECTIVE TISSUE GROWTH FACTOR EXPRESSION  
; FILE REFERENCE: RTS-0274  
; CURRENT APPLICATION NUMBER: US/10/006,191

; CURRENT FILING DATE: 2001-12-10  
; NUMBER OF SEQ ID NOS: 153  
; SEQ ID NO 92  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-006-191-92

Query Match 1.9%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1242 TCACATCTCATTTTCCGTA 1261  
|||||  
Db 20 TCACATCTCATTTTCCGTA 1

## RESULT 44

US-10-006-191-93/c  
; Sequence 93, Application US/10006191  
; Publication No. US20030144223A1  
; GENERAL INFORMATION:  
; APPLICANT: William Gaarde  
; APPLICANT: Andrew T. Watt  
; TITLE OF INVENTION: ANTISENSE MODULATION OF CONNECTIVE TISSUE GROWTH FACTOR EXPRESSION  
; FILE REFERENCE: RTS-0274  
; CURRENT APPLICATION NUMBER: US/10/006,191  
; CURRENT FILING DATE: 2001-12-10  
; NUMBER OF SEQ ID NOS: 153  
; SEQ ID NO 93  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-006-191-93

Query Match 1.9%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1274 GTAGCACAAGTTATTAAAT 1293  
|||||  
Db 20 GTAGCACAAGTTATTAAAT 1

## RESULT 45

US-10-006-191-94/c  
; Sequence 94, Application US/10006191  
; Publication No. US20030144223A1  
; GENERAL INFORMATION:  
; APPLICANT: William Gaarde  
; APPLICANT: Andrew T. Watt  
; TITLE OF INVENTION: ANTISENSE MODULATION OF CONNECTIVE TISSUE GROWTH FACTOR EXPRESSION  
; FILE REFERENCE: RTS-0274  
; CURRENT APPLICATION NUMBER: US/10/006,191  
; CURRENT FILING DATE: 2001-12-10  
; NUMBER OF SEQ ID NOS: 153  
; SEQ ID NO 94  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-006-191-94

Query Match 1.9%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1371 CCAGACACTGGTTTCAAGAA 1390

```
Db 20 CCAGACTGGTTGAAGA 1
|||||
Query Match 1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 45
US-10-006-191-95/c
; Sequence 95, Application US/10006191
; Publication No. US20030144223A1
; GENERAL INFORMATION:
; APPLICANT: William Gaarde
; TITLE OF INVENTION: ANTISENSE MODULATION OF CONNECTIVE TISSUE GROWTH FACTOR EXPRESSION
; FILE REFERENCE: RTS-0274
; CURRENT APPLICATION NUMBER: US/10/006,191
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 95
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-006-191-95

Query Match 1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1553 AAATTTAGCGTCTCATG 1572
|||||
Db 20 AAATTTAGCGTCTCATG 1

RESULT 47
US-10-006-191-96/c
; Sequence 96, Application US/10006191
; Publication No. US20030144223A1
; GENERAL INFORMATION:
; APPLICANT: William Gaarde
; TITLE OF INVENTION: ANTISENSE MODULATION OF CONNECTIVE TISSUE GROWTH FACTOR EXPRESSION
; FILE REFERENCE: RTS-0274
; CURRENT APPLICATION NUMBER: US/10/006,191
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 96
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-006-191-96

Query Match 1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1637 GTTGTTCCCTTAAGTCAGAAC 1656
|||||
Db 20 GTTGTTCCCTTAAGTCAGAAC 1

RESULT 48
US-10-006-191-97/c
; Sequence 97, Application US/10006191
; Publication No. US20030144223A1
; GENERAL INFORMATION:
; APPLICANT: William Gaarde
; TITLE OF INVENTION: ANTISENSE MODULATION OF CONNECTIVE TISSUE GROWTH FACTOR EXPRESSION
; FILE REFERENCE: RTS-0274
; CURRENT APPLICATION NUMBER: US/10/006,191
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 97
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-006-191-97

Query Match 1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1713 TGTGATTAGCTGGACAGC 1732
|||||
Db 20 TGTGATTAGCTGGACAGC 1

RESULT 49
US-09-735-363A-20
; Sequence 20, Application US/09735363A
; Patent No. US20010041681A1
; GENERAL INFORMATION:
; APPLICANT: Phillip, Nigel
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
; FILE REFERENCE: 02811-0181
; CURRENT APPLICATION NUMBER: US/09/735,363A
; CURRENT FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/170,325
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 60/228,925
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-735-363A-20

Query Match 1.9%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1794 GTGTGTGTGTGTGTGTGTGT 1813
|||||
Db 1 GTGTGTGTGTGTGTGTGTGT 20

RESULT 50
US-10-385-193-1/c
; Sequence 1, Application US/10385193
; Publication No. US20030229218A1
; GENERAL INFORMATION:
; APPLICANT: Nanda D. Sinha
; TITLE OF INVENTION: Synthesis for Oligonucleotide Synthesis
; FILE REFERENCE: 2733.1001-001
; CURRENT APPLICATION NUMBER: US/10/385,193
; CURRENT FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: US 60/230,685
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-10-385-193-1
```



Query Match 1.9%; Score 20; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTGT 1813  
DB 20 GTGTGTGTGTGTGTGTGT 1

RESULT 51  
US-10-385-193-2  
Sequence 2, Application US/10385193  
Publication No. US20030229218A1  
GENERAL INFORMATION:  
APPLICANT: Nanda D. Sinha  
TITLE OF INVENTION: Synthesis for Oligonucleotide Synthesis  
FILE REFERENCE: 2733.1001-001  
CURRENT APPLICATION NUMBER: US/10/385,193  
CURRENT FILING DATE: 2003-03-07  
PRIOR APPLICATION NUMBER: US 60/230,685  
PRIOR FILING DATE: 2000-09-07  
NUMBER OF SEQ ID NOS: 2  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 2  
LENGTH: 21  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: synthetic  
US-10-385-193-2

Query Match 1.9%; Score 20; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTGT 1813  
DB 1 GTGTGTGTGTGTGTGTGT 20

RESULT 52  
US-09-263-959-774/c  
Sequence 774, Application US/09263959  
Patent No. US20020150891A1  
GENERAL INFORMATION:  
APPLICANT: Hood, Leroy E.  
APPLICANT: Rowen, Lee  
APPLICANT: Koop, Ben F.  
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI  
NUMBER OF SEQUENCES: 1279  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/263,959  
FILING DATE: 05-MAR-1999  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Mcmasters, David D.  
REGISTRATION NUMBER: 33,963  
REFERENCE/DOCKET NUMBER: 920010.426C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 774:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 23 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-263-959-774

Query Match 1.9%; Score 19.8; DB 1; Length 23;  
Best Local Similarity 91.3%; Pred. No. 16;  
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTAT 1815  
DB 23 TGTGTGTGTGTGTGTGTGT 1

RESULT 53  
US-10-357-488-5  
Sequence 5, Application US/10357488  
Publication No. US20030194730A1  
GENERAL INFORMATION:  
APPLICANT: Centre For DNA Fingerprinting and Diagnostics  
TITLE OF INVENTION: No. US20030194730A1 FISSR-PCR primers and markers and a method c  
TITLE OF INVENTION: Primers and markers for identifying genetic constitution and bree  
TITLE OF INVENTION: varieties.  
FILE REFERENCE: 782-indian  
CURRENT APPLICATION NUMBER: US/10/357,488  
CURRENT FILING DATE: 2003-02-04  
PRIOR APPLICATION NUMBER: 260/MAS/2002  
PRIOR FILING DATE: 2002-04-08  
NUMBER OF SEQ ID NOS: 37  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 5  
LENGTH: 23  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: A novel FISSR-PCR primer for genotyping eukaryotes  
US-10-357-488-5

Query Match 1.8%; Score 19.4; DB 1; Length 23;  
Best Local Similarity 95.2%; Pred. No. 18;  
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGT 1813  
DB 3 TATGTGTGTGTGTGTGTGT 23

RESULT 54  
US-09-557-423-7/c  
Sequence 7, Application US/09557423  
Patent No. US20020094555A1  
GENERAL INFORMATION:  
APPLICANT: Belotserkovskii, Boris  
APPLICANT: Reddy, Gurucharan  
APPLICANT: Zarling, David A.  
TITLE OF INVENTION: Locked Nucleic Acid Hybrids and Methods of Use  
FILE REFERENCE: A-68112-1/RPT/RMS/BTC  
CURRENT APPLICATION NUMBER: US/09/557,423  
CURRENT FILING DATE: 2000-04-21  
PRIOR APPLICATION NUMBER: USSN 60/130,345  
PRIOR FILING DATE: 1999-04-21  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 7  
LENGTH: 19  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Z-DNA

US-09-557-423-7

Query Match 1.8%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGT 1811  
DB 19 TGTGTGTGTGTGTGTGTGT 1

RESULT 55

US-09-557-423-8  
; Sequence 8, Application US/09557423  
; Patent No. US20020094555A1  
; GENERAL INFORMATION:  
; APPLICANT: Belotserkovskii, Boris  
; APPLICANT: Reddy, Gurucharan  
; APPLICANT: Zarling, David A.  
; TITLE OF INVENTION: Locked Nucleic Acid Hybrids and Methods of Use  
; FILE REFERENCE: A-68112-1/RFT/RMS/BTC  
; CURRENT APPLICATION NUMBER: US/09/557,423  
; CURRENT FILING DATE: 2000-04-21  
; PRIOR APPLICATION NUMBER: USSN 60/130,345  
; PRIOR FILING DATE: 1999-04-21  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 8  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Z-DNA

US-09-557-423-8

Query Match 1.8%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGT 1811  
DB 1 TGTGTGTGTGTGTGTGTGT 19

RESULT 56

US-09-969-373-3086/c  
; Sequence 3086, Application US/09969373  
; Patent No. US20020133852A1  
; GENERAL INFORMATION:  
; APPLICANT: Haug, Brian M.  
; APPLICANT: Effertz, Roger J.  
; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping  
; FILE REFERENCE: 39-10(52679)A  
; CURRENT APPLICATION NUMBER: US/09/969,373  
; CURRENT FILING DATE: 2001-10-02  
; PRIOR APPLICATION NUMBER: US 09/754,853  
; PRIOR FILING DATE: 2001-01-05  
; PRIOR APPLICATION NUMBER: US 09/760,427  
; PRIOR FILING DATE: 2001-01-13  
; PRIOR APPLICATION NUMBER: US 09/855,768  
; PRIOR FILING DATE: 2001-05-15  
; NUMBER OF SEQ ID NOS: 4593  
; SEQ ID NO 3086  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: Glycine max  
; OTHER INFORMATION: Glycine max

US-09-969-373-3086

Query Match 1.8%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGT 1811

Db 19 TGTGTGTGTGTGTGTGTGT 1

RESULT 57

US-10-006-191-153/c  
; Sequence 153, Application US/10006191  
; Publication No. US20030144223A1  
; GENERAL INFORMATION:  
; APPLICANT: William Gaarde  
; APPLICANT: Andrew T. Watt  
; TITLE OF INVENTION: ANTISENSE MODULATION OF CONNECTIVE TISSUE GROWTH FACTOR EXPRESSION  
; FILE REFERENCE: RFS-0274  
; CURRENT APPLICATION NUMBER: US/10/006,191  
; CURRENT FILING DATE: 2001-12-10  
; NUMBER OF SEQ ID NOS: 153  
; SEQ ID NO 153  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
; US-10-006-191-153

Query Match 1.8%; Score 18.4; DB 1; Length 20;  
Best Local Similarity 95.0%; Pred. No. 23;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2247 TAGTTGAAATAAAGTGTAT 2266  
DB 20 TAGTTGAAATAAAGTATAT 1

RESULT 58

US-09-735-363A-17  
; Sequence 17, Application US/09735363A  
; Patent No. US20010041681A1  
; GENERAL INFORMATION:  
; APPLICANT: Fillon, Mario  
; APPLICANT: Phillip, Nigel  
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides  
; FILE REFERENCE: 02811-0181  
; CURRENT APPLICATION NUMBER: US/09/735,363A  
; CURRENT FILING DATE: 2000-12-12  
; PRIOR APPLICATION NUMBER: 60/170,325  
; PRIOR FILING DATE: 1999-12-13  
; PRIOR APPLICATION NUMBER: 60/228,925  
; PRIOR FILING DATE: 2000-08-29  
; NUMBER OF SEQ ID NOS: 87  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 17  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Oligonucleotide  
; US-09-735-363A-17

Query Match 1.7%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGT 1810  
DB 1 TGTGTGTGTGTGTGTGTGT 18

RESULT 59

US-09-735-363A-18  
; Sequence 18, Application US/09735363A  
; Patent No. US20010041681A1  
; GENERAL INFORMATION:  
; APPLICANT: Fillon, Mario

APPLICANT: Phillip, Nigel  
TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides  
FILE REFERENCE: 02811-0181  
CURRENT APPLICATION NUMBER: US/09/735,363A  
CURRENT FILING DATE: 2000-12-12  
PRIOR APPLICATION NUMBER: 60/170,325  
PRIOR FILING DATE: 1999-12-13  
PRIOR APPLICATION NUMBER: 60/228,925  
PRIOR FILING DATE: 2000-08-29  
NUMBER OF SEQ ID NOS: 87  
SOFTWARE: Patent in version 3.0  
SEQ ID NO 18  
LENGTH: 18  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic Oligonucleotide  
US-09-735-363A-18  
Query Match 1.7%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1794 GTGTGTGTGTGTGTGT 1811  
Db 1 GTGTGTGTGTGTGTGT 18  
RESULT 60  
US-09-896-650A-28  
Sequence 28, Application US/09896650A  
Patent No. US20020146704A1  
GENERAL INFORMATION:  
APPLICANT: Head, Steven  
APPLICANT: Boyce-Jacino, Michael  
APPLICANT: Karn, Jonathan  
APPLICANT: Golet, Philip  
TITLE OF INVENTION: De No. US20020146704A1 or "Universal" Sequencing Array  
FILE REFERENCE: 13019-2  
CURRENT APPLICATION NUMBER: US/09/896,650A  
CURRENT FILING DATE: 2001-06-29  
NUMBER OF SEQ ID NOS: 31  
SOFTWARE: Patent in version 3.1  
SEQ ID NO 28  
LENGTH: 18  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Reagent Sequence  
US-09-896-650A-28  
Query Match 1.7%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1793 TGTGTGTGTGTGTGTGT 1810  
Db 1 TGTGTGTGTGTGTGTGT 18  
RESULT 61  
US-10-011-204-1/c  
Sequence 1, Application US/10011204  
Publication No. US20020182617A1  
GENERAL INFORMATION:  
APPLICANT: EKINS, Roger P  
TITLE OF INVENTION: Binding assay using binding agents with tail groups  
FILE REFERENCE: 0380-P01180US0  
CURRENT APPLICATION NUMBER: US/10/011,204  
CURRENT FILING DATE: 2001-11-08  
PRIOR APPLICATION NUMBER: US/08/700,530  
PRIOR FILING DATE: 1996-10-23  
PRIOR APPLICATION NUMBER: PCT/GB95/00521

PRIOR FILING DATE: 1995-03-10  
PRIOR APPLICATION NUMBER: GB 9404709.9  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: Patent in Ver. 2.1  
SEQ ID NO 1  
LENGTH: 18  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:  
OTHER INFORMATION: Oligonucleotide  
US-10-011-204-1  
Query Match 1.7%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1793 TGTGTGTGTGTGTGTGT 1810  
Db 18 TGTGTGTGTGTGTGTGT 18  
RESULT 62  
US-10-011-204-2  
Sequence 2, Application US/10011204  
Publication No. US20020182617A1  
GENERAL INFORMATION:  
APPLICANT: EKINS, Roger P  
TITLE OF INVENTION: Binding assay using binding agents with tail groups  
FILE REFERENCE: 0380-P01180US0  
CURRENT APPLICATION NUMBER: US/10/011,204  
CURRENT FILING DATE: 2001-11-08  
PRIOR APPLICATION NUMBER: US/08/700,530  
PRIOR FILING DATE: 1996-10-23  
PRIOR APPLICATION NUMBER: PCT/GB95/00521  
PRIOR FILING DATE: 1995-03-10  
PRIOR APPLICATION NUMBER: GB 9404709.9  
PRIOR FILING DATE: 1994-03-11  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: Patent in Ver. 2.1  
SEQ ID NO 2  
LENGTH: 18  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:  
OTHER INFORMATION: Oligonucleotide  
US-10-011-204-2  
Query Match 1.7%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1794 GTGTGTGTGTGTGTGT 1811  
Db 1 GTGTGTGTGTGTGTGT 18  
RESULT 63  
US-10-357-488-26  
Sequence 26, Application US/10357488  
Publication No. US20030194730A1  
GENERAL INFORMATION:  
APPLICANT: Centre For DNA Fingerprinting and Diagnostics  
TITLE OF INVENTION: No. US20030194730A1el FISRR-PCR primers and markers and a method c  
TITLE OF INVENTION: primers and markers for identifying genetic constitution and bree  
TITLE OF INVENTION: varieties.  
FILE REFERENCE: 782-indian  
CURRENT APPLICATION NUMBER: US/10/357,488  
CURRENT FILING DATE: 2003-02-04  
PRIOR APPLICATION NUMBER: 260/MAS/2002  
PRIOR FILING DATE: 2002-04-08

NUMBER OF SEQ ID NOS: 37  
SOFTWARE: Patent version 3.1  
SEQ ID NO 26  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: A novel FISSR-PCR primer for genotyping eukaryotes  
US-10-357-488-26

Query Match 1.7%; Score 18; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1798 GTGTGTGTGTGTGTAT 1815  
|||||  
DB 1 GTGTGTGTGTGTGTAT 18

RESULT 64  
US-09-918-186A-235/c  
Sequence 235, Application US/09918186A  
Patent No. US20020137708A1  
GENERAL INFORMATION:  
APPLICANT: C. Frank Bennett  
APPLICANT: Elizabeth J. Ackermann  
APPLICANT: Eric E. Swayze  
APPLICANT: Lex M. Cowsett  
TITLE OF INVENTION: ANTISENSE MODULATION OF SURVIVIN EXPRESSION  
FILE REFERENCE: ISPH-0585  
CURRENT APPLICATION NUMBER: US/09/918,186A  
CURRENT FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 09/496,594  
PRIOR FILING DATE: 2000-02-02  
PRIOR APPLICATION NUMBER: 09/286,407  
PRIOR FILING DATE: 1999-04-05  
PRIOR APPLICATION NUMBER: 09/163,162  
PRIOR FILING DATE: 1998-09-29  
NUMBER OF SEQ ID NOS: 250  
SEQ ID NO 235  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Antisense Oligonucleotide  
US-09-918-186A-235

Query Match 1.7%; Score 17.4; DB 1; Length 20;  
Best Local Similarity 94.7%; Pred. No. 32;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1811 TGTATATATATATATGT 1829  
|||||  
DB 19 TGTATATATATATATGT 1

RESULT 65  
US-09-263-959-557  
Sequence 557, Application US/09263959  
Patent No. US20020150891A1  
GENERAL INFORMATION:  
APPLICANT: Hood, Leroy E.  
APPLICANT: Rowen, Lee  
APPLICANT: Koop, Ben F.  
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI  
NUMBER OF SEQUENCES: 1279  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/263,959  
FILING DATE: 05-MAR-1999  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: McMasters, David D.  
REGISTRATION NUMBER: 33,963  
REFERENCE/DOCKET NUMBER: 920010.426C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 557:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-263-959-557

Query Match 1.6%; Score 17; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGT 1809  
|||||  
DB 1 TGTGTGTGTGTGTGT 17

RESULT 66  
US-09-263-959-705  
Sequence 705, Application US/09263959  
Patent No. US20020150891A1  
GENERAL INFORMATION:  
APPLICANT: Hood, Leroy E.  
APPLICANT: Koop, Ben F.  
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI  
NUMBER OF SEQUENCES: 1279  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/263,959  
FILING DATE: 05-MAR-1999  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: McMasters, David D.  
REGISTRATION NUMBER: 33,963  
REFERENCE/DOCKET NUMBER: 920010.426C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 705:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-263-959-705

Query Match 1.6%; Score 17; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGT 1809  
DB 1 TGTGTGTGTGTGTGTGT 17

## RESULT 67

US-09-959-970  
; Sequence 970, Application US/09263959  
; Patent No. US20020150891A1  
; GENERAL INFORMATION:  
; APPLICANT: Hood, Leroy E.  
; APPLICANT: Koop, Ben F.  
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI  
; NUMBER OF SEQUENCES: 1279  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Seed and Berry LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: US  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/263,959  
; FILING DATE: 05-MAR-1999  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McMasters, David D.  
; REGISTRATION NUMBER: 33,963  
; REFERENCE/POCKET NUMBER: 920010.426C2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 970:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear

## US-09-263-959-970

Query Match 1.6%; Score 17; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGT 1809  
DB 1 TGTGTGTGTGTGTGTGT 17

## RESULT 68

US-10-339-782-333  
; Sequence 333, Application US/10339782  
; Publication No. US20030166026A1  
; GENERAL INFORMATION:  
; APPLICANT: Lynx Therapeutics, Inc.  
; APPLICANT: Goodman, Laurie J.  
; APPLICANT: Bowen, Benjamin A.  
; TITLE OF INVENTION: Identification of Specific Biomarkers for Breast Cancer Cells  
; FILE REFERENCE: 37-000110US  
; CURRENT APPLICATION NUMBER: US/10/339,782  
; CURRENT FILING DATE: 2003-01-08  
; NUMBER OF SEQ ID NOS: 495

; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 333  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-339-782-333

Query Match 1.6%; Score 17; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2141 GATCAGTTTTTTCACCT 2157  
DB 1 GATCAGTTTTTTCACCT 17

## RESULT 69

US-10-340-192-68  
; Sequence 68, Application US/10340192  
; Publication No. US20030170700A1  
; GENERAL INFORMATION:  
; APPLICANT: Lynx Therapeutics, Inc.  
; APPLICANT: Shang, Jin  
; APPLICANT: Bowen, Benjamin A.  
; TITLE OF INVENTION: SECRETED AND CELL SURFACE POLYPEPTIDES AFFECTED BY CHOLESTEROL ANI  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: 37-000610US  
; CURRENT APPLICATION NUMBER: US/10/340,192  
; CURRENT FILING DATE: 2003-01-08  
; NUMBER OF SEQ ID NOS: 88  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 68  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-340-192-68

Query Match 1.6%; Score 17; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2141 GATCAGTTTTTTCACCT 2157  
DB 1 GATCAGTTTTTTCACCT 17

## RESULT 70

US-09-969-373-2420  
; Sequence 2420, Application US/09969373  
; Patent No. US20020133852A1  
; GENERAL INFORMATION:  
; APPLICANT: Effertz, Roger J.  
; APPLICANT: Hauger, Brian M.  
; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping  
; FILE REFERENCE: 38-10(52679)A  
; CURRENT APPLICATION NUMBER: US/09/969,373  
; CURRENT FILING DATE: 2001-10-02  
; PRIOR APPLICATION NUMBER: US 09/754,853  
; PRIOR FILING DATE: 2001-01-05  
; PRIOR APPLICATION NUMBER: US 09/760,427  
; PRIOR FILING DATE: 2001-01-13  
; PRIOR APPLICATION NUMBER: US 09/855,768  
; PRIOR FILING DATE: 2001-05-15  
; NUMBER OF SEQ ID NOS: 4593  
; SEQ ID NO 2420  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Glycine max  
US-09-969-373-2420

Query Match 1.6%; Score 16.8; DB 1; Length 20;  
Best Local Similarity 90.0%; Pred. No. 39;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTG 1812  
Db 1 TCTGTGTGTGTGTGTGTG 20

RESULT 71  
US-09-969-373-2422  
; Sequence 2422, Application US/09969373  
; Patent No. US20020133852A1  
; GENERAL INFORMATION:  
; APPLICANT: Effertz, Roger J.  
; APPLICANT: Haug, Brian M.  
; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping  
; FILE REFERENCE: 38-10(52679)A  
; CURRENT APPLICATION NUMBER: US/09/969,373  
; CURRENT FILING DATE: 2001-10-02  
; PRIOR APPLICATION NUMBER: US 09/754,853  
; PRIOR FILING DATE: 2001-01-05  
; PRIOR APPLICATION NUMBER: US 09/760,427  
; PRIOR FILING DATE: 2001-01-13  
; PRIOR APPLICATION NUMBER: US 09/855,768  
; PRIOR FILING DATE: 2001-05-15  
; NUMBER OF SEQ ID NOS: 4593  
; SEQ ID NO 2422  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Glycine max  
US-09-969-373-2422

Query Match 1.6%; Score 16.8; DB 1; Length 20;  
Best Local Similarity 90.0%; Pred. No. 39;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTG 1812  
Db 1 TCTGTGTGTGTGTGTGTG 20

RESULT 72  
US-10-006-191-135/c  
; Sequence 135, Application US/10006191  
; Publication No. US20030144223A1  
; GENERAL INFORMATION:  
; APPLICANT: William Gaarde  
; APPLICANT: Andrew T. Watt  
; TITLE OF INVENTION: ANTISENSE MODULATION OF CONNECTIVE TISSUE GROWTH FACTOR EXPRESSION  
; FILE REFERENCE: R1S-0274  
; CURRENT APPLICATION NUMBER: US/10/006,191  
; CURRENT FILING DATE: 2001-12-10  
; NUMBER OF SEQ ID NOS: 153  
; SEQ ID NO 135  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-006-191-135

Query Match 1.6%; Score 16.8; DB 1; Length 20;  
Best Local Similarity 90.0%; Pred. No. 39;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1675 ATTCTGATTCGAATGACACT 1694  
Db 20 ATTCTGATTCGAATGACACT 1

RESULT 73  
US-09-768-917-10/c  
; Sequence 10, Application US/09768917  
; Patent No. US20020034494A1  
; GENERAL INFORMATION:  
; APPLICANT: Vicari, Alain P.  
; APPLICANT: Caux, Christophe  
; TITLE OF INVENTION: Chemokines as Adjuvants of Immune Response  
; FILE REFERENCE: SF0896K US  
; CURRENT APPLICATION NUMBER: US/09/768,917  
; CURRENT FILING DATE: 2001-01-24  
; PRIOR APPLICATION NUMBER: EP 0 974 357  
; PRIOR FILING DATE: 1998-07-16  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 10  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: primer  
US-09-768-917-10

Query Match 1.6%; Score 16.8; DB 1; Length 21;  
Best Local Similarity 90.0%; Pred. No. 39;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTGT 1813  
Db 21 GTGTGTGTGTGTGTGTGT 2

RESULT 74  
US-10-085-906-412  
; Sequence 412, Application US/10085906  
; Publication No. US20030054371A1  
; GENERAL INFORMATION:  
; APPLICANT: Ying, Vincent  
; APPLICANT: Wu, Paul  
; APPLICANT: Gray, Gary S.  
; TITLE OF INVENTION: POLYMORPHIC ELEMENTS IN THE  
; TITLE OF INVENTION: COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF  
; FILE REFERENCE: GNN-5343CP2  
; CURRENT APPLICATION NUMBER: US/10/085,906  
; CURRENT FILING DATE: 2002-02-27  
; PRIOR APPLICATION NUMBER: US 60/126,215  
; PRIOR FILING DATE: 1999-03-25  
; PRIOR APPLICATION NUMBER: US 09/534,061  
; PRIOR FILING DATE: 2000-03-24  
; PRIOR APPLICATION NUMBER: PCT/US00/07938  
; PRIOR FILING DATE: 2000-03-24  
; NUMBER OF SEQ ID NOS: 545  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 412  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-085-906-412

Query Match 1.6%; Score 16.8; DB 1; Length 21;  
Best Local Similarity 90.0%; Pred. No. 39;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTGT 1813  
Db 1 GTGTGTGTGTGTGTGTGT 20

RESULT 75  
US-09-263-959-983/c  
; Sequence 983, Application US/09263959  
; Patent No. US20020150891A1  
; GENERAL INFORMATION:  
; APPLICANT: Hood, Leroy E.  
; APPLICANT: Rowen, Lee  
; APPLICANT: Koop, Ben F.  
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI

NUMBER OF SEQUENCES: 1279  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION NUMBER: US/09/263.959  
FILING DATE: 05-MAR-1999  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: McMasters, David D.  
REGISTRATION NUMBER: 33,963  
REFERENCE/DOCKET NUMBER: 920010.426C2,  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 983:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-263-959-983

Query Match 1.6%; Score 16.4; DB 1; Length 18;  
Best Local Similarity 94.4%; Pred. No. 42;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTG 1810  
DB 18 TGTGTGTGTGTGTGTGTG 1

RESULT 76  
US-10-085-906-135  
Sequence 135, Application US/10085906  
Publication No. US20030054371A1  
GENERAL INFORMATION:  
APPLICANT: Ying, Vincent  
APPLICANT: Wu, Paul  
APPLICANT: Gray, Gary S.  
TITLE OF INVENTION: POLYMORPHIC ELEMENTS IN THE  
FILE REFERENCE: GNN-5343P2  
CURRENT APPLICATION NUMBER: US/10/085.906  
CURRENT FILING DATE: 2002-02-27  
PRIOR FILING DATE: 1999-03-25  
PRIOR FILING DATE: 1999-03-25  
PRIOR FILING DATE: 2000-03-24  
PRIOR FILING DATE: 2000-03-24  
PRIOR FILING DATE: 2000-03-24  
NUMBER OF SEQ ID NOS: 545  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 135  
LENGTH: 18  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-085-906-135

Query Match 1.6%; Score 16.4; DB 1; Length 18;  
Best Local Similarity 94.4%; Pred. No. 42;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTGT 1811

DB 1 GTGTGTGTGTGTGTGTGT 18  
RESULT 77  
US-10-301-844-26  
Sequence 26, Application US/10301844  
Publication No. US20030100747A1  
GENERAL INFORMATION:  
APPLICANT: Ruddy, David A.  
TITLE OF INVENTION: POLYMORPHISMS IN THE REGION OF THE HUMAN  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds, LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10036-2811  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: Windows  
SOFTWARE: FastSeq for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/301,844  
FILING DATE: 20-NOV-2003  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/852,495C  
FILING DATE: 07-MAY-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Poissant, Brian M  
REGISTRATION NUMBER: 28,462  
REFERENCE/DOCKET NUMBER: 9907-0057-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-493-4935  
TELEFAX: 650-493-5556  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 26:  
US-10-301-844-26

Query Match 1.6%; Score 16.4; DB 1; Length 20;  
Best Local Similarity 94.4%; Pred. No. 44;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1813 TATATATATATATATGTA 1830  
DB 2 TATATATATATATATA 19

RESULT 78  
US-10-301-844-26/c  
Sequence 26, Application US/10301844  
Publication No. US20030100747A1  
GENERAL INFORMATION:  
APPLICANT: Ruddy, David A.  
TITLE OF INVENTION: POLYMORPHISMS IN THE REGION OF THE HUMAN  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds, LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York

STATE: NY  
COUNTRY: USA  
ZIP: 10036-2811  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: Windows  
SOFTWARE: FastSeq for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/301-844  
FILING DATE: 20-NOV-1997  
CLASSIFICATION: <Unknown>  
PRIORITY APPLICATION NUMBER: US/08/852,495C  
FILING DATE: 07-MAY-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Poissant, Brian M  
REGISTRATION NUMBER: 28,462  
REFERENCE/DOCKET NUMBER: 8907-0057-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-493-4935  
TELEFAX: 650-493-5556  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 26:  
US-10-301-844-26

Query Match 1.6%; Score 16.4; DB 1; Length 20;  
Best Local Similarity 94.4%; Pred. No. 44;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1813 TATATATATATATGTA 1830  
DB 19 TATATATATATATATA 2

RESULT 79  
US-10-092-885-27  
Sequence 27, Application US/10092885  
Publication No. US20030190618A1  
GENERAL INFORMATION:  
APPLICANT: SAWAL, BABRU  
APPLICANT: LI, YUAN  
APPLICANT: HERMIDA, LEANDRO C.  
APPLICANT: HOPPA, NANCY L.  
APPLICANT: JOHE, KARL K.  
TITLE OF INVENTION: METHOD FOR GENERATING FIVE PRIME BIASED TANDEM TAG  
FILE REFERENCE: 0109015/026  
CURRENT APPLICATION NUMBER: US/10/092,885  
CURRENT FILING DATE: 2002-03-06  
NUMBER OF SEQ ID NOS: 60  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO: 27  
LENGTH: 16  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-092-885-27

Query Match 1.5%; Score 16; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 46;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGT 1809  
DB 1 GTGTGTGTGTGTGTGT 16

RESULT 80  
US-09-263-959-971  
Sequence 971, Application US/09263959  
Patent No. US20020150891A1  
GENERAL INFORMATION:  
APPLICANT: Rowen, Lee  
APPLICANT: Hood, Leroy E.  
APPLICANT: Koop, Ben F.  
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI  
NUMBER OF SEQUENCES: 1279  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/263,959  
FILING DATE: 05-MAR-1999  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: McWaters, David D.  
REGISTRATION NUMBER: 33,963  
REFERENCE/DOCKET NUMBER: 920010.426C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 971:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-263-959-971

Query Match 1.5%; Score 15.4; DB 1; Length 18;  
Best Local Similarity 94.1%; Pred. No. 57;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1816 ATATATATATATGTACA 1832  
DB 1 ATATATATATATGTATA 17

RESULT 81  
US-09-888-326-85  
Sequence 85, Application US/09888326  
Publication No. US20030026801A1  
GENERAL INFORMATION:  
APPLICANT: Weiner, George  
APPLICANT: Hartmann, Gunther  
TITLE OF INVENTION: Methods for Enhancing Antibody-Induced  
FILE REFERENCE: C1039/7052 (AWS)  
CURRENT APPLICATION NUMBER: US/09/888,326  
CURRENT FILING DATE: 2001-06-22  
PRIOR APPLICATION NUMBER: US 60/213,346  
PRIOR FILING DATE: 2000-06-22  
NUMBER OF SEQ ID NOS: 848  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO: 85  
LENGTH: 18  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic oligonucleotide  
NAME/KEY: misc\_feature



; LOCATION: (0)...(0)  
; OTHER INFORMATION: phosphorothioate backbone  
US-09-888-326-85

Query Match 1.5%; Score 15.4; DB 1; Length 18;  
Best Local Similarity 94.1%; Pred. No. 57;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1814 ATATATATATATATGTA 1830  
|||||  
Db 1 ATATATATATATATA 17

RESULT 82

US-09-888-326-85/c  
; Sequence 85, Application US/09888326  
; Publication No. US20030026801A1  
; GENERAL INFORMATION:  
; APPLICANT: Weiner, George  
; APPLICANT: Hartmann, Gunther  
; TITLE OF INVENTION: Methods for Enhancing Antibody-Induced  
; TITLE OF INVENTION: Cell Lysis and Treating Cancer  
; FILE REFERENCE: C1039/7052 (AWS)  
; CURRENT APPLICATION NUMBER: US/09/888,326  
; CURRENT FILING DATE: 2001-06-22  
; PRIOR APPLICATION NUMBER: US 60/213,346  
; PRIOR FILING DATE: 2000-06-22  
; NUMBER OF SEQ ID NOS: 848  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 85  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (0)...(0)  
; OTHER INFORMATION: phosphorothioate backbone  
US-09-888-326-85

Query Match 1.5%; Score 15.4; DB 1; Length 18;  
Best Local Similarity 94.1%; Pred. No. 57;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1814 ATATATATATATATGTA 1830  
|||||  
Db 18 ATATATATATATATA 2

RESULT 83

US-09-735-363A-16  
; Sequence 16, Application US/09735363A  
; Patent No. US20010041681A1  
; GENERAL INFORMATION:  
; APPLICANT: Fillion, Mario  
; APPLICANT: Phillip, Nigel  
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides  
; FILE REFERENCE: 02811-0181  
; CURRENT APPLICATION NUMBER: US/09/735,363A  
; CURRENT FILING DATE: 2000-12-12  
; PRIOR APPLICATION NUMBER: 60/170,325  
; PRIOR FILING DATE: 1999-12-13  
; PRIOR APPLICATION NUMBER: 60/228,925  
; PRIOR FILING DATE: 2000-08-29  
; NUMBER OF SEQ ID NOS: 87  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 16  
; LENGTH: 15  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Oligonucleotide  
US-09-735-363A-16

Query Match 1.4%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 61;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTG 1808  
|||||  
Db 1 GTGTGTGTGTGTGTG 15

RESULT 84

US-10-085-906-222  
; Sequence 222, Application US/10085906  
; Publication No. US20030054371A1  
; GENERAL INFORMATION:  
; APPLICANT: Ying, Vincent  
; APPLICANT: Wu, Paul  
; APPLICANT: Gray, Gary S.  
; TITLE OF INVENTION: POLYMORPHIC ELEMENTS IN THE  
; TITLE OF INVENTION: COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF  
; FILE REFERENCE: GNN-5343CP2  
; CURRENT APPLICATION NUMBER: US/10/085,906  
; CURRENT FILING DATE: 2002-02-27  
; PRIOR APPLICATION NUMBER: US 60/126,215  
; PRIOR FILING DATE: 1999-03-25  
; PRIOR APPLICATION NUMBER: US 09/534,061  
; PRIOR FILING DATE: 2000-03-24  
; PRIOR APPLICATION NUMBER: PCT/US00/07938  
; PRIOR FILING DATE: 2000-03-24  
; NUMBER OF SEQ ID NOS: 545  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 222  
; LENGTH: 15  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-085-906-222

Query Match 1.4%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 61;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTG 1807  
|||||  
Db 1 TGTGTGTGTGTGTGTG 15

RESULT 85

US-10-085-906-258/c  
; Sequence 258, Application US/10085906  
; Publication No. US20030054371A1  
; GENERAL INFORMATION:  
; APPLICANT: Ying, Vincent  
; APPLICANT: Wu, Paul  
; APPLICANT: Gray, Gary S.  
; TITLE OF INVENTION: POLYMORPHIC ELEMENTS IN THE  
; TITLE OF INVENTION: COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF  
; FILE REFERENCE: GNN-5343CP2  
; CURRENT APPLICATION NUMBER: US/10/085,906  
; CURRENT FILING DATE: 2002-02-27  
; PRIOR APPLICATION NUMBER: US 60/126,215  
; PRIOR FILING DATE: 1999-03-25  
; PRIOR APPLICATION NUMBER: US 09/534,061  
; PRIOR FILING DATE: 2000-03-24  
; PRIOR APPLICATION NUMBER: PCT/US00/07938  
; PRIOR FILING DATE: 2000-03-24  
; NUMBER OF SEQ ID NOS: 545  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 258  
; LENGTH: 15  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-085-906-258

```
Query Match 1.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1813 TATATATATATAT 1827
    |||||
    15 TATATATATATAT 1
Db

RESULT 86
US-09-263-959-540
; Sequence 540, Application US/09263959
; Patent No. US20020150891A1
; GENERAL INFORMATION:
; APPLICANT: Hood, Leroy E.
; APPLICANT: Rowen, Lee
; APPLICANT: Koop, Ben F.
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
; NUMBER OF SEQUENCES: 1279
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/09/263,959
; FILING DATE: 05-MAR-1999
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 920010.426C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 540:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-263-959-540

Query Match 1.4%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1813 TATATATATATAT 1827
    |||||
    2 TATATATATATAT 16
Db

RESULT 87
US-09-263-959-540/c
; Sequence 540, Application US/09263959
; Patent No. US20020150891A1
; GENERAL INFORMATION:
; APPLICANT: Hood, Leroy E.
; APPLICANT: Rowen, Lee
; APPLICANT: Koop, Ben F.
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
; NUMBER OF SEQUENCES: 1279
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
```

```
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 540:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-263-959-540

Query Match 1.4%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1813 TATATATATATAT 1827
    |||||
    15 TATATATATATAT 1
Db

RESULT 88
US-10-085-906-231
; Sequence 231, Application US/10085906
; Publication No. US20030054371A1
; GENERAL INFORMATION:
; APPLICANT: Ying, Vincent
; APPLICANT: Wu, Paul
; APPLICANT: Gray, Gary S.
; TITLE OF INVENTION: POLYMORPHIC ELEMENTS IN THE
; FILE REFERENCE: GNN-5343CP2
; CURRENT APPLICATION NUMBER: US/10/085,906
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 60/126,215
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: US 09/534,061
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: PCT/US00/07938
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 545
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 231
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-085-906-231

Query Match 1.4%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1813 TATATATATATAT 1827
    |||||
    2 TATATATATATAT 16
Db

RESULT 89
```

US-10-085-906-231/c  
; Sequence 231, Application US/10085906  
; Publication No. US20030054371A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Vincent  
; APPLICANT: Wu, Paul  
; APPLICANT: Gray, Gary S.  
; TITLE OF INVENTION: POLYMORPHIC ELEMENTS IN THE  
; TITLE OF INVENTION: COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF  
; FILE REFERENCE: GNN-5343CP2  
; CURRENT APPLICATION NUMBER: US/10/085,906  
; CURRENT FILING DATE: 2002-02-27  
; PRIOR APPLICATION NUMBER: US 60/126,215  
; PRIOR FILING DATE: 1999-03-25  
; PRIOR APPLICATION NUMBER: US 09/534,061  
; PRIOR FILING DATE: 2000-03-24  
; PRIOR APPLICATION NUMBER: PCT/US00/07938  
; PRIOR FILING DATE: 2000-03-24  
; NUMBER OF SEQ ID NOS: 545  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 231  
; LENGTH: 16  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-085-906-231

Query Match 1.4%; Score 15; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 63;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1813 TATATATATATAT 1827  
DB 15 TATATATATATAT 1

RESULT 90  
US-10-238-700-878  
; Sequence 878, Application US/10238700  
; Publication No. US20030153521A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: McSwiggen, James  
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Level  
; FILE REFERENCE: 400/057 (WEH01-1158-A)  
; CURRENT APPLICATION NUMBER: US/10/238,700  
; CURRENT FILING DATE: 2002-09-18  
; PRIOR APPLICATION NUMBER: PCT/US 02/16840  
; PRIOR FILING DATE: 2002-05-29  
; PRIOR APPLICATION NUMBER: US 60/318,471  
; PRIOR FILING DATE: 2001-09-10  
; NUMBER OF SEQ ID NOS: 4666  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 878  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-238-700-878

Query Match 1.4%; Score 15; DB 1; Length 17;  
Best Local Similarity 66.7%; Pred. No. 64;  
Matches 10; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1391 TGTAAAGACTTGACA 1405  
DB 2 UGUUAAGACUUGACA 16

RESULT 91  
US-08-463-404-57  
; Sequence 57, Application US/08463404  
; Publication No. US20020127634A1  
; GENERAL INFORMATION:  
; APPLICANT: Michael D. West

APPLICANT: Jerry W. Shay  
APPLICANT: Woodring E. Wright  
APPLICANT: Elizabeth Blackburn  
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF CONDITIONS  
TITLE OF INVENTION: RELATED TO TELOMERE LENGTH AND/OR  
TITLE OF INVENTION: RELATED TO TELOMERE LENGTH AND/OR  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/463,404  
FILING DATE: 05-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/060,952  
FILING DATE: May 13, 1993  
APPLICATION NUMBER: 07/882,438  
FILING DATE: May 13, 1992  
APPLICATION NUMBER: 08/038,766  
FILING DATE: March 24, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 202/045  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 57:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-463-404-57

Query Match 1.4%; Score 14.4; DB 1; Length 16;  
Best Local Similarity 93.8%; Pred. No. 75;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTG 1808  
DB 1 TGGGTGTGTGTGTGTG 16

RESULT 92  
US-10-092-885-28  
; Sequence 28, Application US/10092885  
; Publication No. US20030190618A1  
; GENERAL INFORMATION:  
; APPLICANT: SAMAL, BABRU  
; APPLICANT: LI, YUAN  
; APPLICANT: HERMIDA, LEANDRO C.  
; APPLICANT: HOPPA, NANCY L.  
; APPLICANT: JOHE, KARL K.  
; TITLE OF INVENTION: METHOD FOR GENERATING FIVE PRIME BIASED TANDEM TAG  
; TITLE OF INVENTION: LIBRARIES OF CDNAS  
; FILE REFERENCE: 0109015/026  
; CURRENT APPLICATION NUMBER: US/10/092,885  
; CURRENT FILING DATE: 2002-03-06  
; NUMBER OF SEQ ID NOS: 60

SEQUENCE DESCRIPTION: SEQ ID NO: 80;  
US-10-232-927A-80  
Query Match 1.4%; Score 14.4; DB 1; Length 16;  
Best Local Similarity 93.8%; Pred. No. 75;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1793 TGGTGTGTGTGTGTG 1808  
Db 1 TGGTGTGTGTGTGTG 16  
RESULT 94  
US-09-321-005A-13/C  
; Sequence 13; Application US/09321005A  
; Patent No. US20020162622A1  
; GENERAL INFORMATION:  
; APPLICANT: Gut, Ivo  
; TITLE OF INVENTION: Mutation Analysis Using Mass Spectrometry  
; FILE REFERENCE: B0004/7065  
; CURRENT APPLICATION NUMBER: US/09/321,005A  
; CURRENT FILING DATE: 1999-05-27  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 13  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Hypothetical Sequence for Exemplary Purposes  
US-09-321-005A-13  
Query Match 1.4%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 76;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1891 ATATTTCATGTAGC 1906  
Db 16 ATATTTCATGTACG 1  
RESULT 95  
US-10-060-756A-4088  
; Sequence 4088; Application US/10060756A  
; Publication No. US20030046717A1  
; GENERAL INFORMATION:  
; APPLICANT: Zhang, Jian  
; TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN  
; FILE REFERENCE: PB0177  
; CURRENT APPLICATION NUMBER: US/10/060,756A  
; CURRENT FILING DATE: 2002-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 09/864,761  
; PRIOR FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US 60/327,898  
; PRIOR FILING DATE: 2001-10-09  
; NUMBER OF SEQ ID NOS: 4804  
; SOFTWARE: Aecomica Sequence Listing Engine  
; SEQ ID NO 4088  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens

SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 28  
; LENGTH: 16  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-092-895-28  
Query Match 1.4%; Score 14.4; DB 1; Length 16;  
Best Local Similarity 93.8%; Pred. No. 75;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1794 GTGTGTGTGTGTGTG 1809  
Db 1 GTTGTGTGTGTGTG 16  
RESULT 93  
US-10-232-927A-80  
; Sequence 80; Application US/10232927A  
; Publication No. US20030190638A1  
; GENERAL INFORMATION:  
; APPLICANT: Michael D. West  
; Calvin B. Harley  
; Scott L. Weinrich  
; Catherine M. Strahl  
; Michael J. Meeachern  
; Jerry Shay  
; Woodring E. Wright  
; Elizabeth H. Blackburn  
; Nam Woo Kim  
; Homayoun Vaziri  
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF  
; CONDITIONS RELATED TO  
; TELOMERE LENGTH AND/OR  
; TELOMERASE ACTIVITY  
; NUMBER OF SEQUENCES: 80  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: FastSQ for Windows 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/232,927A  
; FILING DATE: 29-Aug-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/378,535  
; FILING DATE: 20-Aug-1999  
; APPLICATION NUMBER: 08/819,867  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Chambers, Daniel M.  
; REGISTRATION NUMBER: 34,561  
; REFERENCE/DOCKET NUMBER: 224/232  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 80:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear

```
US-10-060-756A-4088
Query Match      1.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 76;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2162 GCATTGTTTCTACTT 2177
    |||||
Db 2 GCATTGTTTCTAGTT 17

RESULT 96
US-10-060-756A-4089
; Sequence 4089, Application US/10060756A
; Publication No. US20030046717A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jian
; TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
; FILE REFERENCE: PB0177
; CURRENT APPLICATION NUMBER: US/10/060,756A
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/327,898
; PRIOR FILING DATE: 2001-10-09
; NUMBER OF SEQ ID NOS: 4804
; SOFTWARE: Aeonica Sequence Listing Engine
; SEQ ID NO 4089
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-756A-4089

Query Match      1.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 76;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2162 GCATTGTTTCTACTT 2177
    |||||
Db 1 GCATTGTTTCTAGTT 16

RESULT 97
US-10-297-068-1015
; Sequence 1015, Application US/10297068
; Publication No. US20030228585A1
; GENERAL INFORMATION:
; APPLICANT: INOKO, Hidetoshi
; APPLICANT: KAGIYA, Taeko
; APPLICANT: ICHIHARA, Tatsuo
; APPLICANT: Matsumura, Yoshiyuki
; APPLICANT: MORIYA, Shogo
; APPLICANT: NISHIDA, Michio
; TITLE OF INVENTION: KIT AND METHOD FOR DETERMINING HLA TYPES
; FILE REFERENCE: 13140P1174
; CURRENT APPLICATION NUMBER: US/10/297,068
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: JP 2000-164798
; PRIOR FILING DATE: 2000-06-01
; NUMBER OF SEQ ID NOS: 1298
; SOFTWARE: PatentIn Ver. 2.1
```

```
; SEQ ID NO 1015
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:capture
US-297-068-1015

Query Match      1.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 77;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1470 GGTACCACGACGAGAG 1485
    |||||
Db 2 GGTACCACGACGAGACG 17

RESULT 98
US-09-918-186A-235
; Sequence 235, Application US/09918186A
; Patent No. US20020137708A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Elizabeth J. Ackermann
; APPLICANT: Eric E. Swayze
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF SURVIVIN EXPRESSION
; FILE REFERENCE: ISPH-0595
; CURRENT APPLICATION NUMBER: US/09/918,186A
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 09/496,694
; PRIOR FILING DATE: 2000-02-02
; PRIOR APPLICATION NUMBER: 09/286,407
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: 09/163,162
; PRIOR FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 250
; SEQ ID NO 235
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-918-186A-235

Query Match      1.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 84;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1814 ATATATATATATATGTACA 1832
    |||||
Db 1 ACATATATATATATAACA 19

RESULT 99
US-09-735-363A-15
; Sequence 15, Application US/09735363A
; Patent No. US20010041691A1
; GENERAL INFORMATION:
; APPLICANT: Fillon, Mario
; APPLICANT: Phillip, Nigel
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
; FILE REFERENCE: 02811-0181
; CURRENT APPLICATION NUMBER: US/09/735,363A
; CURRENT FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/170,325
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 60/228,925
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
; LENGTH: 14
```

```

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-735-363A-15

Query Match 1.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTG 1806
Db 1 TGTGTGTGTGTGTG 14

RESULT 100
US-09-263-959-479/c
; Sequence 479, Application US/09263959
; Patent No. US20020150891A1
; GENERAL INFORMATION:
; APPLICANT: Rowen, Lee
; APPLICANT: Hood, Leroy E.
; APPLICANT: Koop, Ben F.
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
; NUMBER OF SEQUENCES: 1279
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/263,959
; FILING DATE: 05-MAR-1999
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 920010.426C2
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 479:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-263-959-479

Query Match 1.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGT 1807
Db 14 GTGTGTGTGTGTGT 1

RESULT 101
US-09-263-959-658
; Sequence 658, Application US/09263959
; Patent No. US20020150891A1
; GENERAL INFORMATION:
; APPLICANT: Rowen, Lee
; APPLICANT: Hood, Leroy E.
; APPLICANT: Koop, Ben F.

```

```

; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
; NUMBER OF SEQUENCES: 1279
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/263,959
; FILING DATE: 05-MAR-1999
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 920010.426C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 658:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-263-959-658

Query Match 1.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTG 1806
Db 1 TGTGTGTGTGTGTG 14

RESULT 102
US-09-263-959-811
; Sequence 811, Application US/09263959
; Patent No. US20020150891A1
; GENERAL INFORMATION:
; APPLICANT: Rowen, Lee
; APPLICANT: Hood, Leroy E.
; APPLICANT: Koop, Ben F.
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
; NUMBER OF SEQUENCES: 1279
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/263,959
; FILING DATE: 05-MAR-1999
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 920010.426C2
; TELECOMMUNICATION INFORMATION:

```

```

, , TELEPHONE: (206) 622-4900
, , TELEFAX: (206) 682-6031
, , INFORMATION FOR SEQ ID NO: 811
, , SEQUENCE CHARACTERISTICS:
, , LENGTH: 14 base pairs
, , TYPE: nucleic acid
, , STRANDEDNESS: single
, , TOPOLOGY: linear
US-09-263-953-811

```

Query Match	1.3%;	Score 14;	DB 1;	Length 14;
Best Local Similarity	100.0%;	Pred. No. 82;		
Matches 14;	Conservative	0;	Mismatches	0;
Indels	0;	Gaps	0;	

RESULT 103  
US-09-263-959-811/c  
; Sequence 811, Application US/09263959  
; Patent No. US20020150891A1  
; GENERAL INFORMATION:  
; APPLICANT: Hoog, Leroy E.  
; APPLICANT: Rowen, Lee  
; APPLICANT: Koop, Ben F.  
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTILIZE  
; NUMBER OF SEQUENCES: 1279  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Seed and Berry LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: US

Query Match	1.3%;	Score 14;	DB 1;	Length 14;
Best Local Similarity	100.0%;			
Matches	14;			
Conservative	0;			
Mismatches	0;			
Indels	0;			
Gaps	0;			

RESULT 104  
US-09-913-514-27  
; Sequence 27, Application US/09913514  
; Publication No. US20030082210A1

```

; GENERAL INFORMATION:
; APPLICANT: GOMI, Yasuyuki
; APPLICANT: SUNAWACHI, Hirotaki
; APPLICANT: TAKAHASHI, Michiaki
; APPLICANT: YAMANISHI, Koichi
; TITLE OF INVENTION: Method for Quality Control of an Attenuated Varicella Live Vaccine
; FILE REFERENCE: 0216-0454P
; CURRENT APPLICATION NUMBER: US/09/913.514
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: PCT/JP01/00678
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: JP 2000-62734
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Varicella virus
; US-09-913-514-27

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Query Match	1.3%;	Score 14;	DB 1;	Length 14;
Best Local Similarity	100.0%;	Pred. No. 82;		
Matches 14;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

RESULT 105  
 US-09-913-514-27/c  
 ; Sequence 27, Application US/09913514  
 ; Publication No. US20030082210A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: GOMI, Yasuyuki  
 ; APPLICANT: SUNAWACHI, Hiroki  
 ; APPLICANT: TAKAHASHI, Michiaki  
 ; APPLICANT: YAMANISHI, Koichi  
 ; TITLE OF INVENTION: Method for Quality Control of an Attenuated Varicella Live Vaccine  
 ; FILE REFERENCE: 0216-0454P  
 ; CURRENT APPLICATION NUMBER: US/09/913,514  
 ; CURRENT FILING DATE: 2001-12-07  
 ; PRIOR APPLICATION NUMBER: PCT/JP01/00678  
 ; PRIOR FILING DATE: 2001-01-31  
 ; PRIOR APPLICATION NUMBER: JP 2000-62734  
 ; PRIOR FILING DATE: 2000-01-31  
 ; NUMBER OF SEQ ID NOS: 42  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 27  
 ; LENGTH: 14  
 ; TYPE: DNA  
 ; ORGANISM: Varicella virus  
 US-09-913-514-27

Query Match	1.3%;	Score 14;	DB 1;	Length 14;
Best Local Similarity	100.0%;	Pred. No. 82;		
Matches 14;	Conservative	0;	Mismatches 0;	Indels 0;
Gaps	0;			

RESULT 106  
US-10-301-844-19  
; Sequence 19, Application US/10301844  
; Publication No. US20030100747A1  
; GENERAL INFORMATION:  
APPLICANT: Ruddy, David A.  
; Welff, Roger K.  
; TITLE OF INVENTION: POLYMORPHISMS IN THE REGION OF THE HUMAN  
; HEMOCHROMATOSIS GENE

NUMBER OF SEQUENCES: 26  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Pennie & Edmonds, LLP  
 STREET: 1155 Avenue of the Americas  
 CITY: New York  
 STATE: NY  
 COUNTRY: USA  
 ZIP: 10036-2811  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: Windows  
 SOFTWARE: FastSeq for Windows Version 2.0b  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/10/301,844  
 FILING DATE: 20-NO. US20030100747A1-2002  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/08/852,495C  
 FILING DATE: 07-MAY-1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Poissant, Brian M  
 REGISTRATION NUMBER: 28,462  
 REFERENCE/DOCKET NUMBER: 8907-0057-999  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 650-493-4935  
 TELEFAX: 650-493-5556  
 TELEX: 66141 PENNIE  
 INFORMATION FOR SEQ ID NO: 19:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 14 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 SEQUENCE DESCRIPTION: SEQ ID NO: 19:  
 US-10-301-844-19  
 Query Match 1.3%; Score 14; DB 1; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 82;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1813 TATATATATATATA 1826  
 Db 1 TATATATATATATA 14  
 RESULT 107  
 US-10-301-844-19/c  
 Sequence 19, Application US/10301844  
 Publication No. US20030100747A1  
 GENERAL INFORMATION:  
 APPLICANT: Ruddy, David A.  
 TITLE OF INVENTION: POLYMORPHISMS IN THE REGION OF THE HUMAN  
 NUMBER OF SEQUENCES: 26  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Pennie & Edmonds, LLP  
 STREET: 1155 Avenue of the Americas  
 CITY: New York  
 STATE: NY  
 COUNTRY: USA  
 ZIP: 10036-2811  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: Windows  
 SOFTWARE: FastSeq for Windows Version 2.0b  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/10/301,844  
 FILING DATE: 20-NO. US20030100747A1-2002  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/852,495C  
 FILING DATE: 07-MAY-1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Poissant, Brian M  
 REGISTRATION NUMBER: 28,462  
 REFERENCE/DOCKET NUMBER: 8907-0057-999  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 650-493-4935  
 TELEFAX: 650-493-5556  
 TELEX: 66141 PENNIE  
 INFORMATION FOR SEQ ID NO: 19:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 14 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 SEQUENCE DESCRIPTION: SEQ ID NO: 19:  
 US-10-301-844-19  
 Query Match 1.3%; Score 14; DB 1; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 82;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1813 TATATATATATATA 1826  
 Db 14 TATATATATATATA 1  
 RESULT 108  
 US-10-085-906-258  
 Sequence 258, Application US/10085906  
 Publication No. US20030054371A1  
 GENERAL INFORMATION:  
 APPLICANT: Ying, Vincent  
 APPLICANT: Wu, Paul  
 APPLICANT: Gray, Gary S.  
 TITLE OF INVENTION: POLYMORPHIC ELEMENTS IN THE  
 FILE REFERENCE: COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF  
 CURRENT FILING DATE: 2002-02-27  
 PRIOR APPLICATION NUMBER: US/10/085,906  
 PRIOR FILING DATE: 1999-03-25  
 PRIOR APPLICATION NUMBER: US 09/534,061  
 PRIOR FILING DATE: 2000-03-24  
 PRIOR APPLICATION NUMBER: PCT/US00/07938  
 PRIOR FILING DATE: 2000-03-24  
 NUMBER OF SEQ ID NOS: 545  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 258  
 LENGTH: 15  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 US-10-085-906-258  
 Query Match 1.3%; Score 14; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 83;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1814 ATATATATATATAT 1827  
 Db 1 ATATATATATATAT 14  
 RESULT 109  
 US-09-827-998-384  
 Sequence 384, Application US/09827998  
 Patent No. US20020102252A1  
 GENERAL INFORMATION:  
 APPLICANT: Gu, Yizhong  
 APPLICANT: Shannon, Mark  
 TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E  
 FILE REFERENCE: MDHMORF-8



```

, CURRENT APPLICATION NUMBER: US/09/827,998
, CURRENT FILING DATE: 2001-04-06
, PRIOR APPLICATION NUMBER: US 60/207,456
, PRIOR FILING DATE: 2000-05-26
, PRIOR APPLICATION NUMBER: US 60/236,359
, PRIOR FILING DATE: 2000-09-27
, NUMBER OF SEQ ID NOS: 1881
, SOFTWARE: Aecomica Sequence Listing Engine
, SEQ ID NO 384
, LENGTH: 17
, TYPE: DNA
, ORGANISM: Homo sapiens
US-09-827-998-384

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Query Match 1.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 91;  
Matches 15; Conservative 0; Mismatches 2; Indels

Qy 1794 GTGTGTGTGTGTGTG 1810  
Db 1 GTGTGTGTTTGTGAGTG 17

RESULT 110

US-09-827-998-385  
; Sequence 385, Application US/09827998  
; Patent No. US20020102252A1  
; GENERAL INFORMATION:

```

/ APPLICANT: Gu, Yizhong
/ APPLICANT: Shannon, Mark
/ TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
/ FILE REFERENCE: MDW0RF-8
/ CURRENT APPLICATION NUMBER: US/09/827,998
/ CURRENT FILING DATE: 2001-04-06
/ PRIOR APPLICATION NUMBER: US 60/207,456
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: US 60/236,359
/ PRIOR FILING DATE: 2000-09-27
/ NUMBER OF SEQ ID NOS: 1881
/ SOFTWARE: Aecomica Sequence Listing Engine
/ SEQ ID NO 385

```

Query Match	1.3%;	Score 13.8;	DB 1;	Length 17;
Best Local Similarity	88.2%;	Pred. No. 91;		
Matches	15;	Conservative	0;	Mismatches
			2;	Indels

Qy 1793 TGTGTGTGTGTGTGT 1809  
|||||  
pb 1 TGTGTGTGTGTGTGT 17

RESULT 111

US-09-827-998-386  
; Sequence 386, Application US/09827998  
; Patent No. US20020102252A1  
: GENERAL INFORMATION:

```

1 / APPLICANT: Guo, Yizhong
2 /
3 / APPLICANT: Shannon, Mark
4 /
5 / TITLE OF INVENTION: NOVEL
6 /
7 / FILE REFERENCE: MDHMOF-8
8 /
9 / CURRENT APPLICATION NUMBER: US/09/827,998
10 /
11 / CURRENT FILING DATE: 2001-04-06
12 /
13 / PRIOR APPLICATION NUMBER: US 60/207,456
14 /
15 / PRIOR FILING DATE: 2000-05-26
16 /
17 / PRIOR APPLICATION NUMBER: US 60/236,359
18 /
19 / PRIOR FILING DATE: 2000-09-27
20 /
21 / NUMBER OF SEQ ID NOS: 1881
22 /
23 / SOFTWARE: Acomica Sequence Listing Engine
24 /
25 / SEQ ID NO 386

```

QY 1798 GTGTGTGTGTGTGTAT 1814  
|||||  
Db 1 GTGTGTGTGTGTGTAT 17

## RESULT 114

US-09-827-998-389  
; Sequence 389, Application US/09827998  
; Patent No. US20020102252A1  
; GENERAL INFORMATION:  
; APPLICANT: Gu, Yizhong  
; APPLICANT: Shannon, Mark  
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E  
; FILE REFERENCE: MDHMORF-8  
; CURRENT APPLICATION NUMBER: US/09/827,998  
; CURRENT FILING DATE: 2001-04-06  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; NUMBER OF SEQ ID NOS: 1881  
; SOFTWARE: Aeonica Sequence Listing Engine  
; SEQ ID NO 389  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-827-998-389

Query Match 1.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 91;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1799 TGTGTGTGTGTGTAT 1815  
|||||  
Db 1 TGTGTGTGTGTGTAT 17

## RESULT 115

US-09-263-959-546  
; Sequence 546, Application US/09263959  
; Patent No. US20020150891A1  
; GENERAL INFORMATION:  
; APPLICANT: Hood, Leroy E.  
; APPLICANT: Rowen, Lee  
; APPLICANT: Koop, Ben F.  
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI  
; NUMBER OF SEQUENCES: 1279  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Seed and Berry LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: US  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/263,959  
; FILING DATE: 05-MAR-1999  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McMasters, David D.  
; REGISTRATION NUMBER: 33,963  
; REFERENCE/DOCKET NUMBER: 920010.426C2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 546:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 base pairs

; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-09-263-959-546

Query Match 1.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 91;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1814 ATATATATATATATGTA 1830  
|||||  
Db 1 ATGTATGTATATATGTA 17

## RESULT 116

US-09-263-959-837/c  
; Sequence 837, Application US/09263959  
; Patent No. US20020150891A1  
; GENERAL INFORMATION:  
; APPLICANT: Hood, Leroy E.  
; APPLICANT: Rowen, Lee  
; APPLICANT: Koop, Ben F.  
; APPLICANT: Koop, Ben F.  
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI  
; NUMBER OF SEQUENCES: 1279  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Seed and Berry LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: US  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/263,959  
; FILING DATE: 05-MAR-1999  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McMasters, David D.  
; REGISTRATION NUMBER: 33,963  
; REFERENCE/DOCKET NUMBER: 920010.426C2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 837:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-09-263-959-837

Query Match 1.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 91;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1799 TGTGTGTGTGTGTAT 1815  
|||||  
Db 17 TGTATGTGTGTATGTA 1

## RESULT 117

US-09-843-676-132  
; Sequence 132, Application US/09843676  
; Patent No. US20020164786A1  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; APPLICANT: Lingner, Joachim  
; APPLICANT: Nakamura, Toru  
; APPLICANT: Chapman, Karen B.

```

; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: NO. US20020164786A1el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/843,676
; FILING DATE: 26-Apr-2001
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US/08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US/08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US/08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 132:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 132:
;
; US-09-843-676-132
;
; Query Match 1.3%; Score 13.8; DB 1; Length 17;
; Best Local Similarity 88.2%; Pred. No. 91;
; Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
;
; QY 1865 TTTTATTTTGTGTTTT 1881
; Db 1 TTTTATTTTGTGTTTT 17
;
; RESULT 118
; US-09-766-253-132
; Sequence 132, Application US/09766253
; Publication No. US2002018747A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Linger, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: NO. US2002018747A1el Telomerase
; NUMBER OF SEQUENCES: 171
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco

```

```

; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/766,253
; FILING DATE: 19-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/846,017
; FILING DATE: 1997-04-25
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002920US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 132:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 132:
;
; US-09-766-253-132
;
; Query Match 1.3%; Score 13.8; DB 1; Length 17;
; Best Local Similarity 88.2%; Pred. No. 91;
; Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
;
; QY 1865 TTTTATTTTGTGTTTT 1881
; Db 1 TTTTATTTTGTGTTTT 17
;
; RESULT 119
; US-09-438-486-132
; Sequence 132, Application US/09438486
; Publication No. US20030009019A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Linger, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: NO. US20030009019A1el Telomerase
; NUMBER OF SEQUENCES: 223
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/438,486
; FILING DATE: 12-NOV-1999
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:

```

; APPLICATION NUMBER: US 08/851,843  
; FILING DATE: 06-MAY-1997  
; CLASSIFICATION: 536  
; PRIORITY INFORMATION DATA: US 08/846,017  
; FILING DATE: 25-APR-1997  
; CLASSIFICATION: 536  
; PRIORITY INFORMATION DATA: US 08/844,419  
; FILING DATE: 18-APR-1997  
; CLASSIFICATION: 536  
; PRIORITY INFORMATION DATA: US 08/724,643  
; FILING DATE: 01-OCT-1996  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Apple, Randolph T.  
; REGISTRATION NUMBER: 36,429  
; REFERENCE/DOCKET NUMBER: 015389-002931US  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 132:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-09-438-486-132

Query Match 1.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 91;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1865 TTTTATTTTGTGTTT 1881  
Db 1 TTTTATTTTGTGTTT 17

## RESULT 120

US-09-848-754A-2098/c  
; Sequence 2098, Application US/09848754A  
; Publication No. US20030073207A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to  
; TITLE OF INVENTION: Levels of Epidermal Growth Factor Receptors  
; FILE REFERENCE: MEH800-958-I (400/018)  
; CURRENT APPLICATION NUMBER: US/09/848,754A  
; CURRENT FILING DATE: 2001-05-03  
; NUMBER OF SEQ ID NOS: 9645  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 2098  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
; US-09-848-754A-2098

Query Match 1.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 91;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1789 ATATTGTGTGTGTGT 1805  
Db 17 ATTTGTATGTGTGTGT 1

## RESULT 121

US-10-208-357-23/c  
; Sequence 23, Application US/10208357  
; Publication No. US20020182687A1  
; GENERAL INFORMATION:  
; APPLICANT: Kurz, Markus

; APPLICANT: Lohse, Peter  
; APPLICANT: Wagner, Richard  
; TITLE OF INVENTION: Peptide Acceptor Ligation Methods  
; FILE REFERENCE: 50036/031002  
; CURRENT APPLICATION NUMBER: US/10/208,357  
; CURRENT FILING DATE: 2002-07-30  
; PRIOR APPLICATION NUMBER: US/09/619,103  
; PRIOR FILING DATE: 2000-07-19  
; PRIOR APPLICATION NUMBER: 60/145,834  
; PRIOR FILING DATE: 1999-07-27  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 23  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: designed sequence for nucleic acid purification  
; US-10-208-357-23

Query Match 1.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 91;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1865 TTTTATTTTGTGTTT 1881  
Db 17 TTTTATTTTGTGTTT 1

## RESULT 122

US-10-053-758-132  
; Sequence 132, Application US/10053758  
; Publication No. US20030032075A1  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; Lingner, Joachim  
; Nakamura, Toru  
; Chapman, Karen B.  
; Morin, Gregg B.  
; Harley, Calvin  
; Andrews, William H.  
; TITLE OF INVENTION: No. US20030032075A1el Telomerase  
; NUMBER OF SEQUENCES: 225  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 94111

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/053,758  
FILING DATE: 18-Jan-2002  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/854,050  
FILING DATE: 09-MAY-1997  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph T.  
REGISTRATION NUMBER: 36,429

REFERENCE/DOCKET NUMBER: 015389-002930US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 132:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 132:  
US-10-053-758-132

Query Match 1.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 91;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1865 TTTTATTTTGTGTTTT 1881  
Db 1 TTTTATTTTGTGTTTT 17

## RESULT 123

US-10-054-295-132  
; Sequence 132, Application US/10054295  
; Publication No. US2003004495A1  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; Lingner, Joachim  
; Nakamura, Toru  
; Chapman, Karen B.  
; Morin, Gregg B.  
; Harley, Calvin  
; Andrews, William H.  
; TITLE OF INVENTION: NO. US20030044953A1el Telomerase  
; NUMBER OF SEQUENCES: 225  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 94111

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/054,295  
FILING DATE: 18-Jan-2002  
CLASSIFICATION: 536

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/854,050  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 23-APR-1997  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph T.  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002930US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 132:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single

TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 132:  
US-10-054-295-132

Query Match 1.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 91;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1865 TTTTATTTTGTGTTTT 1881  
Db 1 TTTTATTTTGTGTTTT 17

## RESULT 124

US-10-117-267-5  
; Sequence 5, Application US/10117267  
; Publication No. US20030045698A1  
; GENERAL INFORMATION:  
; APPLICANT: Manoharan, Muthiah  
; TITLE OF INVENTION: Compounds, Processes And Intermediates For Synthesis Of Mixed Back  
; TITLE OF INVENTION: Oligomeric Compounds  
; FILE REFERENCE: ISIS-5039  
; CURRENT APPLICATION NUMBER: US/10/117,267  
; CURRENT FILING DATE: 2002-04-05  
; PRIOR APPLICATION NUMBER: 09/726,096  
; PRIOR FILING DATE: 2000-11-29  
; PRIOR APPLICATION NUMBER: 09/250,075  
; PRIOR FILING DATE: 1999-02-12  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 5  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Construct  
; NAME/KEY: misc feature  
; LOCATION: (1)..(19)  
; OTHER INFORMATION: 2'-methoxyethoxy (MOE); phosphorothioate  
; OTHER INFORMATION: internucleoside linkage  
US-10-117-267-5

Query Match 1.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 91;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1865 TTTTATTTTGTGTTTT 1881  
Db 1 TTTTATTTTGTGTTTT 17

## RESULT 125

US-10-060-756A-4087  
; Sequence 4087, Application US/10060756A  
; Publication No. US2003004617A1  
; GENERAL INFORMATION:  
; APPLICANT: Zhang, Jian  
; TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN  
; FILE REFERENCE: PB0177  
; CURRENT APPLICATION NUMBER: US/10/060,756A  
; CURRENT FILING DATE: 2002-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30

;; PRIOR APPLICATION NUMBER: PCT/US01/00663  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: US 09/864,761  
;; PRIOR FILING DATE: 2001-05-23  
;; PRIOR APPLICATION NUMBER: US 60/327,898  
;; PRIOR FILING DATE: 2001-10-09  
;; NUMBER OF SEQ ID NOS: 4804  
;; SOFTWARE: Acemica Sequence Listing Engine  
;; SEQ ID NO 4087  
;; LENGTH: 17  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-10-060-756A-4087

Query Match 1.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 91;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2160 AAGCATTGTTCTACT 2176  
Db 1 ATGCATTGTTCTACT 17

## RESULT 126

US-10-054-611-132  
; Sequence 132, Application US/10054611  
; Publication No. US20030059787A1

## GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.

Lingner, Joachim

Nakamura, Toru

Chapman, Karen B.

Morin, Gregg B.

Harley, Calvin

Andrews, William H.

TITLE OF INVENTION: No. US20030059787A1el Telomerase

NUMBER OF SEQUENCES: 225

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, 8th Floor

CITY: San Francisco

STATE: California

COUNTRY: United States of America

ZIP: 94111

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/054,611

FILING DATE: 18-Jan-2002

CLASSIFICATION: 536

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/854,050

FILING DATE: &lt;Unknown&gt;

APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

APPLICATION NUMBER: US 08/724,643

FILING DATE: 01-OCT-1996

## ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph T.

REGISTRATION NUMBER: 36,429

REFERENCE/DOCKET NUMBER: 015389-002930US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 132:

SEQUENCE CHARACTERISTICS:

LENGTH: 17 base pairs

TYPE: nucleic acid

;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; SEQUENCE DESCRIPTION: SEQ ID NO: 132:  
US-10-054-611-132

Query Match 1.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 91;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1865 TTTTATTTTCTTTT 1881  
Db 1 TTTTATTTTCTTTT 17

## RESULT 127

US-10-156-306-1628/c

; Sequence 1628, Application US/10156306

; Publication No. US20030119017A1

## GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

McSwiggen, James

TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related

FILE REFERENCE: MEH01-664-A (400/050)

CURRENT APPLICATION NUMBER: US/10/156,306

CURRENT FILING DATE: 2002-05-28

NUMBER OF SEQ ID NOS: 8013

SOFTWARE: PatentIn version 3.0

SEQ ID NO 1628

LENGTH: 17

TYPE: RNA

ORGANISM: Homo sapiens

US-10-156-306-1628

## Query Match

Best Local Similarity 88.2%; Pred. No. 91;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1476 CAGCAGAAAGTTAGTA 1492  
Db 17 CTGCAGAAAGATTAGTA 1

## RESULT 128

US-09-263-959-971/c

; Sequence 971, Application US/09263959

; Patent No. US20020150891A1

## GENERAL INFORMATION:

APPLICANT: Hood, Leroy E.

APPLICANT: Koop, Ben F.

TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI

NUMBER OF SEQUENCES: 1279

CORRESPONDENCE ADDRESS:

ADDRESSEE: Seed and Berry LLP

STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle

STATE: Washington

COUNTRY: US

ZIP: 98104-7092

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/263,959

FILING DATE: 05-MAR-1999

## CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Mcmasters, David D.

REGISTRATION NUMBER: 33,963

REFERENCE/DOCKET NUMBER: 920010.426C2

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 971:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-263-959-971

Query Match 1.3%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 92;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1811 TGTATATATATATAT 1827
Db 17 TATACATATATATAT 1

RESULT 129
US-10-187-251A-2/c
; Sequence 2, Application US/10187251A
; Publication No. US2003010897A1
; GENERAL INFORMATION:
; APPLICANT: Dmanac, Radoje
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION OR QUANTIFICATION OF NUCLE
; FILE REFERENCE: 30311/0018A
; CURRENT APPLICATION NUMBER: US/10/187,251A
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: US 08/947,779
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: US 08/912,885
; PRIOR FILING DATE: 1997-08-15
; PRIOR APPLICATION NUMBER: US 08/892,503
; PRIOR FILING DATE: 1997-07-14
; PRIOR APPLICATION NUMBER: US 08/812,951
; PRIOR FILING DATE: 1997-03-04
; PRIOR APPLICATION NUMBER: US 08/784,787
; PRIOR FILING DATE: 1997-01-16
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 2
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic primer
US-10-187-251A-2

Query Match 1.3%; Score 13.6; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 94;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1863 CCTTTTATTTTG 1876
Db 15 CCTTTTITTTTG 2

RESULT 130
US-08-463-404-51
; Sequence 51, Application US/08463404
; Publication No. US20020127634A1
; GENERAL INFORMATION:
; APPLICANT: Michael D. West
; APPLICANT: Jerry W. Shay
; APPLICANT: Woodring E. Wright
; APPLICANT: Elizabeth Blackburn
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF CONDITIONS
; TITLE OF INVENTION: RELATED TO TELOMERE LENGTH AND/OR
; TITLE OF INVENTION: TELOMERASE ACTIVITY
; NUMBER OF SEQUENCES: 57

```

```

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; STATE: Los Angeles
; COUNTRY: California
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,404
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/060,952
; FILING DATE: May 13, 1993
; APPLICATION NUMBER: 07/882,438
; FILING DATE: May 13, 1992
; APPLICATION NUMBER: 08/038,766
; FILING DATE: March 24, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Waizburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 202/045
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-463-404-51

Query Match 1.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 99;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1792 TTGTGTGTGTGTGTG 1806
Db 1 TGGTGTGTGTGTGTG 15

RESULT 131
US-09-263-959-543/c
; Sequence 543, Application US/09263959
; Patent No. US20020150891A1
; GENERAL INFORMATION:
; APPLICANT: Hoog, Leroy E.
; APPLICANT: Rower, Lee
; APPLICANT: Koop, Ben F.
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
; NUMBER OF SEQUENCES: 1279
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

```

APPLICATION NUMBER: US/09/263,959  
FILING DATE: 05-MAR-1999  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Mcmasters, David D.  
REGISTRATION NUMBER: 33,963  
REFERENCE/DOCKET NUMBER: 920010.426C2  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 622-6031  
INFORMATION FOR SEQ ID NO: 543:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-263-959-543

Query Match 1.3%; Score 13.4; DB 1; Length 15;  
Best Local Similarity 93.3%; Pred. No. 99;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1813 TATATATATATAT 1827  
Db 15 TATATATATATAT 1

RESULT 132  
US-09-263-959-545/c  
Sequence 545, Application US/09263959  
Patent No. US20020150891A1  
GENERAL INFORMATION:  
APPLICANT: Hood, Leroy E.  
APPLICANT: Rowen, Lee  
APPLICANT: Koop, Ben F.  
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI  
NUMBER OF SEQUENCES: 1279  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/263,959  
FILING DATE: 05-MAR-1999

CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Mcmasters, David D.  
REGISTRATION NUMBER: 33,963  
REFERENCE/DOCKET NUMBER: 920010.426C2  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 622-6031  
INFORMATION FOR SEQ ID NO: 545:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-263-959-545

Query Match 1.3%; Score 13.4; DB 1; Length 15;  
Best Local Similarity 93.3%; Pred. No. 99;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1813 TATATATATATAT 1827

Db 15 TATATATATATAT 1

RESULT 133  
US-09-263-959-877/c  
Sequence 877, Application US/09263959  
Patent No. US20020150891A1  
GENERAL INFORMATION:  
APPLICANT: Hood, Leroy E.  
APPLICANT: Rowen, Lee  
APPLICANT: Koop, Ben F.  
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI  
NUMBER OF SEQUENCES: 1279  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/263,959  
FILING DATE: 05-MAR-1999  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Mcmasters, David D.  
REGISTRATION NUMBER: 33,963  
REFERENCE/DOCKET NUMBER: 920010.426C2  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 622-6031  
INFORMATION FOR SEQ ID NO: 877:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-263-959-877

Query Match 1.3%; Score 13.4; DB 1; Length 15;  
Best Local Similarity 93.3%; Pred. No. 99;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1813 TATATATATATAT 1827  
Db 15 TATATATATATAT 1

RESULT 134  
US-10-287-919-592/c  
Sequence 582, Application US/10287919  
Publication No. US20030085830A1  
GENERAL INFORMATION:  
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.  
TITLE OF INVENTION: Methanococcus jannaschii complete genome.  
FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333  
CURRENT APPLICATION NUMBER: US/10/287,919  
CURRENT FILING DATE: 2002-11-05  
NUMBER OF SEQ ID NOS: 2706  
SOFTWARE: Proprietary  
SEQ ID NO 582  
LENGTH: 15  
TYPE: DNA  
ORGANISM: Methanococcus jannaschii complete genome.  
FEATURE:  
LOCATION: (167867)...(167881)  
OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectionObjectNumber = 690



## US-10-287-919-582

Query Match 1.3%; Score 13.4; DB 1; Length 15;  
Best Local Similarity 93.3%; Pred. No. 99;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1866 TTTTATTTTGTGTTT 1880  
|||||  
DB 15 TTTTATTTTGTGTTT 1

## RESULT 135

US-10-287-919-583/c  
; Sequence 583, Application US/10287919  
; Publication No. US20030085830A1  
; GENERAL INFORMATION:  
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.  
; TITLE OF INVENTION: Methanococcus jannaschii complete genome.  
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333  
; CURRENT APPLICATION NUMBER: US/10/287,919  
; CURRENT FILING DATE: 2002-11-05  
; NUMBER OF SEQ ID NOS: 2706  
; SOFTWARE: Proprietary  
; SEQ ID NO 583  
; LENGTH: 15  
; TYPE: DNA  
; ORGANISM: Methanococcus jannaschii complete genome.  
; FEATURE:  
; LOCATION: (167867)...(167881)  
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 589  
US-10-287-919-583

Query Match 1.3%; Score 13.4; DB 1; Length 15;  
Best Local Similarity 93.3%; Pred. No. 99;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1866 TTTTATTTTGTGTTT 1880  
|||||  
DB 15 TTTTATTTTGTGTTT 1

## RESULT 136

US-10-287-919-2620/c  
; Sequence 2620, Application US/10287919  
; Publication No. US20030085830A1  
; GENERAL INFORMATION:  
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.  
; TITLE OF INVENTION: Methanococcus jannaschii complete genome.  
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333  
; CURRENT APPLICATION NUMBER: US/10/287,919  
; CURRENT FILING DATE: 2002-11-05  
; NUMBER OF SEQ ID NOS: 2706  
; SOFTWARE: Proprietary  
; SEQ ID NO 2620  
; LENGTH: 15  
; TYPE: DNA  
; ORGANISM: Methanococcus jannaschii complete genome.  
; FEATURE:  
; LOCATION: (1596075)...(1596090)  
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 3341  
US-10-287-919-2620

Query Match 1.3%; Score 13.4; DB 1; Length 15;  
Best Local Similarity 93.3%; Pred. No. 99;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1879 TTTAATGCTTTGATA 1893  
|||||  
DB 15 TTTAATGCTTTAATA 1

## RESULT 137

US-10-232-927A-79

; Sequence 79, Application US/10232927A  
; Publication No. US20030190638A1  
; GENERAL INFORMATION:

APPLICANT: Michael D. West  
Calvin B. Harley  
Scott L. Weinrich  
Catherine M. Strahl  
Michael J. Mceachern  
Jerry Shay  
Woodring E. Wright  
Elizabeth H. Blackburn  
Nam Woo Kim  
Homayoun Vaziri

TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF  
CONDITIONS RELATED TO  
TELOMERE LENGTH AND/OR  
TELOMERASE ACTIVITY

NUMBER OF SEQUENCES: 80  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
Suite 4700

CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq for Windows 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/232,927A  
FILING DATE: 29-Aug-2002  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/378,535  
FILING DATE: 20-Aug-1999  
APPLICATION NUMBER: 08/819,867  
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Chambers, Daniel M.  
REGISTRATION NUMBER: 34,561  
REFERENCE/DOCKET NUMBER: 224/232  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 79:

SEQUENCE CHARACTERISTICS:  
LENGTH: 15 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 79:

US-10-232-927A-79

Query Match 1.3%; Score 13.4; DB 1; Length 15;  
Best Local Similarity 93.3%; Pred. No. 99;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1792 TTGTGTGTGTGTGTG 1806  
|||||  
DB 1 TGGTGTGTGTGTGTG 15

## RESULT 138

US-10-271-602B-208  
; Sequence 208, Application US/10271602B  
; Publication No. US20040002073A1  
; GENERAL INFORMATION:  
; APPLICANT: Alice Xiang Li

```

; APPLICANT: Ghazala Hashmi
; APPLICANT: Michael Seul
; TITLE OF INVENTION: MULTIPLEXED ANALYSIS OF POLYMORPHIC LOCI
; TITLE OF INVENTION: BY CONCURRENT INTERROGATION AND ENZYME-MEDIATED DETECTION
; FILE REFERENCE: ewap-us
; CURRENT APPLICATION NUMBER: US/10/271.602B
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/329,427
; PRIOR FILING DATE: 2001-10-14
; PRIOR APPLICATION NUMBER: 60/329,620
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 60/329,428
; PRIOR FILING DATE: 2001-10-14
; PRIOR APPLICATION NUMBER: 60/329,619
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 60/364,416
; PRIOR FILING DATE: 2002-03-14
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 208
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe sequence derived from human genomic sequence
; US-10-271-602B-208

Query Match      1.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 99;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1580 TGTAGCCCGAGTGAC 1594
Db 1 TGTACCCCGAGTGAC 15

RESULT 139
US-09-263-959-541
; Sequence 541, Application US/09263959
; Patent No. US20020150891A1
; GENERAL INFORMATION:
; APPLICANT: Hood, Leroy E.
; APPLICANT: Koop, Ben F.
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
; NUMBER OF SEQUENCES: 1279
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/263,959
; FILING DATE: 05-MAR-1999
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 920010.426C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 541:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-263-959-541

Query Match      1.3%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 1e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1813 TATATATATATAT 1827
Db 16 TATATATATATAT 2

RESULT 141
US-09-263-959-544
; Sequence 544, Application US/09263959
; Patent No. US20020150891A1
; GENERAL INFORMATION:
; APPLICANT: Hood, Leroy E.
; APPLICANT: Rowen, Lee
; APPLICANT: Koop, Ben F.
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
; NUMBER OF SEQUENCES: 1279

```

```

; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-263-959-541

Query Match      1.3%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 1e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1813 TATATATATATAT 1827
Db 1 TATATATATATAT 15

RESULT 140
US-09-263-959-541/c
; Sequence 541, Application US/09263959
; Patent No. US20020150891A1
; GENERAL INFORMATION:
; APPLICANT: Hood, Leroy E.
; APPLICANT: Rowen, Lee
; APPLICANT: Koop, Ben F.
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
; NUMBER OF SEQUENCES: 1279
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/263,959
; FILING DATE: 05-MAR-1999
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 920010.426C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 541:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-263-959-541

Query Match      1.3%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 1e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1813 TATATATATATAT 1827
Db 16 TATATATATATAT 2

RESULT 141
US-09-263-959-544
; Sequence 544, Application US/09263959
; Patent No. US20020150891A1
; GENERAL INFORMATION:
; APPLICANT: Hood, Leroy E.
; APPLICANT: Rowen, Lee
; APPLICANT: Koop, Ben F.
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
; NUMBER OF SEQUENCES: 1279

```

;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Seed and Berry LLP  
;; STREET: 6300 Columbia Center, 701 Fifth Avenue  
;; CITY: Seattle  
;; STATE: Washington  
;; COUNTRY: US  
;; ZIP: 98104-7092  
;;  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;;  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/263,959  
;; FILING DATE: 05-MAR-1999  
;;  
;; CLASSIFICATION:  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Mcmasters, David D.  
;; REGISTRATION NUMBER: 33,963  
;; REFERENCE/DOCKET NUMBER: 920010.426C2  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (206) 622-4900  
;; TELEFAX: (206) 682-6031  
;;  
;; INFORMATION FOR SEQ ID NO: 544:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 16 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;;  
;; US-09-263-959-544

Query Match 1.3%; Score 13.4; DB 1; Length 16;  
Best Local Similarity 93.3%; Pred. No. 1e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1813 TATATATATATATAT 1827  
Db 1 TATATATGATATAT 15

RESULT 142  
US-09-263-959-544/c  
; Sequence 544, Application US/09263959  
; Patent No. US20020150891A1  
; GENERAL INFORMATION:  
; APPLICANT: Hood, Leroy E.  
; APPLICANT: Rowen, Lee  
; APPLICANT: Koop, Ben F.  
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI  
; NUMBER OF SEQUENCES: 1279  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Seed and Berry LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: US  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/263,959  
; FILING DATE: 05-MAR-1999  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mcmasters, David D.  
; REGISTRATION NUMBER: 33,963  
; REFERENCE/DOCKET NUMBER: 920010.426C2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031

;; INFORMATION FOR SEQ ID NO: 544:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 16 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;;  
;; US-09-263-959-544

Query Match 1.3%; Score 13.4; DB 1; Length 16;  
Best Local Similarity 93.3%; Pred. No. 1e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1813 TATATATATATATAT 1827  
Db 16 TATATATACATATAT 2

RESULT 143  
US-09-263-959-508  
; Sequence 508, Application US/09263959  
; Patent No. US20020150891A1  
; GENERAL INFORMATION:  
; APPLICANT: Hood, Leroy E.  
; APPLICANT: Rowen, Lee  
; APPLICANT: Koop, Ben F.  
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI  
; NUMBER OF SEQUENCES: 1279  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Seed and Berry LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: US  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/263,959  
; FILING DATE: 05-MAR-1999  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mcmasters, David D.  
; REGISTRATION NUMBER: 33,963  
; REFERENCE/DOCKET NUMBER: 920010.426C2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 508:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 13 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-09-263-959-508

Query Match 1.2%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGT 1805  
Db 1 TGTGTGTGTGTGT 13

RESULT 144  
US-09-263-959-548  
; Sequence 548, Application US/09263959  
; Patent No. US20020150891A1  
; GENERAL INFORMATION:  
; APPLICANT: Hood, Leroy E.

APPLICANT: Rowen, Lee  
APPLICANT: Koop, Ben F.  
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI  
NUMBER OF SEQUENCES: 1279  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
FILING DATE: 05-MAR-1999  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: McMasters, David D.  
REGISTRATION NUMBER: 33,963  
REFERENCE/DOCKET NUMBER: 920010.426C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 548:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-263-959-548

Query Match 1.2%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1814 ATATATATATATA 1826  
DB 1 ATATATATATATA 13

RESULT 145  
US-09-263-959-548/C  
Sequence 548, Application US/09263959  
Patent No. US20020150891A1  
GENERAL INFORMATION:  
APPLICANT: Hood, Leroy E.  
APPLICANT: Rowen, Lee  
APPLICANT: Koop, Ben F.  
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI  
NUMBER OF SEQUENCES: 1279  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
FILING DATE: 05-MAR-1999  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: McMasters, David D.  
REGISTRATION NUMBER: 33,963

REFERENCE/DOCKET NUMBER: 920010.426C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 548:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-263-959-548

Query Match 1.2%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1813 TATATATATATAT 1825  
DB 13 TATATATATATAT 1

RESULT 146  
US-09-263-959-704  
Sequence 704, Application US/09263959  
Patent No. US20020150891A1  
GENERAL INFORMATION:  
APPLICANT: Hood, Leroy E.  
APPLICANT: Rowen, Lee  
APPLICANT: Koop, Ben F.  
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI  
NUMBER OF SEQUENCES: 1279  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
FILING DATE: 05-MAR-1999  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: McMasters, David D.  
REGISTRATION NUMBER: 33,963  
REFERENCE/DOCKET NUMBER: 920010.426C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 704:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-263-959-704

Query Match 1.2%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTG 1806  
DB 1 GTGTGTGTGTGTG 13

RESULT 147  
US-09-263-959-723

```
; Sequence 723, Application US/09263959
; Patent No. US20020150891A1
; GENERAL INFORMATION:
; APPLICANT: Hood, Leroy E.
; APPLICANT: Rowen, Lee
; APPLICANT: Koop, Ben F.
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
; NUMBER OF SEQUENCES: 1279
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/263,959
; FILING DATE: 05-MAR-1999
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 920010.426C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 723:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-263-959-723

Query Match 1.2%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1813 TATATATATATAT 1825
Db 1 TATATATATATAT 13

RESULT 148
US-09-263-959-723/c
; Sequence 723, Application US/09263959
; Patent No. US20020150891A1
; GENERAL INFORMATION:
; APPLICANT: Hood, Leroy E.
; APPLICANT: Rowen, Lee
; APPLICANT: Koop, Ben F.
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
; NUMBER OF SEQUENCES: 1279
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/263,959
; FILING DATE: 05-MAR-1999
```

```
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 920010.426C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 723:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-263-959-723

Query Match 1.2%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1814 ATATATATATATA 1826
Db 13 ATATATATATATA 1

RESULT 149
US-08-892-503-1
; Sequence 1, Application US/08892503
; Publication No. US20020042048A1
; GENERAL INFORMATION:
; APPLICANT: Dmanac, Radoje
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION
; FILE REFERENCE: 9598-0013-999
; CURRENT APPLICATION NUMBER: US/08/892,503
; CURRENT FILING DATE: 1997-07-14
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially synthesized oligonucleotide
; NAME/KEY: misc feature
; LOCATION: (1)..(15)
; OTHER INFORMATION: n = A,T,C or G
; US-08-892-503-1

Query Match 1.2%; Score 13; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1863 CCTTTTATTTTG 1876
Db 1 CCTTTTNTTTTG 14

RESULT 150
US-08-892-503-2/c
; Sequence 2, Application US/08892503
; Publication No. US20020042048A1
; GENERAL INFORMATION:
; APPLICANT: Dmanac, Radoje
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION
; FILE REFERENCE: 9598-0013-999
; CURRENT APPLICATION NUMBER: US/08/892,503
; CURRENT FILING DATE: 1997-07-14
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 15
```

```

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially synthesized oligonucleotide
; NAME/KEY: misc feature
; LOCATION: (1)...(15)
; OTHER INFORMATION: n = A,T,C or G
US-08-892-503-2

```

```

Query Match      1.2%; Score 13; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1863 CCTTTTATTTTGG 1876
Db 15 CCTTTTNTTTTGG 2

```

```

RESULT 151
US-09-918-995-38044
; Sequence 38044, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 38044
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Exemplary oligonucleotide primer used in sequence
; OTHER INFORMATION: assembly process
; NAME/KEY: misc feature
; LOCATION: (8)...(8)
; OTHER INFORMATION: n=a, t, c, g or
; OTHER INFORMATION: 1-(2-deoxy-D-ribofuranosyl)-3-nitropyrrrole
US-09-918-995-38044

```

```

Query Match      1.2%; Score 13; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1863 CCTTTTATTTTGG 1876
Db 1 CCTTTTNTTTTGG 14

```

```

RESULT 152
US-09-918-995-38045/c
; Sequence 38045, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 38045
; LENGTH: 15

```

```

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Exemplary oligonucleotide primer used in sequence
; OTHER INFORMATION: assembly process
; NAME/KEY: misc feature
; LOCATION: (8)...(8)
; OTHER INFORMATION: n=a, t, c, g or
; OTHER INFORMATION: 1-(2-deoxy-D-ribofuranosyl)-3-nitropyrrrole
US-09-918-995-38045

```

```

Query Match      1.2%; Score 13; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1863 CCTTTTATTTTGG 1876
Db 15 CCTTTTNTTTTGG 2

```

```

RESULT 153
US-09-896-095-245/c
; Sequence 245, Application US/09896095
; Publication No. US20030219886A1
; GENERAL INFORMATION:
; APPLICANT: LADNER, Charles C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: LEY, Arthur C.
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: DIRECTED EVOLUTION OF NOVEL BINDING PROTEINS
; FILE REFERENCE: LADNER-7L
; CURRENT APPLICATION NUMBER: US/09/896,095
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 08/415,922
; PRIOR FILING DATE: 1995-03-04
; PRIOR APPLICATION NUMBER: 08/009,319
; PRIOR FILING DATE: 1993-01-26
; PRIOR APPLICATION NUMBER: 07/664,989
; PRIOR FILING DATE: 1991-03-01
; PRIOR APPLICATION NUMBER: 08/993,776
; PRIOR FILING DATE: 1997-12-18
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 245
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic 805:814 junction
US-09-896-095-245

```

```

Query Match      1.2%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1846 ATTAAAGTTGTT 1858
Db 13 ATTAAAGTTGTT 1

```

```

RESULT 154
US-10-056-414-121/c
; Sequence 121, Application US/10056414
; Publication No. US2003003469A1
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth G.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; DISEASES OR CONDITIONS

```

RELATED TO LEVELS OF  
NF-KB  
NUMBER OF SEQUENCES: 830  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/056,414  
FILING DATE: 23-Jan-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/291,932A  
FILING DATE: August 15, 1994  
APPLICATION NUMBER: 08/245,466  
FILING DATE: May 18, 1994  
APPLICATION NUMBER: 07/987,132  
FILING DATE: December 7, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 208/157  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 121:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 121:  
US-10-056-414-121  
Query Match 1.2%; Score 13; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred.No. 1.1e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 2152 TCACCTGGAAGCA 2164  
DB 15 TCACCTGGAAGCA 3  
RESULT 155  
US-10-056-414-194/c  
; Sequence 194, Application US/10056414  
; Publication No. US20030003469A1  
; GENERAL INFORMATION:  
; APPLICANT: Stinchcomb, Dan T.  
; Draper, Kenneth G.  
; McSwiggen, James  
; TITLE OF INVENTION: RIBOZYME TREATMENT OF  
; DISEASES OR CONDITIONS  
; RELATED TO LEVELS OF  
; NF-KB  
; NUMBER OF SEQUENCES: 830  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; Suite 4700  
; CITY: Los Angeles  
; STATE: California

COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/056,414  
FILING DATE: 23-Jan-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/291,932A  
FILING DATE: August 15, 1994  
APPLICATION NUMBER: 08/245,466  
FILING DATE: May 18, 1994  
APPLICATION NUMBER: 07/987,132  
FILING DATE: December 7, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 208/157  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 194:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 194:  
US-10-056-414-194  
Query Match 1.2%; Score 13; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred.No. 1.1e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 2152 TCACCTGGAAGCA 2164  
DB 15 TCACCTGGAAGCA 3  
RESULT 156  
US-10-056-414-310/c  
; Sequence 310, Application US/10056414  
; Publication No. US20030003469A1  
; GENERAL INFORMATION:  
; APPLICANT: Stinchcomb, Dan T.  
; Draper, Kenneth G.  
; McSwiggen, James  
; TITLE OF INVENTION: RIBOZYME TREATMENT OF  
; DISEASES OR CONDITIONS  
; RELATED TO LEVELS OF  
; NF-KB  
; NUMBER OF SEQUENCES: 830  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/056,414  
FILING DATE: 23-Jan-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/291,932A  
FILING DATE: August 15, 1994  
APPLICATION NUMBER: 08/245,466  
FILING DATE: May 18, 1994  
APPLICATION NUMBER: 07/987,132  
FILING DATE: December 7, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 208/157  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 310:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 base pairs  
TYPE: nucleic acid  
STRAINEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 310:  
US-10-056-414-310

Query Match 1.2%; Score 13; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2152 TCACCTGGAAGCA 2164  
Db 15 TCACCTGGAAGCA 3

## RESULT 157

US-10-187-251A-1  
Sequence 1, Application US/10187251A  
Publication No. US20030108897A1

GENERAL INFORMATION:  
APPLICANT: Drmanac, Radoje  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION OR QUANTIFICATION OF NUCLEIC ACID SPECIES  
FILE REFERENCE: 30311/0015A  
CURRENT APPLICATION NUMBER: US/10/187,251A  
CURRENT FILING DATE: 2003-02-14  
PRIOR APPLICATION NUMBER: US 08/947,779  
PRIOR FILING DATE: 1997-10-09  
PRIOR APPLICATION NUMBER: US 08/912,885  
PRIOR FILING DATE: 1997-08-15  
PRIOR APPLICATION NUMBER: US 08/892,503  
PRIOR FILING DATE: 1997-07-14  
PRIOR APPLICATION NUMBER: US 08/812,951  
PRIOR FILING DATE: 1997-03-04  
PRIOR APPLICATION NUMBER: US 08/784,787  
PRIOR FILING DATE: 1997-01-16  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: Patent in version 3.1  
SEQ ID NO 1  
LENGTH: 15  
TYPE: DNA  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: Synthetic primer  
NAME/KEY: misc feature  
LOCATION: (8)  
OTHER INFORMATION: n = A or T or G or C or M  
US-10-187-251A-1

Query Match 1.2%; Score 13; DB 1; Length 15;  
Best Local Similarity 92.9%; Pred. No. 1.1e+02;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1863 CCTTTTATTG 1876  
Db 1 CCTTTTATTG 14

## RESULT 158

US-10-191-997-67  
Sequence 67, Application US/10191997  
Publication No. US20030207834A1  
GENERAL INFORMATION:  
APPLICANT: Oligos Etc., Inc.  
APPLICANT: DALE, Roderic M. K.  
APPLICANT: ARROW, Amy  
TITLE OF INVENTION: Oligonucleotide-Containing Pharmacological Compositions And Their Use  
FILE REFERENCE: 54800-5019  
CURRENT APPLICATION NUMBER: US/10/191,997  
CURRENT FILING DATE: 2002-07-10  
PRIOR APPLICATION NUMBER: US 60/303,820  
PRIOR FILING DATE: 2001-07-10  
NUMBER OF SEQ ID NOS: 132  
SOFTWARE: Patent in version 3.1  
SEQ ID NO 67  
LENGTH: 16  
TYPE: DNA  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: CD4OL oligonucleotide  
US-10-191-997-67

Query Match 1.2%; Score 13; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1688 TGACACTGTTTCAG 1700  
Db 4 TGACACTGTTTCAG 16

## RESULT 159

US-09-739-928-2  
Sequence 2, Application US/09739928  
Patent No. US20020052482A1  
GENERAL INFORMATION:  
APPLICANT: Kutyavin, Igor V.  
Lukhtanov, Eugeny A.  
Gamber, Howard B.  
Meyer Jr., Rich B.  
TITLE OF INVENTION: Covalently Linked Oligonucleotide Minor Groove Binder Conjugates  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/739,928  
FILING DATE: 11-May-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/415,370  
FILING DATE: 03-APR-1995  
APPLICATION NUMBER: US 09/141,764



FILING DATE: 27-AUG-1998  
APPLICATION NUMBER: US 09/507,345  
FILING DATE: 18-FEB-2000  
ATTORNEY/AGENT INFORMATION:  
NAME: Kezer, William B.  
REGISTRATION NUMBER: 37,369  
REFERENCE/DOCKET NUMBER: 17682A-003510US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-09-739-928-2

Query Match 1.2%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 1.2e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTT 1880  
DB 1 TTTTATTTTGTGTTT 16

RESULT 160  
US-09-152-059-70  
Sequence 70, Application US/09152059  
Patent No. US20020068708A1  
GENERAL INFORMATION:  
APPLICANT: WENGEL, JESPER  
APPLICANT: NIELSEN, POUL  
TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES  
FILE REFERENCE: 49165 (71994)  
CURRENT APPLICATION NUMBER: US/09/152,059  
CURRENT FILING DATE: 1998-09-11  
PRIOR APPLICATION NUMBER: 60/058,541  
PRIOR FILING DATE: 1997-09-12  
PRIOR APPLICATION NUMBER: 60/068,293  
PRIOR FILING DATE: 1997-12-19  
PRIOR APPLICATION NUMBER: 60/071,682  
PRIOR FILING DATE: 1998-01-16  
PRIOR APPLICATION NUMBER: 60/076,591  
PRIOR FILING DATE: 1998-03-03  
PRIOR APPLICATION NUMBER: 60/083,507  
PRIOR FILING DATE: 1998-04-23  
PRIOR APPLICATION NUMBER: 60/088,309  
PRIOR FILING DATE: 1998-06-05  
PRIOR APPLICATION NUMBER: 60/094,355  
PRIOR FILING DATE: 1998-07-28  
NUMBER OF SEQ ID NOS: 146  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 70  
LENGTH: 16  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-152-059-70

Query Match 1.2%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 1.2e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTT 1880  
DB 1 TTTTATTTTGTGTTT 16

RESULT 161  
US-09-263-959-950  
Sequence 950, Application US/09263959  
Patent No. US20020150891A1  
GENERAL INFORMATION:  
APPLICANT: Hood, Leroy E.  
APPLICANT: Koop, Ben F.  
APPLICANT: Rowen, Lee  
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI  
NUMBER OF SEQUENCES: 1279  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/263,959  
FILING DATE: 05-MAR-1999

CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: McMasters, David D.  
REGISTRATION NUMBER: 33,963  
REFERENCE/DOCKET NUMBER: 920010.426C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 950:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-263-959-950

Query Match 1.2%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 1.2e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1866 TTTTATTTTGTGTTT 1881  
DB 1 TTTTATTTTGTGTTT 16

RESULT 162  
US-09-805-296D-9  
Sequence 9, Application US/09805296D  
Patent No. US20020155989A1  
GENERAL INFORMATION:  
APPLICANT: Active Motif  
APPLICANT: Efimov, Vladimir  
APPLICANT: Fernandez, Joseph  
APPLICANT: Archdeacon, Dorothy  
APPLICANT: Archdeacon, John  
APPLICANT: Chakmakchcheau, Oksana  
APPLICANT: Buryakova, Alla  
APPLICANT: Choob, Mikhail  
APPLICANT: Hondorp, Kyle  
TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES, METHODS OF SYNTHESIS AND METHODS OF USE  
FILE REFERENCE: AM102.P.1US  
CURRENT APPLICATION NUMBER: US/09/805,296D  
CURRENT FILING DATE: 2001-03-13  
PRIOR APPLICATION NUMBER: US 60/189,190  
PRIOR FILING DATE: 2000-03-14  
PRIOR APPLICATION NUMBER: US 60/250,334  
PRIOR FILING DATE: 2000-11-30

```
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin version 3.1
; SEQ ID NO: 9
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
; NAME/KEY: misc feature
; OTHER INFORMATION: Synthetic Construct
;
US-09-805-296D-9

Query Match      1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTT 1880
Db 1 TTTTATTTTGTGTTT 16

RESULT 163
US-09-843-676-131/c
; Sequence 131, Application US/09843676
; Patent No. US20020164786A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Linger, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. US20020164786A1el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/843,676
; FILING DATE: 26-Apr-2001
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US/08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US/08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US/08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 131:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
```

```
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 131:
US-09-843-676-131
Query Match      1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTT 1880
Db 16 TTTTATTTTGTGTTT 1

RESULT 164
US-09-766-253-131/c
; Sequence 131, Application US/09766253
; Publication No. US20020187471A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. US20020187471A1el Telomerase
; NUMBER OF SEQUENCES: 171
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/766,253
; FILING DATE: 19-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/846,017
; FILING DATE: 1997-04-25
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002920US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 131:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 131:
US-09-766-253-131

Query Match      1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTT 1880
Db 16 TTTTATTTTGTGTTT 1

RESULT 165
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US-09-438-486-131/c
; Sequence 131, Application US/09438486
; Publication No. US20030009019A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: NO. US20030009019A1el Telomerase
; NUMBER OF SEQUENCES: 223
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/438,486
; FILING DATE: 12-NOV-1999
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 08-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002931US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 131:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-438-486-131
Query Match 1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTT 1880
DB 16 TTTTATTTTGTGTTT 1

RESULT 166
US-10-208-357-22/c
; Sequence 22, Application US/10208357
; Publication No. US20020182687A1
; GENERAL INFORMATION:
; APPLICANT: Kurz, Markus
; APPLICANT: Lohse, Peter
; APPLICANT: Wagner, Richard
; TITLE OF INVENTION: Peptide Acceptor Ligation Methods
; FILE REFERENCE: 50036/031002
; CURRENT APPLICATION NUMBER: US/10/208,357
; CURRENT FILING DATE: 2002-07-30
; PRIOR APPLICATION NUMBER: US/09/619,103
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 60/145,834
; PRIOR FILING DATE: 1999-07-27
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: designed sequence for nucleic acid purification
US-10-208-357-22
Query Match 1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTT 1880
DB 16 TTTTATTTTGTGTTT 1

RESULT 167
US-10-053-758-131/c
; Sequence 131, Application US/10053758
; Publication No. US20030032075A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: NO. US20030032075A1el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/053,758
; FILING DATE: 18-Jan-2002
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:

```

NAME: Apple, Randolph T.  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002930US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 131:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 131:  
US-10-053-758-131

Query Match 1.2%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 1.2e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTGTTT 1880  
Db 16 TTTTATTTT 1

RESULT 168  
US-10-054-295-131/c  
; Sequence 131, Application US/10054295  
; Publication No. US20030044953A1  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; Lingner, Joachim  
; Nakamura, Toru  
; Chapman, Karen B.  
; Morin, Gregg B.  
; Andrews, William H.  
; TITLE OF INVENTION: No. US20030044953A1 Telomerase  
; NUMBER OF SEQUENCES: 225  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/054,295  
; FILING DATE: 18-Jan-2002  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/854,050  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: US 08/846,017  
; FILING DATE: 25-APR-1997  
; APPLICATION NUMBER: US 08/844,419  
; FILING DATE: 18-APR-1997  
; APPLICATION NUMBER: US 08/724,643  
; FILING DATE: 01-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Apple, Randolph T.  
; REGISTRATION NUMBER: 36,429  
; REFERENCE/DOCKET NUMBER: 015389-002930US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 131:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 131:  
US-10-054-295-131

Query Match 1.2%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 1.2e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 131:  
US-10-054-295-131

Query Match 1.2%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 1.2e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTGTTT 1880  
Db 16 TTTTATTTT 1

RESULT 169  
US-10-054-611-131/c  
; Sequence 131, Application US/10054611  
; Publication No. US20030059787A1  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; Lingner, Joachim  
; Nakamura, Toru  
; Chapman, Karen B.  
; Morin, Gregg B.  
; Andrews, William H.  
; TITLE OF INVENTION: No. US20030059787A1 Telomerase  
; NUMBER OF SEQUENCES: 225  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/054,611  
; FILING DATE: 18-Jan-2002  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/854,050  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: US 08/846,017  
; FILING DATE: 25-APR-1997  
; APPLICATION NUMBER: US 08/844,419  
; FILING DATE: 18-APR-1997  
; APPLICATION NUMBER: US 08/724,643  
; FILING DATE: 01-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Apple, Randolph T.  
; REGISTRATION NUMBER: 36,429  
; REFERENCE/DOCKET NUMBER: 015389-002930US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 131:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 131:  
US-10-054-611-131

Query Match 1.2%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 1.2e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTT 1880  
DB 16 TTTTATTTTGTGTTT 1

## RESULT 170

US-10-072-975-9  
; Sequence 9, Application US/10072975  
; Publication No. US20030059789A1  
; GENERAL INFORMATION:  
; APPLICANT: Active Motif  
; APPLICANT: Efimov, Vladimir  
; APPLICANT: Fernandez, Joseph  
; APPLICANT: Archdeacon, Dorothy  
; APPLICANT: Archdeacon, John  
; APPLICANT: Chakmakheau, Oksana  
; APPLICANT: Buryakova, Alla  
; APPLICANT: Choob, Mikhail  
; APPLICANT: Hondorp, Kyle  
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES, METHODS OF SYNTHESIS AND METHODS OF USE  
; FILE REFERENCE: AM102.P.1.1US  
; CURRENT APPLICATION NUMBER: US/10/072,975  
; CURRENT FILING DATE: 2002-02-09  
; PRIOR APPLICATION NUMBER: US 60/189,190  
; PRIOR FILING DATE: 2000-03-14  
; PRIOR APPLICATION NUMBER: US 60/250,334  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: 09/805,296  
; PRIOR FILING DATE: 2001-03-13  
; PRIOR APPLICATION NUMBER: PCT/US01/0811  
; PRIOR FILING DATE: 2001-03-13  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 9  
; LENGTH: 16  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Construct  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Synthetic Construct  
US-10-072-975-9

Query Match 1.2%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 1.2e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTT 1880  
DB 1 TTTTATTTTGTGTTT 16

## RESULT 171

US-10-287-919-1350  
; Sequence 1350, Application US/10287919  
; Publication No. US20030085830A1  
; GENERAL INFORMATION:  
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.  
; TITLE OF INVENTION: Methanococcus jannaschii complete genome.  
; FILE REFERENCE: Jim Zegger Law Offices - 703-684-8333  
; CURRENT APPLICATION NUMBER: US/10/287,919  
; CURRENT FILING DATE: 2002-11-05  
; NUMBER OF SEQ ID NOS: 2706  
; SOFTWARE: Proprietary  
; SEQ ID NO 1350  
; LENGTH: 16  
; TYPE: DNA  
; ORGANISM: Methanococcus jannaschii complete genome.  
; FEATURE:  
; LOCATION: (644443)...(644458)  
; OTHER INFORMATION: Chromosome = 1 Strand = negative  
US-10-287-919-1350

Query Match 1.2%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 1.2e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Query Match 1.2%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 1.2e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1869 TATTTTGTGTTTAAAT 1884  
DB 1 TATTTTGTGTTTAAAT 16

## RESULT 172

US-10-287-919-2293  
; Sequence 2293, Application US/10287919  
; Publication No. US20030085830A1  
; GENERAL INFORMATION:  
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.  
; TITLE OF INVENTION: Methanococcus jannaschii complete genome.  
; FILE REFERENCE: Jim Zegger Law Offices - 703-684-8333  
; CURRENT APPLICATION NUMBER: US/10/287,919  
; CURRENT FILING DATE: 2002-11-05  
; NUMBER OF SEQ ID NOS: 2706  
; SOFTWARE: Proprietary  
; SEQ ID NO 2293  
; LENGTH: 16  
; TYPE: DNA  
; ORGANISM: Methanococcus jannaschii complete genome.  
; FEATURE:  
; LOCATION: (1424659)...(1424675)  
; OTHER INFORMATION: Chromosome = 1 Strand = negative  
US-10-287-919-2293

Query Match 1.2%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 1.2e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1869 TATTTTGTGTTTAAAT 1884  
DB 1 TATTTTGTGTTTAAAT 16

## RESULT 173

US-10-227-001-21  
; Sequence 21, Application US/10227001  
; Publication No. US20030113765A1  
; GENERAL INFORMATION:  
; APPLICANT: Demcoy, Robert O.  
; APPLICANT: Afonina, Irina Aleksandrovna  
; APPLICANT: Vermeulen, Nicolaas M.J.  
; APPLICANT: Epoch Biosciences, Inc.  
; TITLE OF INVENTION: Hybridization-Triggered Fluorescent  
; FILE REFERENCE: 17682A-004210US  
; CURRENT APPLICATION NUMBER: US/10/227,001  
; CURRENT FILING DATE: 2002-08-21  
; PRIOR APPLICATION NUMBER: US 05/428,236  
; PRIOR FILING DATE: 1999-10-26  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 21  
; LENGTH: 16  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: R2 (ODN) of fluorophore-MGB-ODN  
; OTHER INFORMATION: conjugate  
US-10-227-001-21

Query Match 1.2%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 1.2e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTT 1880  
DB 1 TTTTATTTTGTGTTT 16

```
Db 1 TTTTATTTTGT 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Synthetic Construct
US-10-051-436-9

Query Match 1.2% Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGT 1880
Db 1 TTTTATTTTGT 16

RESULT 174
US-10-008-029-70
; Sequence 70, Application US/10008029
; Publication No. US2003013480A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 70
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-008-029-70

Query Match 1.2% Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGT 1880
Db 1 TTTTATTTTGT 16

RESULT 175
US-10-051-436-9
; Sequence 9, Application US/10051436
; Publication No. US20030138045A1
; GENERAL INFORMATION:
; APPLICANT: Active Motif
; APPLICANT: Efimov, Vladimir
; APPLICANT: Fernandez, Joseph
; APPLICANT: Archdeacon, Dorothy
; APPLICANT: Archdeacon, John
; APPLICANT: Chakmakicheau, Oksana
; APPLICANT: Buryakova, Alla
; APPLICANT: Choob, Mikhail
; APPLICANT: Hondorp, Kyle
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES, METHODS OF SYNTHESIS AND METHODS OF USE
; FILE REFERENCE: AM102.P1US
; CURRENT APPLICATION NUMBER: US/10/051,436
; CURRENT FILING DATE: 2002-01-19
; PRIOR APPLICATION NUMBER: US 60/189,190
; PRIOR FILING DATE: 2000-03-14
; PRIOR APPLICATION NUMBER: US 60/250,334
; PRIOR FILING DATE: 2000-11-30
; NUMBER OF SEQ ID NOS: 18

; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Synthetic Construct
US-10-051-436-9

Query Match 1.2% Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGT 1880
Db 1 TTTTATTTTGT 16

RESULT 177
US-10-203-780-9
; Sequence 9, Application US/10203780
; Publication No. US20030165914A1
; GENERAL INFORMATION:
```

```

; APPLICANT: CUZIN, MARC
; APPLICANT: PELTIE, PHILIPPE
; APPLICANT: FONTECAVE, MARC
; APPLICANT: DECOU, JEAN-LUC
; APPLICANT: DUEYRES, CECILE
; TITLE OF INVENTION: ANALYSIS OF BIOLOGICAL TARGETS USING A BIOCHIP COMPRISING A FLUOR
; FILE REFERENCE: MARKER
; CURRENT APPLICATION NUMBER: US/10/203,780
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: PCT/FR01/00516
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: FR 00 02236
; PRIOR FILING DATE: 2000-02-23
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 9
; LENGTH: 16
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
; NAME/KEY: modified base
; LOCATION: (1)..(1)
; OTHER INFORMATION: t is modified with a covalent linkage to flavin
US-10-203-780-9

Query Match 1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTGTTT 1880
DB 1 TTTTATTGTTT 16

RESULT 178
US-10-309-775A-71
; Sequence 71, Application US/10309775A
; Publication No. US20040006032A1
; GENERAL INFORMATION:
; APPLICANT: LOPEZ, Ricardo A.
; TITLE OF INVENTION: IMMUNOSTIMULATORY OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 2901/0M327
; CURRENT APPLICATION NUMBER: US/10/309,775A
; CURRENT FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: CA 2,388,049
; PRIOR FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 71
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR primer
US-10-309-775A-71

Query Match 1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1866 TTTTATTGTTT 1881
DB 1 TTTTATTGTTT 16

RESULT 179
US-10-360-275-9
; Sequence 9, Application US/10360275
; Publication No. US20040014644A1
; GENERAL INFORMATION:
; APPLICANT: CUZIN, MARC
; APPLICANT: PELTIE, PHILIPPE
; APPLICANT: FONTECAVE, MARC
; APPLICANT: DECOU, JEAN-LUC
; APPLICANT: DUEYRES, CECILE
; TITLE OF INVENTION: ANALYSIS OF BIOLOGICAL TARGETS USING A BIOCHIP COMPRISING A FLUOR
; FILE REFERENCE: MARKER
; CURRENT APPLICATION NUMBER: US/10/203,780
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: PCT/FR01/00516
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: FR 00 02236
; PRIOR FILING DATE: 2000-02-23
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 9
; LENGTH: 16
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
; NAME/KEY: modified base
; LOCATION: (1)..(1)
; OTHER INFORMATION: t is modified with a covalent linkage to flavin
US-10-203-780-9

Query Match 1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTGTTT 1880
DB 1 TTTTATTGTTT 16

RESULT 180
US-08-463-404-56
; Sequence 56, Application US/08463404
; Publication No. US20020127634A1
; GENERAL INFORMATION:
; APPLICANT: Michael D. West
; APPLICANT: Jerry W. Shay
; APPLICANT: Woodring E. Wright
; APPLICANT: Elizabeth Blackburn
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF CONDITIONS
; TITLE OF INVENTION: RELATED TO TELOMERE LENGTH AND/OR
; TITLE OF INVENTION: TELOMERASE ACTIVITY
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2086
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,404
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/060,952
; FILING DATE: May 13, 1993

```

```

; APPLICANT: Active Motif
; APPLICANT: Efimov, Vladimir
; APPLICANT: Fernandez, Joseph
; APPLICANT: Archdeacon, Dorothy
; APPLICANT: Archdeacon, John
; APPLICANT: Choob, Mikhail
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES AND METHODS OF USE FOR MODULATING GENE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: AM102.P.1.1.1US
; CURRENT APPLICATION NUMBER: US/10/360,275
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US 10/072,975
; PRIOR FILING DATE: 2002-02-09
; PRIOR APPLICATION NUMBER: US 09/805,296
; PRIOR FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: US 60/189,190
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 9
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
; NAME/KEY: misc feature
; OTHER INFORMATION: Synthetic Construct
US-10-360-275-9

Query Match 1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTGTTT 1880
DB 1 TTTTATTGTTT 16

RESULT 180
US-08-463-404-56
; Sequence 56, Application US/08463404
; Publication No. US20020127634A1
; GENERAL INFORMATION:
; APPLICANT: Michael D. West
; APPLICANT: Jerry W. Shay
; APPLICANT: Woodring E. Wright
; APPLICANT: Elizabeth Blackburn
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF CONDITIONS
; TITLE OF INVENTION: RELATED TO TELOMERE LENGTH AND/OR
; TITLE OF INVENTION: TELOMERASE ACTIVITY
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2086
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,404
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/060,952
; FILING DATE: May 13, 1993

```





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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/263,959
; FILING DATE: 05-MAR-1999
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 920010.426C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 532:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-263-959-532

Query Match 1.2%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 1.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1814 ATATATATATATAT 1827
DB 1 ATATATCTATATAT 14

RESULT 185
US-09-263-959-562
; Sequence 562, Application US/09263959
; Patent No. US20020150891A1
; GENERAL INFORMATION:
; APPLICANT: Hood, Leroy E.
; APPLICANT: Rowen, Lee
; APPLICANT: Koop, Ben F.
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
; NUMBER OF SEQUENCES: 1279
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/263,959
; FILING DATE: 05-MAR-1999
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 920010.426C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 562:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-263-959-562

Query Match 1.2%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 1.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1814 ATATATATATATAT 1827
DB 1 ATATATCTATATAT 14

RESULT 186
US-09-263-959-562/c
; Sequence 562, Application US/09263959
; Patent No. US20020150891A1
; GENERAL INFORMATION:
; APPLICANT: Hood, Leroy E.
; APPLICANT: Rowen, Lee
; APPLICANT: Koop, Ben F.
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
; NUMBER OF SEQUENCES: 1279
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/263,959
; FILING DATE: 05-MAR-1999
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 920010.426C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 532:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-263-959-532

Query Match 1.2%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 1.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1814 ATATATATATATAT 1827
DB 1 ATATATCTATATAT 14

RESULT 184
US-09-263-959-532/c
; Sequence 532, Application US/09263959
; Patent No. US20020150891A1
; GENERAL INFORMATION:
; APPLICANT: Hood, Leroy E.
; APPLICANT: Rowen, Lee
; APPLICANT: Koop, Ben F.
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
; NUMBER OF SEQUENCES: 1279
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/263,959
; FILING DATE: 05-MAR-1999
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 920010.426C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 532:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-263-959-532
```



; NUMBER OF SEQUENCES: 1279  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Seed and Berry LLP  
 ; STREET: 6300 Columbia Center, 701 Fifth Avenue  
 ; CITY: Seattle  
 ; STATE: Washington  
 ; COUNTRY: US  
 ; ZIP: 98104-7092  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/263,959  
 ; FILING DATE: 05-MAR-1999  
 ; CLASSIFICATION:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: McMasters, David D.  
 ; REGISTRATION NUMBER: 33,963  
 ; REFERENCE/DOCKET NUMBER: 920010.426C2  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (206) 622-4900  
 ; TELEFAX: (206) 682-6031  
 ; INFORMATION FOR SEQ ID NO: 726:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 14 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; US-09-263-959-726

Query Match 1.2%; Score 12.4; DB 1; Length 14;  
 Best Local Similarity 92.9%; Pred. No. 1.3e+02;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1814 ATATATATATATAT 1827  
 Db 1 ATATATGATATATAT 14

RESULT 190  
 US-09-263-959-726/c  
 ; Sequence 726, Application US/09263959  
 ; Patent No. US20020150891A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hood, Leroy E.  
 ; APPLICANT: Rowen, Lee  
 ; APPLICANT: Koop, Ben F.  
 ; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI  
 ; NUMBER OF SEQUENCES: 1279  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Seed and Berry LLP  
 ; STREET: 6300 Columbia Center, 701 Fifth Avenue  
 ; CITY: Seattle  
 ; STATE: Washington  
 ; COUNTRY: US  
 ; ZIP: 98104-7092  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/263,959  
 ; FILING DATE: 05-MAR-1999  
 ; CLASSIFICATION:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: McMasters, David D.  
 ; REGISTRATION NUMBER: 33,963  
 ; REFERENCE/DOCKET NUMBER: 920010.426C2  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (206) 622-4900

; TELEFAX: (206) 682-6031  
 ; INFORMATION FOR SEQ ID NO: 726:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 14 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; US-09-263-959-726

Query Match 1.2%; Score 12.4; DB 1; Length 14;  
 Best Local Similarity 92.9%; Pred. No. 1.3e+02;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1814 ATATATATATATAT 1827  
 Db 14 ATATATACATATAT 1

RESULT 191  
 US-09-263-959-730  
 ; Sequence 730, Application US/09263959  
 ; Patent No. US20020150891A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hood, Leroy E.  
 ; APPLICANT: Rowen, Lee  
 ; APPLICANT: Koop, Ben F.  
 ; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI  
 ; NUMBER OF SEQUENCES: 1279  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Seed and Berry LLP  
 ; STREET: 6300 Columbia Center, 701 Fifth Avenue  
 ; CITY: Seattle  
 ; STATE: Washington  
 ; COUNTRY: US  
 ; ZIP: 98104-7092  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/263,959  
 ; FILING DATE: 05-MAR-1999  
 ; CLASSIFICATION:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: McMasters, David D.  
 ; REGISTRATION NUMBER: 33,963  
 ; REFERENCE/DOCKET NUMBER: 920010.426C2  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (206) 622-4900  
 ; TELEFAX: (206) 682-6031  
 ; INFORMATION FOR SEQ ID NO: 730:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 14 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; US-09-263-959-730

Query Match 1.2%; Score 12.4; DB 1; Length 14;  
 Best Local Similarity 92.9%; Pred. No. 1.3e+02;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1813 TATATATATATATAT 1826  
 Db 1 TATATATAATATA 14

RESULT 192  
 US-09-263-959-730/c  
 ; Sequence 730, Application US/09263959  
 ; Patent No. US20020150891A1  
 ; GENERAL INFORMATION:

APPLICANT: Hood, Leroy E.  
APPLICANT: Rowen, Lee  
APPLICANT: Koop, Ben F.  
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI  
NUMBER OF SEQUENCES: 1279  
CORRESPONDENCE ADDRESS:  
ADDRESS: Seed and Berry LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/263,959  
FILING DATE: 05-MAR-1999  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: McMasters, David D.  
REGISTRATION NUMBER: 33,963  
REFERENCE/DOCKET NUMBER: 920010.426C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 730:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-263-959-730

Query Match 1.2%; Score 12.4; DB 1; Length 14;  
Best Local Similarity 92.9%; Pred. No. 1.3e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1813 TATATATATATATA 1826  
DB 14 TATATTTATATATA 1

## RESULT 193

US-09-263-959-752  
Sequence 752, Application US/09263959  
Patent No. US20020150891A1  
GENERAL INFORMATION:  
APPLICANT: Hood, Leroy E.  
APPLICANT: Rowen, Lee  
APPLICANT: Koop, Ben F.  
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI  
NUMBER OF SEQUENCES: 1279  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/263,959  
FILING DATE: 05-MAR-1999  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: McMasters, David D.

REGISTRATION NUMBER: 33,963  
REFERENCE/DOCKET NUMBER: 920010.426C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 752:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-263-959-752

Query Match 1.2%; Score 12.4; DB 1; Length 14;  
Best Local Similarity 92.9%; Pred. No. 1.3e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1814 ATATATATATATAT 1827  
DB 1 ATATATACATATAT 14

## RESULT 194

US-09-263-959-752/c  
Sequence 752, Application US/09263959  
Patent No. US20020150891A1  
GENERAL INFORMATION:  
APPLICANT: Hood, Leroy E.  
APPLICANT: Rowen, Lee  
APPLICANT: Koop, Ben F.  
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI  
NUMBER OF SEQUENCES: 1279  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/263,959  
FILING DATE: 05-MAR-1999  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: McMasters, David D.  
REGISTRATION NUMBER: 33,963  
REFERENCE/DOCKET NUMBER: 920010.426C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 752:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-263-959-752

Query Match 1.2%; Score 12.4; DB 1; Length 14;  
Best Local Similarity 92.9%; Pred. No. 1.3e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1814 ATATATATATATAT 1827  
DB 14 ATATATGTATATAT 1

## RESULT 195

```
US-09-263-959-764
; Sequence 764, Application US/09263959
; Patent No. US20020150891A1
; GENERAL INFORMATION:
; APPLICANT: Hood, Leroy E.
; APPLICANT: Rowen, Lee
; APPLICANT: Koop, Ben F.
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
; NUMBER OF SEQUENCES: 1279
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/263,959
; FILING DATE: 05-MAR-1999
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 920010.426C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 764:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-263-959-764

Query Match 1.2%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 1.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1814 ATATATATATATAT 1827
DB 1 ATATATATATATAT 14

RESULT 196
US-09-263-959-764/c
; Sequence 764, Application US/09263959
; Patent No. US20020150891A1
; GENERAL INFORMATION:
; APPLICANT: Hood, Leroy E.
; APPLICANT: Rowen, Lee
; APPLICANT: Koop, Ben F.
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
; NUMBER OF SEQUENCES: 1279
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/263,959
```

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US-09-263-959-764
; FILING DATE: 05-MAR-1999
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 920010.426C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 764:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-263-959-764

Query Match 1.2%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 1.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1814 ATATATATATATAT 1827
DB 14 ATATATATATATAT 1

RESULT 197
US-09-263-959-822
; Sequence 822, Application US/09263959
; Patent No. US20020150891A1
; GENERAL INFORMATION:
; APPLICANT: Hood, Leroy E.
; APPLICANT: Rowen, Lee
; APPLICANT: Koop, Ben F.
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
; NUMBER OF SEQUENCES: 1279
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/263,959
; FILING DATE: 05-MAR-1999
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 920010.426C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 822:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-263-959-822

Query Match 1.2%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 1.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1814 ATATATATATATAT 1827
DB 14 ATATATATATATAT 14
```

Db 1 ATATATGATATAT 14

RESULT 198

US-09-263-959-822/c

Sequence 822, Application US/09263959

Patent No. US20020150891A1

GENERAL INFORMATION:

APPLICANT: Hood, Leroy E.

APPLICANT: Rowen, Lee

APPLICANT: Koop, Ben F.

TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI

NUMBER OF SEQUENCES: 1279

CORRESPONDENCE ADDRESS:

ADDRESSEE: Seed and Berry LLP

STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle

STATE: Washington

COUNTRY: US

ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/263,959

FILING DATE: 05-MAR-1999

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: McWaters, David D.

REGISTRATION NUMBER: 33,963

REFERENCE/DOCKET NUMBER: 920010.426C2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 822:

SEQUENCE CHARACTERISTICS:

LENGTH: 14 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-09-263-959-822

Query Match 1.2%; Score 12.4; DB 1; Length 14;

Best Local Similarity 92.9%; Pred. No. 1.3e+02;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1814 ATATATATATAT 1827

Db 14 ATATATACATATAT 1

RESULT 199

US-10-232-927A-78

Sequence 78, Application US/10232927A

Publication No. US20030190638A1

GENERAL INFORMATION:

APPLICANT: Michael D. West

Calvin B. Harley

Scott L. Weinrich

Catherine M. Strahl

Michael J. Mceachern

Jerry Shay

Woodring E. Wright

Elizabeth H. Blackburn

Nam Woo Kim

Homayoun Vaziri

TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF

CONDITIONS RELATED TO

TSOLOMERSE LENGTH AND/OR

TSOLOMERSE ACTIVITY

NUMBER OF SEQUENCES: 80

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon Street

STREET: 633 West Fifth Street

Suite 4700

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90071-2066

COMPUTER READABLE FORM: Diskette, 1.44 Mb

MEDIUM TYPE: 3.5" storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: FastSeq for Windows 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/232,927A

FILING DATE: 29-Aug-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/378,535

FILING DATE: 20-Aug-1999

APPLICATION NUMBER: 08/819,867

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Chambers, Daniel M.

REGISTRATION NUMBER: 34,561

REFERENCE/DOCKET NUMBER: 224/232

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 78:

SEQUENCE CHARACTERISTICS:

LENGTH: 14 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 78:

US-10-232-927A-78

Query Match 1.2%; Score 12.4; DB 1; Length 14;

Best Local Similarity 92.9%; Pred. No. 1.3e+02;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTGTG 1806

Db 1 TCGGTGTGTGTGTG 14

RESULT 200

US-09-263-959-543

Sequence 543, Application US/09263959

Patent No. US20020150891A1

GENERAL INFORMATION:

APPLICANT: Hood, Leroy E.

APPLICANT: Koop, Ben F.

TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI

NUMBER OF SEQUENCES: 1279

CORRESPONDENCE ADDRESS:

ADDRESSEE: Seed and Berry LLP

STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle

STATE: Washington

COUNTRY: US

ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/263,959

```
/ FILING DATE: 05-MAR-1999
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: McMasters, David D.
/ REGISTRATION NUMBER: 33,963
/ REFERENCE/DOCKET NUMBER: 920010.426C2
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (206) 622-4900
/ TELEFAX: (206) 682-6031
/ INFORMATION FOR SEQ ID NO: 543:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 15 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-09-263-959-543

Query Match 1.2%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 1.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1814 ATATATATATATAT 1827
Db 1 ATATATGATATAT 14

RESULT 201
US-09-263-959-545
; Sequence 545, Application US/09263959
; Patent No. US20020150891A1
; GENERAL INFORMATION:
; APPLICANT: Hood, Leroy E.
; APPLICANT: Koop, Ben F.
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
; NUMBER OF SEQUENCES: 1279
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/263,959
; FILING DATE: 05-MAR-1999
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 920010.426C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 545:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-263-959-545

Query Match 1.2%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 1.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1814 ATATATATATATAT 1827
Db 1 ATATATGATATAT 14

RESULT 202
US-09-263-959-877
; Sequence 877, Application US/09263959
; Patent No. US20020150891A1
; GENERAL INFORMATION:
; APPLICANT: Hood, Leroy E.
; APPLICANT: Rowen, Lee
; APPLICANT: Koop, Ben F.
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
; NUMBER OF SEQUENCES: 1279
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/263,959
; FILING DATE: 05-MAR-1999
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 920010.426C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 877:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-263-959-877

Query Match 1.2%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 1.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1814 ATATATATATATAT 1827
Db 1 ATATATGATATAT 14

RESULT 203
US-09-877-478-6011/c
; Sequence 6011, Application US/09877478
; Publication No. US20030068301A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Draper, Kenneth
; APPLICANT: Blatt, Larry
; APPLICANT: McSwigen, Jim
; APPLICANT: Morrissey, Dave
; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
; FILE REFERENCE: MHS00-845-H (400/029)
; CURRENT APPLICATION NUMBER: US/09/877,478
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: US 07/882,712
; PRIOR FILING DATE: 1992-05-14
; PRIOR APPLICATION NUMBER: US 09/531,025
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 09/636,385
; PRIOR FILING DATE: 2000-08-09
```

;; PRIOR APPLICATION NUMBER: US 09/696,347  
;; PRIOR FILING DATE: 2000-10-24  
;; PRIOR APPLICATION NUMBER: US 08/193,627  
;; PRIOR FILING DATE: 1994-02-07  
;; PRIOR APPLICATION NUMBER: US 08/433,993  
;; PRIOR FILING DATE: 1995-05-04  
;; PRIOR APPLICATION NUMBER: US 08/434,504  
;; PRIOR FILING DATE: 1995-05-04  
;; PRIOR APPLICATION NUMBER: US 09/436,430  
;; PRIOR FILING DATE: 1999-11-08  
;; NUMBER OF SEQ ID NOS: 6586  
;; SOFTWARE: PatentIn version 3.0  
;; SEQ ID NO 6011  
;; LENGTH: 15  
;; TYPE: RNA  
;; ORGANISM: Hepatitis B virus  
US-09-877-478-6011

Query Match 1.2%; Score 12.4; DB 1; Length 15;  
Best Local Similarity 92.9%; Pred. No. 1.3e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2095 AATGACAAATGGC 2108  
DB 15 ACTGAACAATGGC 2

RESULT 204  
US-09-877-478-6085/c  
;; Sequence 6085, Application US/09877478  
;; Publication No. US2003068301A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
;; APPLICANT: Draper, Kenneth  
;; APPLICANT: Blatt, Larry  
;; APPLICANT: McSwiggen, Jim  
;; APPLICANT: Morrissey, Dave  
;; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication  
;; FILE REFERENCE: MHB00-845-H (400/829)  
;; CURRENT APPLICATION NUMBER: US/09/877,478  
;; CURRENT FILING DATE: 2001-12-31  
;; PRIOR APPLICATION NUMBER: US 07/882,712  
;; PRIOR FILING DATE: 1992-05-14  
;; PRIOR APPLICATION NUMBER: US 09/531,025  
;; PRIOR FILING DATE: 2000-03-20  
;; PRIOR APPLICATION NUMBER: US 09/636,385  
;; PRIOR FILING DATE: 2000-08-09  
;; PRIOR APPLICATION NUMBER: US 09/696,347  
;; PRIOR FILING DATE: 2000-10-24  
;; PRIOR APPLICATION NUMBER: US 08/193,627  
;; PRIOR FILING DATE: 1994-02-07  
;; PRIOR APPLICATION NUMBER: US 08/433,993  
;; PRIOR FILING DATE: 1995-05-04  
;; PRIOR APPLICATION NUMBER: US 08/434,504  
;; PRIOR FILING DATE: 1995-05-04  
;; PRIOR APPLICATION NUMBER: US 09/436,430  
;; PRIOR FILING DATE: 1999-11-08  
;; NUMBER OF SEQ ID NOS: 6586  
;; SOFTWARE: PatentIn version 3.0  
;; SEQ ID NO 6085  
;; LENGTH: 15  
;; TYPE: RNA  
;; ORGANISM: Hepatitis B virus  
US-09-877-478-6085

Query Match 1.2%; Score 12.4; DB 1; Length 15;  
Best Local Similarity 92.9%; Pred. No. 1.3e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2095 AATGACAAATGGC 2108  
DB 14 ACTGAACAATGGC 1

RESULT 205  
US-10-342-902-6011/c  
;; Sequence 6011, Application US/10342902  
;; Publication No. US20040054156A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Sirna Therapeutics, Inc.  
;; APPLICANT: Draper, Kenneth  
;; APPLICANT: Blatt, Larry  
;; APPLICANT: McSwiggen, Jim  
;; APPLICANT: Morrissey, Dave  
;; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication  
;; FILE REFERENCE: 400/075 (MHB00-845-1)  
;; CURRENT APPLICATION NUMBER: US/10/342,902  
;; CURRENT FILING DATE: 2003-01-15  
;; PRIOR APPLICATION NUMBER: US 09/877,478  
;; PRIOR FILING DATE: 2001-06-08  
;; PRIOR APPLICATION NUMBER: US 09/531,025  
;; PRIOR FILING DATE: 2000-03-20  
;; PRIOR APPLICATION NUMBER: US 09/636,385  
;; PRIOR FILING DATE: 2000-08-09  
;; PRIOR APPLICATION NUMBER: US 09/696,347  
;; PRIOR FILING DATE: 2000-10-24  
;; PRIOR APPLICATION NUMBER: US 08/193,627  
;; PRIOR FILING DATE: 1994-02-07  
;; PRIOR APPLICATION NUMBER: US 07/882,712  
;; PRIOR FILING DATE: 1992-05-14  
;; PRIOR APPLICATION NUMBER: US 09/436,430  
;; PRIOR FILING DATE: 1999-11-08  
;; NUMBER OF SEQ ID NOS: 6592  
;; SOFTWARE: PatentIn version 3.2  
;; SEQ ID NO 6011  
;; LENGTH: 15  
;; TYPE: RNA  
;; ORGANISM: Hepatitis B virus  
US-10-342-902-6011

Query Match 1.2%; Score 12.4; DB 1; Length 15;  
Best Local Similarity 92.9%; Pred. No. 1.3e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2095 AATGACAAATGGC 2108  
DB 15 ACTGAACAATGGC 2

RESULT 206  
US-10-342-902-6085/c  
;; Sequence 6085, Application US/10342902  
;; Publication No. US20040054156A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Sirna Therapeutics, Inc.  
;; APPLICANT: Draper, Kenneth  
;; APPLICANT: Blatt, Larry  
;; APPLICANT: McSwiggen, Jim  
;; APPLICANT: Morrissey, Dave  
;; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication  
;; FILE REFERENCE: 400/075 (MHB00-845-1)  
;; CURRENT APPLICATION NUMBER: US/10/342,902  
;; CURRENT FILING DATE: 2003-01-15  
;; PRIOR APPLICATION NUMBER: US 09/877,478  
;; PRIOR FILING DATE: 2001-06-08  
;; PRIOR APPLICATION NUMBER: US 09/531,025  
;; PRIOR FILING DATE: 2000-03-20  
;; PRIOR APPLICATION NUMBER: US 09/636,385  
;; PRIOR FILING DATE: 2000-08-09  
;; PRIOR APPLICATION NUMBER: US 09/696,347  
;; PRIOR FILING DATE: 2000-10-24  
;; PRIOR APPLICATION NUMBER: US 08/193,627  
;; PRIOR FILING DATE: 1994-02-07  
;; PRIOR APPLICATION NUMBER: US 07/882,712  
;; PRIOR FILING DATE: 1992-05-14  
;; PRIOR APPLICATION NUMBER: US 09/436,430



;; PRIOR FILING DATE: 1999-11-08  
;; NUMBER OF SEQ ID NOS: 6592  
;; SOFTWARE: PatentIn version 3.2  
;; SEQ ID NO 6085  
;; LENGTH: 15  
;; TYPE: RNA  
;; ORGANISM: Hepatitis B virus  
US-10-342-902-6085

Query Match 1.2%; Score 12.4; DB 1; Length 15;  
Best Local Similarity 92.9%; Pred. No. 1.3e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2095 AATGACAAATGGC 2108  
DB 14 ACTGACAAATGGC 1

## RESULT 207

US-10-287-919-1563/c  
;; Sequence 1563, Application US/10287919  
;; Publication No. US20030085830A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.  
;; TITLE OF INVENTION: Methanococcus jannaschii complete genome.  
;; FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333  
;; CURRENT APPLICATION NUMBER: US/10/287,919  
;; CURRENT FILING DATE: 2002-11-05  
;; NUMBER OF SEQ ID NOS: 2706  
;; SOFTWARE: Proprietary  
;; SEQ ID NO 1563  
;; LENGTH: 15  
;; TYPE: DNA  
;; ORGANISM: Methanococcus jannaschii complete genome.  
;; FEATURE:  
;; LOCATION: (868160)...(868174)  
;; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 1981

Query Match 1.2%; Score 12.4; DB 1; Length 15;  
Best Local Similarity 92.9%; Pred. No. 1.3e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1867 TTTATTTTGTGTTT 1880  
DB 14 TTTATTTTGTGTTAT 1

## RESULT 208

US-10-287-919-2317  
;; Sequence 2317, Application US/10287919  
;; Publication No. US20030085830A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.  
;; TITLE OF INVENTION: Methanococcus jannaschii complete genome.  
;; FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333  
;; CURRENT APPLICATION NUMBER: US/10/287,919  
;; CURRENT FILING DATE: 2002-11-05  
;; NUMBER OF SEQ ID NOS: 2706  
;; SOFTWARE: Proprietary  
;; SEQ ID NO 2317  
;; LENGTH: 15  
;; TYPE: DNA  
;; ORGANISM: Methanococcus jannaschii complete genome.  
;; FEATURE:  
;; LOCATION: (1438072)...(1438086)  
;; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 2967

Query Match 1.2%; Score 12.4; DB 1; Length 15;  
Best Local Similarity 92.9%; Pred. No. 1.3e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1966 ATGATACTTATAT 1979  
DB 1 ATGAAACTTATAT 14

## RESULT 209

US-10-287-919-2441/c  
;; Sequence 2441, Application US/10287919  
;; Publication No. US20030085830A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.  
;; TITLE OF INVENTION: Methanococcus jannaschii complete genome.  
;; FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333  
;; CURRENT APPLICATION NUMBER: US/10/287,919  
;; CURRENT FILING DATE: 2002-11-05  
;; NUMBER OF SEQ ID NOS: 2706  
;; SOFTWARE: Proprietary  
;; SEQ ID NO 2441  
;; LENGTH: 15  
;; TYPE: DNA  
;; ORGANISM: Methanococcus jannaschii complete genome.  
;; FEATURE:  
;; LOCATION: (1512879)...(1512893)  
;; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 3130

US-10-287-919-2441  
Query Match 1.2%; Score 12.4; DB 1; Length 15;  
Best Local Similarity 92.9%; Pred. No. 1.3e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1867 TTTATTTTGTGTTT 1880  
DB 14 TTTATTTTGTGTTAT 1

## RESULT 210

US-10-091-281-81/c  
;; Sequence 81, Application US/10091281  
;; Publication No. US20030490617A1  
;; GENERAL INFORMATION:  
;; APPLICANT: RAYMOND, VINCENT  
;; APPLICANT: ST. ERWIN  
;; APPLICANT: MORISSETTE, JEAN  
;; TITLE OF INVENTION: OPTINEURIN NUCLEIC ACID MOLECULES AND USES THEREOF  
;; FILE REFERENCE: 13587.338  
;; CURRENT APPLICATION NUMBER: US/10/091,281  
;; CURRENT FILING DATE: 2002-03-06  
;; NUMBER OF SEQ ID NOS: 463  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 81  
;; LENGTH: 15  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
;; FEATURE:  
;; OTHER INFORMATION: Putative OCTB/TST1.01 motif

US-10-091-281-81  
Query Match 1.2%; Score 12.4; DB 1; Length 15;  
Best Local Similarity 92.9%; Pred. No. 1.3e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1535 AAGTGAATTGAGA 1548  
DB 14 AAGTGAATTGAAA 1

## RESULT 211

US-10-271-602B-184  
;; Sequence 184, Application US/10271602B  
;; Publication No. US20040002073A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Alice Xiang Li  
;; APPLICANT: Ghazala Hashmi

```
APPLICANT: Michael Seul
; TITLE OF INVENTION: MULTIPLEXED ANALYSIS OF POLYMORPHIC LOCI
; FILE REFERENCE: eWAP-US
; CURRENT APPLICATION NUMBER: US/10/271,602B
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/329,427
; PRIOR FILING DATE: 2001-10-14
; PRIOR APPLICATION NUMBER: 60/329,620
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 60/329,428
; PRIOR FILING DATE: 2001-10-14
; PRIOR APPLICATION NUMBER: 60/329,619
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 60/364,416
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 184
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe sequence derived from human genomic sequence
US-10-271-602B-184

Query Match      1.2%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 1.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1581 GTAGCCCCAGTGAC 1594
DB 2 GTAGCCCCAGTGAC 15

RESULT 212
US-10-271-602B-192
; Sequence 192, Application US/10271602B
; Publication No. US20040002073A1
; GENERAL INFORMATION:
; APPLICANT: Alice Xiang Li
; APPLICANT: Ghazala Hashmi
; APPLICANT: Michael Seul
; TITLE OF INVENTION: MULTIPLEXED ANALYSIS OF POLYMORPHIC LOCI
; FILE REFERENCE: eWAP-US
; CURRENT APPLICATION NUMBER: US/10/271,602B
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/329,427
; PRIOR FILING DATE: 2001-10-14
; PRIOR APPLICATION NUMBER: 60/329,620
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 60/329,428
; PRIOR FILING DATE: 2001-10-14
; PRIOR APPLICATION NUMBER: 60/329,619
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 60/364,416
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 192
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe sequence derived from human genomic sequence
US-10-271-602B-192

Query Match      1.2%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 1.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1581 GTAGCCCCAGTGAC 1594
DB 2 GTAGCCCCAGTGAC 15
```

```
APPLICANT: Michael Seul
; TITLE OF INVENTION: MULTIPLEXED ANALYSIS OF POLYMORPHIC LOCI
; FILE REFERENCE: eWAP-US
; CURRENT APPLICATION NUMBER: US/10/271,602B
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/329,427
; PRIOR FILING DATE: 2001-10-14
; PRIOR APPLICATION NUMBER: 60/329,620
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 60/329,428
; PRIOR FILING DATE: 2001-10-14
; PRIOR APPLICATION NUMBER: 60/329,619
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 60/364,416
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 200
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe sequence derived from human genomic sequence
US-10-271-602B-200

Query Match      1.2%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 1.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1581 GTAGCCCCAGTGAC 1594
DB 2 GTAGCCCCAGTGAC 15

RESULT 214
US-10-271-602B-207
; Sequence 207, Application US/10271602B
; Publication No. US20040002073A1
; GENERAL INFORMATION:
; APPLICANT: Alice Xiang Li
; APPLICANT: Ghazala Hashmi
; APPLICANT: Michael Seul
; TITLE OF INVENTION: MULTIPLEXED ANALYSIS OF POLYMORPHIC LOCI
; FILE REFERENCE: eWAP-US
; CURRENT APPLICATION NUMBER: US/10/271,602B
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/329,427
; PRIOR FILING DATE: 2001-10-14
; PRIOR APPLICATION NUMBER: 60/329,620
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 60/329,428
; PRIOR FILING DATE: 2001-10-14
; PRIOR APPLICATION NUMBER: 60/329,619
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 60/364,416
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 207
; LENGTH: 15
```

TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Probe sequence derived from human genomic sequence  
US-10-271-602B-207

Query Match 1.1%; Score 12.4; DB 1; Length 15;  
Best Local Similarity 92.9%; Pred. No. 1.3e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1580 TGTAGCCCCAGTGA 1593  
DB 1 TGTACCCCCAGTGA 14

RESULT 215  
US-09-735-363A-13  
Sequence 13, Application US/09735363A  
Patent No. US20010041681A1

GENERAL INFORMATION:  
APPLICANT: Fillon, Mario  
APPLICANT: Phillip, Nigel  
TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides  
FILE REFERENCE: 02811-0181  
CURRENT APPLICATION NUMBER: US/09/735,363A  
CURRENT FILING DATE: 2000-12-12  
PRIOR APPLICATION NUMBER: 60/170,325  
PRIOR FILING DATE: 1999-12-13  
PRIOR APPLICATION NUMBER: 60/228,925  
PRIOR FILING DATE: 2000-08-29  
NUMBER OF SEQ ID NOS: 87  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 13  
LENGTH: 12  
TYPE: DNA

ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic Oligonucleotide  
US-09-735-363A-13

Query Match 1.1%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTG 1804  
DB 1 TGTGTGTGTGTG 12

RESULT 216  
US-09-735-363A-14  
Sequence 14, Application US/09735363A  
Patent No. US20010041681A1

GENERAL INFORMATION:  
APPLICANT: Fillon, Mario  
APPLICANT: Phillip, Nigel  
TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides  
FILE REFERENCE: 02811-0181  
CURRENT APPLICATION NUMBER: US/09/735,363A  
CURRENT FILING DATE: 2000-12-12  
PRIOR APPLICATION NUMBER: 60/170,325  
PRIOR FILING DATE: 1999-12-13  
PRIOR APPLICATION NUMBER: 60/228,925  
PRIOR FILING DATE: 2000-08-29  
NUMBER OF SEQ ID NOS: 87  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 14  
LENGTH: 12  
TYPE: DNA

ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic Oligonucleotide  
US-09-735-363A-14

Query Match 1.1%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTG 1805  
DB 1 GTGTGTGTGTG 12

RESULT 217  
US-09-263-959-649  
Sequence 649, Application US/09263959  
Patent No. US20020150891A1

GENERAL INFORMATION:  
APPLICANT: Hood, Leroy E.  
APPLICANT: Koop, Ben F.  
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI  
NUMBER OF SEQUENCES: 1279  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/263,959  
FILING DATE: 05-MAR-1999  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: McMasters, David D.  
REGISTRATION NUMBER: 33,963  
REFERENCE/DOCKET NUMBER: 920010.426C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 649:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

US-09-263-959-649

Query Match 1.1%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1814 ATATATATATAT 1825  
DB 1 ATATATATATAT 12

RESULT 218  
US-09-263-959-649/c  
Sequence 649, Application US/09263959  
Patent No. US20020150891A1

GENERAL INFORMATION:  
APPLICANT: Hood, Leroy E.  
APPLICANT: Koop, Ben F.  
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI  
NUMBER OF SEQUENCES: 1279  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue

City: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/263,959  
FILING DATE: 05-MAR-1999  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: McMasters, David D.  
REGISTRATION NUMBER: 33,963  
REFERENCE/DOCKET NUMBER: 920010.426C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 649:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-263-959-649

Query Match 1.1%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1814 ATATATATATAT 1825  
DB 12 ATATATATATAT 1

RESULT 219  
US-09-263-959-768  
Sequence 768, Application US/09263959  
Patent No. US20020150891A1  
GENERAL INFORMATION:  
APPLICANT: Hood, Leroy E.  
APPLICANT: Koop, Ben F.  
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI  
NUMBER OF SEQUENCES: 1279  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/263,959  
FILING DATE: 05-MAR-1999  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: McMasters, David D.  
REGISTRATION NUMBER: 33,963  
REFERENCE/DOCKET NUMBER: 920010.426C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 768:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 base pairs

TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-263-959-768

Query Match 1.1%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1814 ATATATATATAT 1825  
DB 12 ATATATATATAT 1

RESULT 220  
US-09-263-959-768/c  
Sequence 768, Application US/09263959  
Patent No. US20020150891A1  
GENERAL INFORMATION:  
APPLICANT: Hood, Leroy E.  
APPLICANT: Koop, Ben F.  
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI  
NUMBER OF SEQUENCES: 1279  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/263,959  
FILING DATE: 05-MAR-1999  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: McMasters, David D.  
REGISTRATION NUMBER: 33,963  
REFERENCE/DOCKET NUMBER: 920010.426C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 768:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-263-959-768

Query Match 1.1%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1814 ATATATATATAT 1825  
DB 12 ATATATATATAT 1

RESULT 221  
US-09-263-959-832/c  
Sequence 832, Application US/09263959  
Patent No. US20020150891A1  
GENERAL INFORMATION:  
APPLICANT: Hood, Leroy E.  
APPLICANT: Koop, Ben F.  
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI

NUMBER OF SEQUENCES: 1279  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/263,959  
FILING DATE: 05-MAR-1999  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: McMasters, David D.  
REGISTRATION NUMBER: 33,963  
REFERENCE/DOCKET NUMBER: 920010.426C2  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 832:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-263-959-832  
Query Match 1.1%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1793 TGTGTGTGTGTG 1804  
Db 12 TGTGTGTGTGTG 1  
RESULT 222  
US-09-263-959-838/c  
Sequence 838, Application US/09263959  
Patent No. US20020150891A1  
GENERAL INFORMATION:  
APPLICANT: Hood, Leroy E.  
APPLICANT: Koop, Ben F.  
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI  
NUMBER OF SEQUENCES: 1279  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/263,959  
FILING DATE: 05-MAR-1999  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: McMasters, David D.  
REGISTRATION NUMBER: 33,963  
REFERENCE/DOCKET NUMBER: 920010.426C2  
TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 838:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-263-959-838  
Query Match 1.1%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1793 TGTGTGTGTGTG 1804  
Db 12 TGTGTGTGTGTG 1  
RESULT 223  
US-09-263-959-972/c  
Sequence 972, Application US/09263959  
Patent No. US20020150891A1  
GENERAL INFORMATION:  
APPLICANT: Hood, Leroy E.  
APPLICANT: Koop, Ben F.  
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI  
NUMBER OF SEQUENCES: 1279  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/263,959  
FILING DATE: 05-MAR-1999  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: McMasters, David D.  
REGISTRATION NUMBER: 33,963  
REFERENCE/DOCKET NUMBER: 920010.426C2  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 972:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-263-959-972  
Query Match 1.1%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1793 TGTGTGTGTGTG 1804  
Db 12 TGTGTGTGTGTG 1  
RESULT 224  
US-09-263-959-975/c  
Sequence 975, Application US/09263959  
Patent No. US20020150891A1  
GENERAL INFORMATION:

APPLICANT: Hood, Leroy E.  
APPLICANT: Rowen, Lee  
APPLICANT: Koop, Ben F.  
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI  
NUMBER OF SEQUENCES: 1279  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/263,959  
FILING DATE: 05-MAR-1999  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: McMasters, David D.  
REGISTRATION NUMBER: 33,963  
REFERENCE/DOCKET NUMBER: 920010.426C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 975:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-263-959-975

Query Match 1.1%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTG 1804  
|||||  
Db 12 TGTGTGTGTGTG 1

RESULT 225  
US-09-263-959-981/c  
Sequence 981, Application US/09263959  
Patent No. US20020150891A1  
GENERAL INFORMATION:  
APPLICANT: Hood, Leroy E.  
APPLICANT: Koop, Ben F.  
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI  
NUMBER OF SEQUENCES: 1279  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/263,959  
FILING DATE: 05-MAR-1999  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: McMasters, David D.

REGISTRATION NUMBER: 33,963  
REFERENCE/DOCKET NUMBER: 920010.426C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 981:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-263-959-981

Query Match 1.1%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTG 1804  
|||||  
Db 12 TGTGTGTGTGTG 1

RESULT 226  
US-09-841-157A-11  
Sequence 11, Application US/09841157A  
Publication No. US20020192648A1  
GENERAL INFORMATION:  
APPLICANT: NISHIGAKI, KOICHI  
APPLICANT: TAKASAWA, TSUTOMU  
APPLICANT: HAWANO, KEIICHI  
TITLE OF INVENTION: METHODS OF IDENTIFYING AN ORGANISM BASED ON ITS GENOTYPE  
FILE REFERENCE: 12637/P66602USO  
CURRENT APPLICATION NUMBER: US/09/841,157A  
CURRENT FILING DATE: 2001-04-25  
NUMBER OF SEQ ID NOS: 44  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 11  
LENGTH: 12  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Primer  
US-09-841-157A-11

Query Match 1.1%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1814 ATATATATATAT 1825  
|||||  
Db 1 ATATATATATAT 12

RESULT 227  
US-09-841-157A-11/c  
Sequence 11, Application US/09841157A  
Publication No. US20020192648A1  
GENERAL INFORMATION:  
APPLICANT: NISHIGAKI, KOICHI  
APPLICANT: TAKASAWA, TSUTOMU  
APPLICANT: HAWANO, KEIICHI  
TITLE OF INVENTION: METHODS OF IDENTIFYING AN ORGANISM BASED ON ITS GENOTYPE  
FILE REFERENCE: 12637/P66602USO  
CURRENT APPLICATION NUMBER: US/09/841,157A  
CURRENT FILING DATE: 2001-04-25  
NUMBER OF SEQ ID NOS: 44  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 11  
LENGTH: 12  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Primer

US-09-841-157A-11

Query Match 1.1%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1814 ATATATATATAT 1825

Db 12 ATATATATATAT 1

RESULT 228

US-10-077-275A-1

; Sequence 1, Application US/10077275A

; Publication No. US20030032028A1

; GENERAL INFORMATION:

; APPLICANT: Dace, Gayle

; APPLICANT: Kimmerly, William

; APPLICANT: Goff, Stephen

; APPLICANT: Oeller, Paul

; TITLE OF INVENTION: In vitro capture of nucleic acids via modified oligonucleotides

; TITLE OF INVENTION: magnetic beads.

; FILE REFERENCE: TM0076-CIP

; CURRENT APPLICATION NUMBER: US/10/077,275A

; CURRENT FILING DATE: 2002-02-15

; PRIOR APPLICATION NUMBER: US 09/879,279

; PRIOR FILING DATE: 2001-06-12

; NUMBER OF SEQ ID NOS: 1

; SEQ ID NO 1

; LENGTH: 12

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: LNA Homopolymer

US-10-077-275A-1

Query Match 1.1%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGT 1805

Db 1 GTGTGTGTGTGT 12

RESULT 229

US-10-331-780-2/c

; Sequence 2, Application US/10331780

; Publication No. US20030162210A1

; GENERAL INFORMATION:

; APPLICANT: Chetverin, Alexander B.

; APPLICANT: Kramer, Fred Russel

; TITLE OF INVENTION: NOVEL OLIGONUCLEOTIDE ARRAYS AND THEIR USE FOR SORTING,

; TITLE OF INVENTION: ISOLATING, SEQUENCING, AND MANIPULATING NUCLEIC ACIDS

; FILE REFERENCE: 07763-004002

; CURRENT APPLICATION NUMBER: US/10/331,780

; CURRENT FILING DATE: 2002-12-31

; PRIOR APPLICATION NUMBER: US/08/473,010

; PRIOR FILING DATE: 1995-06-07

; PRIOR APPLICATION NUMBER: US 08/247,530

; PRIOR FILING DATE: 1994-05-25

; PRIOR APPLICATION NUMBER: US 07/833,607

; PRIOR FILING DATE: 1992-02-19

; NUMBER OF SEQ ID NOS: 19

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 2

; LENGTH: 12

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthetically derived DNA

US-10-331-780-2

Query Match 1.1%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGT 1805

Db 12 GTGTGTGTGTGT 1

RESULT 230

US-09-877-478-6010/c

; Sequence 6010, Application US/09877478

; Publication No. US20030068301A1

; GENERAL INFORMATION:

; APPLICANT: Ribozyme Pharmaceuticals, Inc.

; APPLICANT: Draper, Kenneth

; APPLICANT: Blatt, Larry

; APPLICANT: McSwiggen, Jim

; APPLICANT: Morrissey, Dave

; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication

; FILE REFERENCE: MBH00-845-H (400/029)

; CURRENT APPLICATION NUMBER: US/09/877,478

; CURRENT FILING DATE: 2001-12-31

; PRIOR APPLICATION NUMBER: US 07/882,712

; PRIOR FILING DATE: 1992-05-14

; PRIOR APPLICATION NUMBER: US 09/531,025

; PRIOR FILING DATE: 2000-03-20

; PRIOR APPLICATION NUMBER: US 09/636,385

; PRIOR FILING DATE: 2000-08-09

; PRIOR APPLICATION NUMBER: US 09/696,347

; PRIOR FILING DATE: 2000-10-24

; PRIOR APPLICATION NUMBER: US 08/193,627

; PRIOR FILING DATE: 1994-02-07

; PRIOR APPLICATION NUMBER: US 08/433,993

; PRIOR FILING DATE: 1995-05-04

; PRIOR APPLICATION NUMBER: US 08/434,504

; PRIOR FILING DATE: 1995-05-04

; PRIOR APPLICATION NUMBER: US 09/436,430

; PRIOR FILING DATE: 1999-11-08

; NUMBER OF SEQ ID NOS: 6586

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 6010

; LENGTH: 15

; TYPE: RNA

; ORGANISM: Hepatitis B virus

US-09-877-478-6010

Query Match 1.1%; Score 12; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2097 TGAACAAATGTC 2108

Db 14 TGAACAAATGTC 3

RESULT 231

US-09-848-754A-9167/c

; Sequence 9167, Application US/09848754A

; Publication No. US20030073207A1

; GENERAL INFORMATION:

; APPLICANT: Ribozyme Pharmaceuticals, Inc.

; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related

; TITLE OF INVENTION: Levels of Epidermal Growth Factor Receptors

; FILE REFERENCE: MBH00-958-1 (400/018)

; CURRENT APPLICATION NUMBER: US/09/848,754A

; CURRENT FILING DATE: 2001-05-03

; NUMBER OF SEQ ID NOS: 9645

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 9167

; LENGTH: 15

; TYPE: RNA

; ORGANISM: Artificial Sequence

FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic acid  
US-09-848-754A-9167

Query Match 1.1%; Score 12; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2059 TGATTCTAGGT 2070  
Db 15 TGATTCTAGGT 4

RESULT 232  
US-10-342-902-6010/c  
Sequence 6010, Application US/10342902  
Publication No. US20040054156A1  
GENERAL INFORMATION:  
APPLICANT: Sirna Therapeutics, Inc.  
APPLICANT: Draper, Kenneth  
APPLICANT: Blatt, Larry  
APPLICANT: McSwiggen, Jim  
APPLICANT: Morrissey, Dave  
TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication  
FILE REFERENCE: 400/075 (MBH00-845-1)  
CURRENT APPLICATION NUMBER: US/10/342,902  
CURRENT FILING DATE: 2003-01-15  
PRIORITY APPLICATION NUMBER: US 09/877,478  
PRIORITY FILING DATE: 2001-06-08  
PRIORITY APPLICATION NUMBER: US 09/531,025  
PRIORITY FILING DATE: 2000-03-20  
PRIORITY APPLICATION NUMBER: US 09/636,385  
PRIORITY FILING DATE: 2000-08-09  
PRIORITY APPLICATION NUMBER: US 09/696,347  
PRIORITY FILING DATE: 2000-10-24  
PRIORITY APPLICATION NUMBER: US 08/193,627  
PRIORITY FILING DATE: 1994-02-07  
PRIORITY APPLICATION NUMBER: US 07/882,712  
PRIORITY FILING DATE: 1992-05-14  
PRIORITY APPLICATION NUMBER: US 09/436,430  
PRIORITY FILING DATE: 1999-11-08  
NUMBER OF SEQ ID NOS: 6592  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 6010  
LENGTH: 15  
TYPE: RNA  
ORGANISM: Hepatitis B virus  
US-10-342-902-6010

Query Match 1.1%; Score 12; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2097 TGAACAAATGCC 2108  
Db 14 TGAACAAATGCC 3

RESULT 233  
US-10-056-414-120/c  
Sequence 120, Application US/10056414  
Publication No. US20030003469A1  
GENERAL INFORMATION:  
APPLICANT: Stinchcomb, Dan T.  
APPLICANT: Draper, Kenneth G.  
APPLICANT: McSwiggen, James  
TITLE OF INVENTION: RIBOZYME TREATMENT OF DISEASES OR CONDITIONS RELATED TO LEVELS OF NF-KB  
NUMBER OF SEQUENCES: 830  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon

STREET: 633 West Fifth Street  
Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/056,414  
FILING DATE: 23-Jan-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/291,932A  
FILING DATE: August 15, 1994  
APPLICATION NUMBER: 08/245,466  
FILING DATE: May 18, 1994  
APPLICATION NUMBER: 07/987,132  
FILING DATE: December 7, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 208/157  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 120:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 120:  
US-10-056-414-120

Query Match 1.1%; Score 12; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2153 CACCTGGAGCA 2164  
Db 15 CACCTGGAGCA 4

RESULT 234  
US-10-056-414-193/c  
Sequence 193, Application US/10056414  
Publication No. US20030003469A1  
GENERAL INFORMATION:  
APPLICANT: Stinchcomb, Dan T.  
APPLICANT: Draper, Kenneth G.  
APPLICANT: McSwiggen, James  
TITLE OF INVENTION: RIBOZYME TREATMENT OF DISEASES OR CONDITIONS RELATED TO LEVELS OF NF-KB  
NUMBER OF SEQUENCES: 830  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
storage



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;
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/056,414
; FILING DATE: 23-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/291,932A
; FILING DATE: August 15, 1994
; APPLICATION NUMBER: 08/245,466
; FILING DATE: May 18, 1994
; APPLICATION NUMBER: 07/987,132
; FILING DATE: December 7, 1992
; CLASSIFICATION: <Unknown>
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 193:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 193:
US-10-056-414-193

Query Match 1.1%; Score 12; DB 1; Length 15;
Best Local Similarity 100.0%; Pred.No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2153 CACCTGGAAGCA 2164
Db 15 CACCTGGAAGCA 4

RESULT 235
US-10-056-414-309/c
; Sequence 309, Application US/10056414
; Publication No. US20030003469A1
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; Draper, Kenneth G.
; MCSwiggan, James
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; DISEASES OR CONDITIONS
; RELATED TO LEVELS OF
; NF-KB
; NUMBER OF SEQUENCES: 830
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/056,414
; FILING DATE: 23-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/291,932A
```

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;
; FILING DATE: August 15, 1994
; APPLICATION NUMBER: 08/245,466
; FILING DATE: May 18, 1994
; APPLICATION NUMBER: 07/987,132
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 309:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 309:
US-10-056-414-309

Query Match 1.1%; Score 12; DB 1; Length 15;
Best Local Similarity 100.0%; Pred.No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2153 CACCTGGAAGCA 2164
Db 15 CACCTGGAAGCA 4

RESULT 236
US-10-287-919-590/c
; Sequence 590, Application US/10287919
; Publication No. US20030085830A1
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Methanococcus jannaschii complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/287,919
; CURRENT FILING DATE: 2002-11-05
; NUMBER OF SEQ ID NOS: 2706
; SOFTWARE: Proprietary
; SEQ ID NO 590
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Methanococcus jannaschii complete genome.
; FEATURE:
; LOCATION: (174470)...(174484)
; OTHER INFORMATION: Chromosome = 1 Strand = positive
US-10-287-919-590

Query Match 1.1%; Score 12; DB 1; Length 15;
Best Local Similarity 100.0%; Pred.No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1892 TATTTCAATGTT 1903
Db 14 TATTTCAATGTT 3

RESULT 237
US-10-287-919-2049/c
; Sequence 2049, Application US/10287919
; Publication No. US20030085830A1
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Methanococcus jannaschii complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/287,919
; CURRENT FILING DATE: 2002-11-05
; NUMBER OF SEQ ID NOS: 2706
; SOFTWARE: Proprietary
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SEQ ID NO 2049  
LENGTH: 15  
TYPE: DNA

ORGANISM: Methanococcus jannaschii complete genome.

FEATURE:

LOCATION: (1247186)...(1247200)

OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectionObjectNumber = 2622

US-10-287-919-2049

Query Match 1.1%; Score 12; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1892 TATTCAATGTT 1903

Db 14 TATTCAATGTT 3

RESULT 238

US-10-041-414-52/c

Sequence 52, Application US/10041414

Publication No. US20030087225A1

GENERAL INFORMATION:

APPLICANT: SHIVER, JOHN W.

DAVIES, MARY ELLEN

FREED, DANIEL C.

LIU, MARGARET A.

PERRY, HELEN C.

TITLE OF INVENTION: SYNTHETIC HIV ENV GENES

NUMBER OF SEQUENCES: 53

CORRESPONDENCE ADDRESS:

ADDRESSEE: J. MARK HAND - MERCK & CO., INC.

STREET: 126 E. LINCOLN AVE., - P.O. BOX 2000

CITY: RAHWAY

STATE: NEW JERSEY

COUNTRY: US

ZIP: 07065-0907

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/041,414

FILING DATE: 08-May-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/802,368

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: HAND, J. MARK

REGISTRATION NUMBER: 36,545

REFERENCE/DOCKET NUMBER: 19643

TELECOMMUNICATION INFORMATION:

TELEPHONE: 732-594-3905

TELEFAX: 732-594-4720

INFORMATION FOR SEQ ID NO: 52:

SEQUENCE CHARACTERISTICS:

LENGTH: 15 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "oligonucleotide"

SEQUENCE DESCRIPTION: SEQ ID NO: 52:

US-10-041-414-52

Query Match

Best Local Similarity 1.1%; Score 12; DB 1; Length 15;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1521 ATGCCTGCTATT 1532

|||||

Db

13 ATGCCTGCTATT 2

RESULT 239

US-10-369-121-51/c

Sequence 51, Application US/10369121

Publication No. US20030229214A1

GENERAL INFORMATION:

APPLICANT: SHIVER, JOHN W.

LIU, MARGARET A.

PERRY, HELEN C.

DAVIES, MARY ELLEN

FREED, DANIEL C.

TITLE OF INVENTION: VACCINES COMPRISING SYNTHETIC GENES

NUMBER OF SEQUENCES: 53

CORRESPONDENCE ADDRESS:

ADDRESSEE: J. MARK HAND - MERCK & CO., INC.

STREET: 126 E. LINCOLN AVE., P.O. BOX 2000

CITY: RAHWAY

STATE: NEW JERSEY

COUNTRY: US

ZIP: 07065-0907

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/369,121

FILING DATE: 17-Feb-2003

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/340,798A

FILING DATE: 28-Jun-1999

APPLICATION NUMBER: US/08/877,418

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: HAND, J. MARK

REGISTRATION NUMBER: 36,545

REFERENCE/DOCKET NUMBER: 19729Y

TELECOMMUNICATION INFORMATION:

TELEPHONE: 908-594-3905

TELEFAX: 908-594-4720

INFORMATION FOR SEQ ID NO: 51:

SEQUENCE CHARACTERISTICS:

LENGTH: 15 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "oligonucleotide"

SEQUENCE DESCRIPTION: SEQ ID NO: 51:

US-10-369-121-51

Query Match

Best Local Similarity 1.1%; Score 12; DB 1; Length 15;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1521 ATGCCTGCTATT 1532

|||||

Db 13 ATGCCTGCTATT 2

Search completed: April 2, 2004, 14:38:06

Job time: 4 secs